

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
22 August 2002 (22.08.2002)

PCT

(10) International Publication Number  
WO 02/064766 A2

- (51) International Patent Classification: C12N 15/00
- (21) International Application Number: PCT/EP01/15398
- (22) International Filing Date:  
21 December 2001 (21.12.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
00870318.3 22 December 2000 (22.12.2000) EP  
01870002.1 4 January 2001 (04.01.2001) EP  
01870003.0 9 January 2001 (09.01.2001) EP
- (71) Applicant *for all designated States except US*:  
JANSSEN PHARMACEUTICA N.V. [RIVBE]; Tim-  
houtseweg 30, B-2340 Reerse (BE).
- (72) Inventors; and
- (75) Inventors/Applicants *for US only*: CONTRERAS,  
Roland, Henri [BE/BE]; Molensstraat 55, B-9820  
Scheldene (BE); EBERHARDT, Ines [DE/DE];  
Paulatenstraat 32, B-9530 Zedelgem (BE); LUYTEN,  
Walter, Herman, Maria, Louis [BE/BE]; Janssen  
Pharmaceutica N.V., Timhoutseweg 30, B-2340 Reerse  
(BE); REEKMANS, Rieka, Josephina [BE/BE]; Wijn-  
bergstraat 190, B-8560 Wevelgem (BE).
- (74) Agents: DE CLERCQ, Ann et al.; De Clercq, Brants &  
Partners, D. Gevaertdreef 10 a, B-2830 Sint-Martens-Latem  
(BE).
- (81) Designated States (*national*): AE, AC, AI, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,  
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GR, GT, GU,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MY, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,  
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU,  
ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GU, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),  
European patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,  
GB, GR, IL, IT, LU, MC, NL, PT, SE, TR), OAPI patent  
(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,  
NE, SN, TD, TG).
- Published:  
— without international search report and to be republished  
upon receipt of that report
- For two letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.*



WO 02/064766 A2

(54) Title: RAX RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

**BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI****Field of the invention**

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

10

**Background to the invention**

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively  
15 expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with  
20 complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses,  
25 expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic,  
30 or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular  
35 target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X<sub>L</sub>) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Sato *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996).

Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear.

It is an aim of the present invention to provide new *bax* sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi.

It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.



### Summary of the invention

Since it has been discovered that the mammalian *bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *BAX* gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*.

Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida spp.* homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

### Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of

SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284,  
 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310,  
 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346,  
 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,  
 5 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418,  
 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454,  
 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490,  
 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526,  
 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562,  
 10 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588,  
 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624,  
 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,  
 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710,  
 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional  
 15 equivalent, derivative or bioprecursor of said protein,  
 (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70%  
 similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or  
 95% similar and most preferably more than 97% similar to any of the amino acid sequences  
 as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,  
 20 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,  
 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130,  
 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166,  
 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202,  
 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,  
 25 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274,  
 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300,  
 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326,  
 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372,  
 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408,  
 30 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444,  
 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480,  
 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516,  
 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552,  
 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578,  
 35 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,

- 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means

10 the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly  
15 employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Hype Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between  
20 two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more  
25 nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence  
30 of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,  
37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85,  
35 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, 687, 689, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729, 731, 733, 735, 737, 739, 741, 743, 745, 747, 749, 751, 753, 755, 757, 759, 761, 763, 765, 767, 769, 771, 773, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859, 861, 863, 865, 867, 869, 871, 873, 875, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 899, 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 965, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1015, 1017, 1019, 1021, 1023, 1025, 1027, 1029, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1069, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1135, 1137, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329, 1331, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1347, 1349, 1351, 1353, 1355, 1357, 1359, 1361, 1363, 1365, 1367, 1369, 1371, 1373, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413, 1415, 1417, 1419, 1421, 1423, 1425, 1427, 1429, 1431, 1433, 1435, 1437, 1439, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1455, 1457, 1459, 1461, 1463, 1465, 1467, 1469, 1471, 1473, 1475, 1477, 1479, 1481, 1483, 1485, 1487, 1489, 1491, 1493, 1495, 1497, 1499, 1501, 1503, 1505, 1507, 1509, 1511, 1513, 1515, 1517, 1519, 1521, 1523, 1525, 1527, 1529, 1531, 1533, 1535, 1537, 1539, 1541, 1543, 1545, 1547, 1549, 1551, 1553, 1555, 1557, 1559, 1561, 1563, 1565, 1567, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1587, 1589, 1591, 1593, 1595, 1597, 1599, 1601, 1603, 1605, 1607, 1609, 1611, 1613, 1615, 1617, 1619, 1621, 1623, 1625, 1627, 1629, 1631, 1633, 1635, 1

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOS 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,



815, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 681, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or  
10 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid  
15 sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than  
20 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
- (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and
- (g) the complement of any of the nucleic acids as specified in a) to f),

- 25 for the preparation of a medicament for treating diseases associated with yeast or fungi.

The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

- 30 The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

- 5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising  
10 to a human homologue of at least one yeast or candida nucleic acid described herein.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

- The present invention also advantageously provides nucleic acid molecules of at least  
15 approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the  
20 invention. The primers will specifically amplify any of the nucleic acid molecules of the invention. The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the  
25 sample.

- According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different  
30 probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

- Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50  
35 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as  $^{32}\text{P}$ ,  $^{33}\text{P}$  or  $^{35}\text{S}$ , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

- 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 682, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 580, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,



56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1988). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,  
 5 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,  
 10 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546,  
 20 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the  
 15 invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684 and 686.  
 25 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs  
 30 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,  
 35 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684 and 686.

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- 15 20 25 30

(d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- 5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;
- 10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or the human or mammal homologues thereof can also be used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian  
25 homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 389, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')<sub>2</sub> fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

- 10 According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector
- 15 comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said
- 20 compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound.

- Alternative methods for identifying compounds which selectively modulate expression or
- 30 functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

- Another alternative to the above described method comprises (a) contacting a compound to be
- 35 tested with a genetically modified yeast or fungus in which modification results in the

- overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.
- 15 The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.
- 25 The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.



The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive  $^3\text{H}$  can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which  
5 activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or  
10 all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene  
15 product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators  
20 upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the  
25 nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as  $\beta$ -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for  
30 compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In  
35 addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with  $^{15}\text{N}$  or  $^{13}\text{C}$  are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates

to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* model systems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp.,

*Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botrytis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

10 These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

According to yet another embodiment, the invention relates to a genetically modified yeast or  
15 fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or  
20 fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other  
25 mammals.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof,  
30 which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a  
5 human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable  
15 pharmaceutically acceptable carrier.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast  
20 *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic *bax* gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic BAX-gene for expression in *Candida* spp. selected from the group of:

- 25     a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,  
      b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,  
      c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,  
      d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90%  
30     or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and  
      e) a nucleic acid as defined in any one of (a) to (d) interrupted by intervening DNA sequences,

or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).

The synthetic *BAX* gene shows 73.7% identity with the gene coding for Bax- $\alpha$ . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic *BAX*, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic *BAX* gene and its fusion partner.

The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the invention is a *Candida* spp. cell.

In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death



According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic *BAX* gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic *BAX* gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death comprising the steps of:

- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,  
b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,  
20 c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- 25 a) providing a genetically modified organism as described above,  
b) expressing a cDNA library in said genetically modified organism, and,  
c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- 30 a) providing (a) genetically modified yeast or fungi as described above,  
b) treating said genetically modified yeast or fungi with a mutagen,  
c) isolating resistant yeast or fungal cells, and,  
d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

## FIGURE AND TABLE LEGENDS

**Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 386 and SEQ ID

5

**Figure 2.** *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

10

**YGL080W** (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

15

**YGR243W** (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

20

**YGR183C (QCR9)** (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 398bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

25

**YBR009C** (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

**Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into

30

8 grids, organised in 24 rows and 8 columns. The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

**Figure 4** Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

35

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean  $\pm$  SD, n=3). SD bars are obscured by symbols.

- 5 **Figure 5.** Scheme for the synthesis of the synthetic *BAX* gene using *C. albicans* optimal codons.
- Figure 6.** DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans BAX* gene.
- 10 **Figure 7.** Representation of the expression constructs of the synthetic *CaBAX* gene (A) and the *yEGFP-synth CaBAX* fusion (B).
- Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of *pGAL1P:synthCaBAX* and *pGAL1P:GFP-synthCaBAX* were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.
- 15 **Figure 9.** Growth kinetics of *GAL1P:synthCaBAX* (A) and *GAL1P:GFP-synthCaBAX* (B) on galactose containing minimal medium.
- Figure 10.** Immunoblot analysis of two independent transformants of *GAL1P:synthCaBAX* after 15 hours *Bax* induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the *Bax* protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal *Bax* antibody could be removed by the threathment with *S. cerevisiae* mannan.
- 20 **Figure 11.** Immunoblot analysis of the *GAL1P:GFP-synthCaBAX* strain on galactose containing minimal medium. The band appearing at 45kDa represents the *Gfp-Bax* fusion protein, while the band at 20kDa represents the *Gfp* protein alone.
- 25 **Figure 12.** FACS analysis of two independent *GAL1P:GFP-synthCaBAX* transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the *GFP-fluorescence* peak is not shaded.
- Figure 13.** Viability test *synthCaBAX* (A) and *GFP-synthCaBAX* transformants (B): Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.
- 30 **Table 1.** Oligonucleotides used for construction of the synthetic *CaBAXx* gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.
- 35

**Tables 2- 6.** Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qt values were calculated using the Pathways™ software (Research Genetics).

**Table 7.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qt values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

**Table 8.** Codon usage for the synthetic *BAX* gene.

**Table 9.** Regulation of 23 selected "Bax-specific" functions.

## EXAMPLES

### **Example 1. Differential gene expression analysis upon Bax-induced cell death**

#### **Materials and media**

- 5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schieff and Gietz, 1989) with YipUTyL or YipUTyLMuBax, after linearisation in the Ty  
10  $\delta$  element (Zhu, 1986).

#### **Cloning of mouse BAX cDNA**

- Mouse *bax* cDNA, encoding the mouse Bax- $\alpha$  protein, was cloned by Pfu DNA polymerase (Stratagene®, La Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18  
15 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and

5'-TCAGCCCATCTTCTCCAGATGGTGAG-3' (SEQ ID NO 690).

- The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).  
20

#### **Plasmid constructions**

- The 2 $\mu$  ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII GALI* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI FLP* terminator fragment was inserted into  
25 this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YipUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty  $\delta$  element in the *KpnI-AatII*-opened and blunted YipUT resulted in the plasmid YipUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-openend and blunted YipUTy resulted in the plasmid YipUTyL.

- Mouse *bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned  
30 into the *XbaI-HindIII*-opened plasmid YipUTyL, obtaining the final expression plasmid YipUTyLMuBax.

The plasmid YipUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

**GeneFilters**

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon  
5 membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8  
columns.

10 Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

**The Yeast ORF target**

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived  
15 from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop  
codons. These products were purified and resuspended at 50 nanograms per microliter in a  
20 colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

**Results****25 Induction of Bax-expression in yeast cells**

A preculture of yeast strain INVSc1 containing YlpUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promoter are integrated in the genome near Ty  $\delta$  elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YlpUTyL as a control. The precultures were diluted in 100-ml minimal glucose-  
30 containing medium and grown until an OD<sub>600</sub> of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

**RNA isolation**

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol.  $1.5 \cdot 10^8$  cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells  
5 were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150  $\mu$ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA  
10 pellet was resuspended in 50  $\mu$ l RNase free dH<sub>2</sub>O.

**First strand cDNA synthesis in the presence of  $\alpha$ -<sup>32</sup>P dCTP**

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of  $\alpha$ -<sup>32</sup>P dCTP as follows: 2  $\mu$ l (1  $\mu$ g/ml) of Oligo dT was added to 20  $\mu$ g of total RNA in a maximal  
15 volume of 8  $\mu$ l RNase-free dH<sub>2</sub>O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6  $\mu$ l 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)  
1  $\mu$ l 0,1 M DTT  
20 1  $\mu$ l RNase Block (40 units/ $\mu$ l) (Stratagene)  
1,5  $\mu$ l 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)  
1,5  $\mu$ l SuperScript™ Reverse Transcriptase (200 units/ $\mu$ l) (GIBCO-BRL)  
10  $\mu$ l  $\alpha$ -<sup>32</sup>P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala,  
25 Sweden),

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was  $5 \cdot 10^8$  opm/ $\mu$ g for both  
30 the INVSc1YlpUTyL and the INVSc1 YlpUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.



**Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection**

The Yeast GeneFilters™ were successively hybridised with the  $\alpha$ -<sup>32</sup>P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during  
5 hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5  $\mu$ l polydA (1  $\mu$ g/ml) and incubated for 24 hours at 42°C  
10 whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0.5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a  
15 PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50  $\mu$ m using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

**Example 2. Quantification of Hybridisation Signals**

20 Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time  
25 point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

**Example 3. Comparative gene expression analysis upon Bax-induced cell death and H<sub>2</sub>O<sub>2</sub>-induced cell death*****The oxidative H<sub>2</sub>O<sub>2</sub>-challenge***

A preculture of yeast strain INVSc1 containing YIpUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD<sub>600</sub> of 1 was reached. Subsequently, the yeast cells were  
35 transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H<sub>2</sub>O<sub>2</sub>, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

***First strand cDNA synthesis in the presence of  $\alpha$ -<sup>32</sup>P dCTP***

- 5 RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YlpUTyL yeast cells.  
The specific activity of all probes was  $5.10^8$  cpm/ $\mu$ g.

10

***Quantification of Hybridisation Signals***

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics,  
15 Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

***Identification of Bax-responsive genes***

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and  
20 INVSc1 YlpUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (*replacement*).

- 25 ***Identification of Bax-specific genes within the Bax-responsive pool***

- Pairwise comparisons of the normalised data obtained from INVSc1 YlpUTyLMuBax (B) and INVSc1 YlpUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background  
30 value. The normalised data of the Bax-responsive genes were compared with data obtained from the H<sub>2</sub>O<sub>2</sub>-stressed INVSc1 YlpUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

**Example 4. Search for homologues in *Candida albicans* and human**

- 5 Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and
- 10 Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).
- Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the
- 15 similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.
- The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

20 **Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans***

- The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity
- 25 to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.
- Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more
- 30 sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.
- This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

#### **Example 6. Assay for High Throughput screening for drugs**

35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 µl of R-compound at  $10^{-3}$  M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at  $-70^{\circ}\text{C}$ . The strains are streaked out on selective plates (SD medium) and incubated for two days at  $30^{\circ}\text{C}$ . For the parent strain, CAI-4, the medium is always supplemented with 20 µg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at  $30^{\circ}\text{C}$  for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at  $30^{\circ}\text{C}$  for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at  $30^{\circ}\text{C}$  while shaking at 250 rpm until a final  $\text{OD}_{600}$  of 0.24 ( $\pm 0.04$ ) is reached.

200 µl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at  $30^{\circ}\text{C}$  for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

#### **Example 7. Yeast cell viability assay upon induction of Bax expression**

##### **Materials and media**

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the YGR183C gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

#### Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YlpUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *EcoI*36II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

#### Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD<sub>600</sub>. Cells were pelleted by centrifugation and washed two times with sterile dH<sub>2</sub>O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

#### Example 8. Bax Expression In Candida cells

##### Strains

The *Candida albicans* strain CAI4 (*ura3<sup>+</sup>*) was used to perform the experiments (Fonzi and Irwin 1993).

*E. coli* transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (*F'* *mcnA*  $\Delta$ (*mrr hsdRMS-mcrBC*)  $\Delta$ 80/*lacZ*ΔM15  $\Delta$ *lacX74 deoR recA1 araD139*  $\Delta$ (*ara-leu*)7697 *galU galK rpsL* (Str<sup>R</sup>) *endA1 nupG*).

##### Media

Synthetic cextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CAI4), the media was supplemented with

50 µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic *BAX* gene was performed using 2% galactose as carbon source.

#### Construction of the codon-optimised *BAX* gene

- 5 Construction of the synthetic *BAX* gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic *BAX* gene.
- 10 The synthCa*BAX* gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst* I site and a *Bgl* II site. The *Pst* I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl* II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma* I site, suitable for cloning into the expression vector.
- 15 Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO vector (Stratagene). All three fragments were sequenced to ensure that no mutation was
- 20 introduced by the PCR.
- Subsequently, fragment A was digested with *Pst* I and *Taq* I, fragment B with *Taq* I and *Bam* HI and fragment C with *Bam* HI and *Sma* I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst* I and *Sma* I resulting in the plasmid pUC21:synthCandida*BAX*.
- 25 The sequence of the synthetic *BAX* gene is shown in Figure 6.

#### Construction of synthetic *BAX*- and GFP-synthetic *BAX* expression plasmids

- A *Pst* I-*Sma* I fragment containing the ORF of the synthetic *BAX* gene was cloned into the *Pst* I-*Sma* I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in
- 30 the expression construct pGAL1P:synthCa*BAX* (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.
- The yeast enhanced GFP gene *yEGFP*, (Cormack *et al.* 1997) was amplified by PCR using
- 35 primer 5'-AACTGCAGATGTCTAAAGGTGAAGAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTTCCTTTGTACAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *yEGFP* gene into the pCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

- 5 The *yEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*I-*Bgl*II *yEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Sfu* I digested expression vector pGAL1ACT1LUC. The obtained pGAL1P:*yEGFP*-synthCa*BAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

#### 10 **Creation of the synthetic *BAX* expression strains**

- Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the GAL1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different
- 15 transformants was prepared using the Nucleon<sup>®</sup> extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the pGAL1P:synthCa*BAX* plasmid as template, together with the sense primer 5'-ATGGATGGTTCTGGTGAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCCATTTTTTCCAGATG-3' (SEQ ID NO 14). Standard
- 20 PCR conditions were used. For detection of the *yEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25

#### **Western blot analysis**

- For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were
- 30 prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an
- 35 anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

### Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD<sub>600</sub> of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in  
5 microtitre plates using the Bioscreen C system (Labsystems).

### Viability tests

Cells were pregrown in minimal dextrose medium to an OD<sub>600</sub> of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the  
10 time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

### Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse Bax protein was placed under control of the *Candida albicans* GAL1 promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida*  
15 *albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the yEGFP to allow screening for transformants with a high yEGFP-synthCaBAX expression level  
20 using FACS technology. The newly obtained plasmids pGAL1P:synthCaBAX and pGAL1:GFP-synthCaBAX were transformed into the *C. albicans* CAI4 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all  
25 transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the GAL1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently,  
30 cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was



observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected  
5 molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX  
10 expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of  
15 colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong  
20 enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from  
25 proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Oligo	Sequence 5' → 3'
A1	AACTGCAGGAAGATCTTCCATGGATGGTTCCTGGTGAACAAATGGGTTCTGGTGG TCCAACTCTTCTGAACAAATCATGAAACCGGTGCTTCTTGTTG (SEQ ID NO 3)
A2	TAGAAGCATCTTGTGGTGGTTCCTCAAGGTCAATCTGGGGTTCAACAGCC ATTCTACCAGCTCTATCTTGGATGAAACCTTGCAACAAGAAAGCACC (SEQ ID NO 4)
A3	GGAAATCTCGACATCAGCGATCATCTTTGGCAATTCATGTTAGAAATCCAAATC ATCACCGATTCTTCTCAAAACATTCAGACAATTTTGGTAGAAGCATCTTGTG (SEQ ID NO 5)
B1	GGAAATTCGCTGATGTCGATACCGATTCTCCAAGAGAAGTCTTCTCAGAGTCG CTGCTGATAIGTTGCTGATGGTAACTTCAACTG (SEQ ID NO 6)
B2	AATCTGGGACTTTGGTACACAAAGCTTTCAGACCAATTTAGAAGCGAAGTA GAACAAAGCGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7)
B3	CCAACTTGATCTTGGATCCAGACCAACAATCTTCTCTCAAGAAATCCAAAGGTC CAACCCATGATGGTTCTGATCAATTCCTGGGACTTTG (SEQ ID NO 8)
C1	ATTGTTGGTCTGGATCCAAGATCAAGGTGGTGGGAGGTTGTGTTCTTACTT CGGTACCCCAACCTGGCAACCGTCA (SEQ ID NO 9)
C2	TCCCCCGGGGATTAACCCATTTTTCAGATGGTCAAGAAGCGGTCAAGAC ACCAGCGACGAAGATGGTGACGGTTTGCCAGGTTGGG (SEQ ID NO 10)

**Table 2: Overview of the differentially expressed genes after 30 min Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

YLP	YLB	Normalized expression YLB	YLB/UTL	YLB/UTL	YLB/UTL
<i>Cellular role : Cell cycle control</i>					
YBR139C	HSL7	18932.54	37877.20	↑	2.00
<i>Cellular role : Polymerase II transcription</i>					
YDR259C	MET32	17681.13	45567.17	↑	2.58
YBR112C	SSN6	26698.87	65315.83	↑	2.45
YDR145W	TAF61	38697.96	79117.62	↑	1.89
YBR269W	SNF5	33111.77	72328.70	↑	2.18
YDR216W	ADR1	30127.45	8815.87	↓	3.42
YEL009C	GCN4	16533.76	3030.44	↓	5.46
YBR089C-A	NHP6B	22698.83	6297.49	↓	3.60
YMR043W	MCM1	39141.64	84180.45	↑	2.15
YKR092C	SRP40	5965.63	16105.62	↑	2.70
YMR279C	ZDS1	14899.61	35508.04	↑	2.42
YPL089C	RLM1	34922.61	67858.88	↑	1.94
YOR372C	NDD1	20285.12	44445.20	↑	2.19
YPL037C	EGD1	30633.33	5250.70	↓	5.83
<i>Cellular role : Cell polarity</i>					
YBL065W	BOI1	7693.29	18614.99	↑	2.42
<i>Cellular role : Chromatine structure</i>					
YBR009C	HHF1	16668.00	4178.80	↓	3.99
YNL030W	HHF2	49878.04	12588.98	↓	3.97
YDR224C	HTB1	67355.40	29155.82	↓	2.91
YBL002W	HTB2	25269.02	5383.97	↓	4.69
<i>Cellular role: RNA processing</i>					
YER112W	USS1	12776.74	31470.70	↑	2.46
YPL190C	NAB3	8381.36	17892.11	↑	2.80
YNL112W	DBP2	9956.84	28036.48	↑	2.82
<i>Cellular role: Energy generation</i>					
YPL078C	ATP4	28902.69	5980.38	↓	4.50
YDL004W	ATP16	36525.08	3004.34	↓	12.16
YDR377W	ATP17	14419.41	756.86	↓	19.05
YDR529C	QCR7	35348.95	5394.85	↓	6.55
YGR008C	STF2	13275.51	2276.27	↓	5.83
YEL039C	CYC7	13604.38	2889.66	↓	5.06
YKL150W	MCR1	105337.67	30743.75	↓	3.43
YLR038C	COX12	52687.73	5455.83	↓	9.66
YLR327C		113,966.77	54,014.65	↓	2.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR149W	ARA1	15149.55	4095.17	↓	3.70
YMR094C	HXT1	12526.80	785.73	↓	15.94
YDR345C	HXT3	36643.13	1632.48	↓	22.45
YDR343C	HXT6	77064.71	32060.05	↓	2.40
YDR342C	HXT7	76349.13	27615.15	↓	2.76
<i>Cellular role: Signal transduction</i>					
YER177W	BMH1	22856.29	44771.71	↑	1.96
YDR099W	BMH2	40127.38	74572.38	↑	1.86

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19648.06	↑	2.67
Cellular role: Protein synthesis					
YGR034W	RPL26B	71942.48	74625.22	↑	1.04
Cellular role: Protein folding					
YLA216C	CPR6	9616.80	31126.02	↑	3.24
Cellular role: Protein modification/degradation					
YFR052W	RPN12	5583.57	14855.67	↑	2.66
YDL147W	RPN5	31832.20	52939.11	↑	1.66
YGR132C	PH51	15429.56	5581.19	↓	2.76
YGR135W	PRE9	38921.63	5517.17	↓	7.24
YFR010W	UBP6	1892.76	828.94	↓	2.26
Cellular role: Cell stress					
YIR037W	GPX3	7869.22	21789.00	↑	2.77
YDR513W	TTR1	55986.32	33263.12	↓	1.68
YCL035C	GRX1	70248.30	10069.97	↓	6.40
YFL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.68
YHR055C	CUP1B	71934.03	56799.80	↓	2.77
YMR173W	DDR18	16670.70	5022.40	↓	3.32
YMR251W-A	HOR7	26878.85	417.36	↓	64.41
YLR043C	TRX1	58251.39	4435.79	↓	13.13
YBL084C	PRX1	21525.00	40969.00	↑	1.30
YOL151W	GRE2	2024.55	24152.03	↑	9.20
Cellular role: Unknown					
YBL081W		73834.11	74612.35	↑	1.31
YDR368C		39398.48	57428.80	↑	1.44
YCR004C	YCP4	6869.08	28115.73	↑	4.09
YCR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL108W		18744.60	35440.24	↑	1.80
YDR154C		19565.23	69428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR095W		14426.76	34898.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24248.38	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		16437.52	2652.80	↓	6.20
YHR056C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38258.80	↑	2.13
YLR311C		7982.40	24164.87	↑	3.02
YJR115W		64690.69	102088.34	↑	1.58
YJL188C	BUD19	7580.28	23325.70	↑	2.95
YKR040C		50934.76	100733.41	↑	1.98
YLR053C		8117.68	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98811.28	110534.34	↑	1.12
YOR131C		7941.55	22353.72	↑	2.81
YNL338W		21800.45	38777.28	↑	1.78
YNL179C		13729.36	39513.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.89

YMR107W		65118.70	10042.46	↓	6.48
YKL065C	YET1	69556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16468.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		26879.95	417.36	↓	64.41
YMR173W-A		110104.98	61951.29	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR285W		64074.73	29749.43	↓	2.15
YOR286W		13458.08	733.06	↓	18.36
<i>Cellular role: Cell wall maintenance</i>					
YKR078W	ECM4	2674.15	13040.04	↑	4.89
YLR300W	ECM19	5472.05	15145.35	↑	2.77
<i>Cellular role: Membrane fusion</i>					
YHR138C		19921.35	3707.57	↓	6.37
<i>Cellular role: Vesicular transport</i>					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL085W	SEC16	6668.57	15206.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR028W	YIP2	25434.34	2049.47	↓	12.41
<i>Cellular role: DNA repair/recombination</i>					
YDL059C	RAD59	1948.81	19089.13	↑	6.72
<i>Cellular role: DNA synthesis</i>					
YEL082W	MCM9	23422.85	44327.48	↑	1.89
<i>Cellular role: Amino acid metabolism</i>					
YIL074C	SER33	3978.42	16702.88	↑	4.20
YGF155W	CYS4	4184.59	19270.89	↑	4.61
<i>Cellular role: Fatty acid metabolism</i>					
YHR179W	OYE2	2291.38	40274.02	↑	17.58
<i>Cellular role: Protein translocation</i>					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
<i>Cellular role: Small molecule transport</i>					
YDR276C	SNA1	21140.46	1580.68	↓	19.98
YOR267C	HRK1	82689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27298.15	↑	4.02

**Table 3: Overview of the differentially expressed genes after 1h Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyL8**

Yeast	Gene	INVSc1 YlpUTL	INVSc1 YlpUTyL8	YpUTL	YpUTyL8
Cellular role: Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YBR112C	CYC8	50186.77	84511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.58
YPL089C	RLM1	23440.54	64284.32	↑	2.74
YOR072C	NDN1	26412.58	50804.99	↑	1.92
Cellular role: Cell cycle control					
YBR133C	HSL7	18761.64	53238.86	↑	2.84
Cellular role: Cell polarity					
YBL085W	BOI1	37895.40	57781.52	↑	1.52
Cellular role: Chromatin structure					
YDR224C	HTB1	13661.40	55656.34	↑	4.07
Cellular role: Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C		5054.57	28994.72	↑	5.74
YKL150W	MCR1	43663.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	29801.54	↑	3.79
YOL126C	MDH2	34144.81	65326.97	↑	1.91
YLR327C		97416.84	101651.17	↑	1.04
Cellular role: Vesicular transport					
YHR181C	YAP180A	11602.81	34695.20	↑	2.99
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role: Carbohydrate metabolism					
YDR342C	HXT7	65273.58	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR346C	HXT3	76352.52	40296.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22919.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.93
Cellular role: Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role: Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role: Protein modification/degradation					
YOR261C	APN8	12575.49	32568.47	↑	2.59
Cellular role: Cell stress					
YHR053C	CUP1A	32531.53	63579.94	↑	1.95
YHR055C	CUP1B	27939.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CBS5	2922.32	23848.60	↑	8.16

YLR109W	AMP1	43067.08	6302.46	↓	6.83
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21288.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.98	↑	3.64
YHR056C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR182W		13836.79	33381.84	↑	2.41
YGR243W		30828.66	59765.39	↑	1.91
YBR050C	REG2	14008.24	29603.16	↑	2.11
YEL071W	DLD3	19467.41	35273.39	↑	1.81
YDR135C		83074.54	62986.96	↓	1.32
YDR134C		83111.03	16839.53	↓	4.94
YHL021C		46028.06	8577.00	↓	5.37
YKL054C	VID31	28018.48	66537.91	↑	2.37
YLR311C		7803.52	31180.73	↑	3.99
YMR107W		13459.16	78850.98	↑	5.86
YKL066W		8751.84	24129.32	↑	2.76
YMR173W-A		38398.83	60514.70	↑	1.58
YML053C		23670.86	66254.48	↑	2.80
YOR121C		17039.58	58010.58	↑	3.40
YOL108W		19917.67	69853.68	↑	3.51
YNL338W		17864.90	49911.08	↑	2.79
YJR115W		84858.02	98161.71	↑	1.16
Cellular role: Small molecule transport					
YOR267C	HRK1	90123.84	98824.51	↑	1.07

**Table 4:** Overview of the differentially expressed genes after 2h Bax expression**Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	INVSc1 YlpUTL	INVSc1 YlpUTyLB	Log2 Ratio	Log2 Ratio
<i>Cellular role: Protein modification/degradation</i>					
YCL052C	PBN1	5264.22	8175.70	↑	1.55
YOL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN8	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8458.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
<i>Cellular role: Unknown</i>					
YDR202C	RAY2	7493.71	10089.19	↑	1.35
YBR062C		4893.97	9894.82	↑	2.02
YDR366C		25468.2	59682.92	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	41083.39	↑	1.29
YGR238C	SPG1	18978.52	31419.12	↑	1.85
YGR182C		30569.31	58805.05	↑	1.92
YDR544C		15937.14	24421.98	↑	1.53
YHR162W		28610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		75520.99	62984.50	↓	1.20
YCR010C	ADY2	17240.59	11835.82	↓	1.46
YDR134C		72723.66	9776.23	↓	7.44
YGR059W		65418.73	53767.35	↓	1.22
YIL057C		16510.16	2198.04	↓	7.51
YGL072C		12209.68	6509.91	↓	1.88
YGL080W		22550.78	11525.24	↓	1.96
YLR311C		11095.31	24060.47	↑	2.22
YJR115W		74757.79	108422.48	↑	1.38
YMR099C		7057.15	11477.42	↑	1.63
YMR173W-A		31901.05	48886.91	↑	1.47
YML132W	GOS3	24648.97	34995.33	↑	1.42
YKL066W		13581.94	25433.97	↑	1.87
YIL142C		7205.86	11920.21	↑	1.65
YLR346C		6447.57	11569.63	↑	1.79
YLR053C		41161.10	78636.82	↑	1.91
YMR110C		19410.64	29861.23	↑	1.63
YKR075C		19134.57	29948.72	↑	1.57
YOR121C		36492.56	59452.09	↑	1.63



Cellular role: Unknown					
YOL106W		31382.10	76664.72	↑	2.44
YNL338W		24117.93	38981.22	↑	1.62
YNL134C		9617.33	14613.60	↑	1.52
YKL085C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20666.22	9519.29	↓	2.17
YJL144W		10316.92	3122.77	↓	3.30
YNL128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21938.96	10883.98	↓	2.02
YOL109W	ZEO1	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role: Chromatine structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14261.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.89
Cellular role: Polymerase II transcription					
YBR289W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	66457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role: Signal transduction					
YDR099W	BMH2	55902.13	73874.51	↑	1.32
Cellular role: Cell stress					
YBL064C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.21	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.33	↓	2.78
YGR209C	TRX2	30492.38	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.62	83536.72	↑	1.94
YDR256C	CTA1	9614.29	4232.17	↓	2.27
YCA021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		36796.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17791.14	4231.30	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role: Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6263.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YJL189W	RPL39	2044.64	8010.57	↑	3.92
YIL148W	RPL40A	6052.35	11595.54	↑	2.30
YKR094C	RPL40B	3994.57	10011.19	↑	2.54
YOL139C	CDC33	4132.18	8956.14	↑	2.17

Cellular role : Protein folding					
YLR216C	CPR6	20353.43	32713.37	↑	1.61
YKL117W	SBA1	11144.25	1500.56	↓	7.43
Cellular role: Vesicular transport					
YCR009C	RVS161	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32481.67	↑	1.29
YEL078C	AUT7	16528.81	9843.25	↓	1.68
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8178.94	↑	1.77
YBR149W	ARA1	30706.41	9837.76	↓	3.19
YOR178W	SDH4	14880.91	6237.35	↓	2.39
YMR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.86
YDR345C	HXT3	77025.40	58749.40	↓	1.36
YDR343C	HXT6	73149.70	8676.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32803	41984.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.67	↑	1.46
YDR529C	QCR7	24821.75	16558.87	↓	1.50
YIL168W	QCR8	15554.30	24508.28	↑	1.58
YHR001W-A	QCR10	12416.35	23485.31	↑	1.89
YBR039W	ATP3	11709.79	3088.19	↓	3.79
YPL078C	ATP4	11325.84	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.61	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role: Small molecule transport					
YDR276C	SNA1	19337.39	12392.20	↓	1.56
YGR197C	SNG1	4756.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.98	↓	2.00
YDR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role: RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPI1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PFY1	14459.45	20178.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

**Table 5: Overview of the differentially expressed genes after 3h Bax expression****Comparison: INVSc1 YlpUTL versus INVSc1 YlpUTyLB**

Gene	Gene	Normalised intensity	Normalised intensity	Log2 ratio	Log2 ratio
<i>Cellular role: Cell cycle control</i>					
YBR133C	HSL7	63562.10	43191.28	↓	1.47
<i>Cellular role: Cell polarity</i>					
YBL085W	BOH1	32734.79	23497.41	↓	1.39
<i>Cellular role: Chromatine structure</i>					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
<i>Cellular role: Energy generation</i>					
YCR005C	CIT2	11882.42	25632.94	↑	2.16
YGR183C	QCR9	74474.20	11510.99	↓	8.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
<i>Cellular role: Carbohydrate metabolism</i>					
YBR019C	GAL10	3092.50	15697.52	↑	5.08
YDR345C	HXT3	14086.41	25857.66	↑	1.82
YKR097W	PCK1	50736.44	20858.02	↓	2.43
<i>Cellular role: Signal transduction</i>					
YDR089W	BMH2	63285.16	56028.91	↓	1.13
<i>Cellular role: Protein synthesis</i>					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
<i>Cellular role: Cell stress</i>					
YFL014W	HSP12	40848.44	89781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21763.09	64594.58	↑	2.97
YMR178W	DDR48	75407.16	38354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
<i>Cellular role: Unknown</i>					
YIL057C		7602.78	24104.02	↑	3.17
YHR056C	RSC90	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↓	1.85
YCR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↓	2.87
YJR115W		74889.58	81238.98	↓	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.97	↓	2.07

**Table 6: Overview of the differentially expressed genes after 6h Bax expression****Comparison: INVSc1 YipUTL versus INVSc1 YipUTyLB**

YipUTL	YipUTyLB	Normalised YipUTL	Normalised YipUTyLB	Log2 Ratio	Log2 Ratio
<i>Cellular role: Cell stress</i>					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	25081.08	↓	1.42
YDR513W	TTR1	19985.22	12935.02	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.64	15289.39	↓	5.39
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOR7	18824.54	5914.28	↓	3.18
<i>Cellular role: Signal transduction</i>					
YDR099W	BMH2	29412.99	56588.42	↑	1.99
<i>Cellular role: Protein synthesis</i>					
YGL147C	RPL9A	13655.66	1585.97	↓	9.81
YGR085C	RPL11B	27485.15	3791.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5706.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.40
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.85
YDR471W	RPL27B	14636.79	2613.40	↓	5.60
YOL075W	RPL31A	11969.47	2811.53	↓	4.56
YBL092W	RPL32	7872.80	857.85	↓	9.18
YOL191W	RPL35A	28582.59	6046.25	↓	4.73
YOL136W	RPL35B	25493.49	5064.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YIL148W	RPL40A	47028.95	9543.65	↓	4.93
YKR094C	RPL40B	38900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML065W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.56	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.80	↓	7.50
YBL072C	RPS8A	17198.50	3233.30	↓	5.82
YER102W	RPS8B	16234.93	1791.18	↓	9.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.68
YDR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR084W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37913.71	5674.80	↓	6.68
YML026C	RPS18B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	20725.18	1117.26	↓	2.13
YLR167W	RPS31	38648.54	2811.97	↓	14.80
YJL138C	TIF2	20154.61	7264.66	↓	2.77
<i>Cellular role: Energy metabolism</i>					
YGR183C	QCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↓	2.28
YKL150W	MCR1	50931.48	37076.83	↓	1.37

YLR038C	COX12	39506.08	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14854.81	2242.42	↓	6.94
YDR134C		17025.59	10681.72	↓	1.61
YHR056C	RSC90	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90126.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.67
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.38	↓	4.88
YOR285W		75099.98	61896.00	↓	1.21
YOL109W	ZEO1	66287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HHF1	11173.15	5416.74	↓	2.06
YNL030W	HHF2	31366.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13338.03	5383.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCM4	34617.98	20798.63	↓	1.86
YPL037C	EGD1	17882.37	8229.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.58	13704.48	↓	1.68
Cellular role: Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.61	↓	1.86
Cellular role: Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

**Table 7:**

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHF1			1.77		
SEQ ID NO 25	YBL054C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W		1.01	1.86			
SEQ ID NO 31	YBL085W	BOI1	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W	RPL32			2.76		-9.18
SEQ ID NO 35	YBL109W		1.89	2.76	1.51	-1.13	
SEQ ID NO 37	YBR009C	HHF1	-3.99				-2.06
SEQ ID NO 39	YBR019C	GAL10				5.08	
SEQ ID NO 41	YBR039W	ATP3			-9.70		
SEQ ID NO 43	YBR050C	REG2	3.07	2.11			
SEQ ID NO 45	YBR062C				2.02		
SEQ ID NO 47	YBR089C-A	NMP6B	-3.60				
SEQ ID NO 49	YBR101C				1.43		
SEQ ID NO 51	YBR112C	SSN6	2.45	1.29			
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	1.28	-1.47	
SEQ ID NO 55	YBR139W				-2.60		
SEQ ID NO 57	YBR149W	ARA1	-3.70		-3.11		
SEQ ID NO 59	YBR189W	RPS9B					-4.88
SEQ ID NO 61	YBR191W	RPL21A					-8.46
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-8.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2				2.16	
SEQ ID NO 73	YCR009C	RVS161			1.83		
SEQ ID NO 75	YCR010C				-1.40		
SEQ ID NO 77	YCR013C		3.80				
SEQ ID NO 79	YCR021C	HSP30			-2.20		
SEQ ID NO 81	YDL004W	ATP16	-12.16				-2.28
SEQ ID NO 83	YDL059C	RAD59	6.72				
SEQ ID NO 85	YDL075W	RPL31A					-4.58
SEQ ID NO 87	YDL147W	RPN5	1.88		2.14		
SEQ ID NO 89	YDR064W	RPS13					-6.13
SEQ ID NO 91	YDR073W	SNF11			1.89		
SEQ ID NO 93	YDR099W	BMH2	1.86	1.29	1.32	-1.13	1.99
SEQ ID NO 95	YDR133C			-1.32	-1.20		
SEQ ID NO 97	YDR134C			-4.84	-7.40		-1.61
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.65	1.58		
SEQ ID NO 103	YDR171W	HSP42					2.02
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR278C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 119	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT8	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-19.05				
SEQ ID NO 129	YDR399W	HPT1					-2.50
SEQ ID NO 131	YDR418W	RPL12B					-9.27
SEQ ID NO 133	YDR513W	TTR1	-1.68				-1.54
SEQ ID NO 135	YDR544C		1.99	2.55	1.53	-1.85	
SEQ ID NO 137	YDR545W	YRF1-1				-1.75	
SEQ ID NO 139	YEL009C	GCN4	-5.46				-1.68
SEQ ID NO 897	YEL032W	MCM3	1.89				
SEQ ID NO 141	YEL039C	CYC7	-5.06				
SEQ ID NO 143	YEL071W	DLD3	3.09	1.21	1.29		
SEQ ID NO 145	YER103W	SSA4			1.80		
SEQ ID NO 147	YER112W	USS1	2.46				
SEQ ID NO 149	YER150W	SPH1			-2.40		
SEQ ID NO 151	YER177W	BMH1	1.96	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28				
SEQ ID NO 155	YFR033C	QCR6			1.46		
SEQ ID NO 157	YFR052W	RPN12	2.66				
SEQ ID NO 159	YGL072C		-6.20		-1.80		
SEQ ID NO 161	YGL080W		-7.28		-1.90		
SEQ ID NO 163	YGL123W	RPS2					-5.57
SEQ ID NO 165	YGR008C	STF2	-5.83				
SEQ ID NO 167	YGR023W	MTL1	2.67				
SEQ ID NO 169	YGR034W	RPL26B	1.04				
SEQ ID NO 171	YGR069W		1.67		-1.20		
SEQ ID NO 173	YGR070W	ROM1	2.34				
SEQ ID NO 175	YGR086C				-1.50		
SEQ ID NO 177	YGR132C	PHB1	-2.76		1.61		
SEQ ID NO 179	YGR135W	PRE9	-7.24				
SEQ ID NO 181	YGR155W	CYS4	4.61				
SEQ ID NO 183	YGR192C	TDH3		-2.72			
SEQ ID NO 185	YGR197C	SNG1			2.20		
SEQ ID NO 187	YGR209C	TRX2			1.24		-1.14
SEQ ID NO 189	YGR243W			1.94			
SEQ ID NO 191	YGR250C				1.89		
SEQ ID NO 193	YHL021C			-5.37			
SEQ ID NO 195	YHR001W-A	QCR10			1.89		
SEQ ID NO 197	YHR039C-B	VMA10	-7.08		-2.00		-1.86
SEQ ID NO 199	YHR053C	CUP1A	-1.68	1.95	1.94	3.19	-5.33
SEQ ID NO 201	YHR055C	CUP1B	-2.77	2.33	4.12	2.97	-4.08
SEQ ID NO 203	YHR056C		-1.25	2.41	2.05	1.56	-2.59
SEQ ID NO 205	YHR094C	HXT1	-15.94		-1.80		
SEQ ID NO 207	YHR095W		2.42				
SEQ ID NO 209	YHR138C		-5.37				
SEQ ID NO 211	YHR161C	YAP180A	2.30	2.99	1.29		
SEQ ID NO 213	YHR162W			2.41	1.27		
SEQ ID NO 215	YHR175W	OYE2	17.58				
SEQ ID NO 217	YIL057C		31.34		-7.50	3.17	
SEQ ID NO 219	YIL074C	SER33	4.20				
SEQ ID NO 221	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YJL138C	TIF2					-2.77
SEQ ID NO 225	YJL142C				1.65		
SEQ ID NO 227	YJL144W				-3.30		
SEQ ID NO 229	YJL161W		-6.29				
SEQ ID NO 231	YJL166W	OCR8			1.58		
SEQ ID NO 233	YJR096W		-2.04				
SEQ ID NO 235	YJR115W		1.58	1.16	1.38	-1.08	
SEQ ID NO 237	YKL054C	VID31	2.13	2.37			
SEQ ID NO 239	YKL060C	FBA1			1.31		-3.21
SEQ ID NO 241	YKL065C	YET1	-5.43		-1.55		
SEQ ID NO 243	YKL066W			2.76	1.87		
SEQ ID NO 245	YKL087W-A	CWP2					-8.37
SEQ ID NO 247	YKL117W	SBA1			-7.43		
SEQ ID NO 249	YKL150W	MCR1	-3.43	1.38			-1.37
SEQ ID NO 251	YKL156W	RPS27A					-2.13
SEQ ID NO 253	YKL196C	YKT6	-6.55				
SEQ ID NO 255	YKR040C		1.98			1.24	1.86
SEQ ID NO 257	YKR075C				1.57		
SEQ ID NO 259	YKR076W	ECM4	4.88				
SEQ ID NO 261	YKR092C	SRP46	2.70				
SEQ ID NO 263	YKR097W	PCK1		1.67		-2.43	
SEQ ID NO 265	YLR029C	RPL15A					-3.98
SEQ ID NO 267	YLR038C	COX12	-9.66				-1.34
SEQ ID NO 269	YLR043C	TRX1	-13.13		-2.78		
SEQ ID NO 271	YLR053C		2.50		1.91		
SEQ ID NO 273	YLR109W	AHP1		-6.83			
SEQ ID NO 275	YLR110C			-9.13	-6.07		
SEQ ID NO 277	YLR206W	ENT2		2.40			
SEQ ID NO 279	YLR216C	CPR6	3.24		1.61		
SEQ ID NO 281	YLR294C			5.74	2.43		
SEQ ID NO 283	YLR311C		3.02	3.99	2.22		
SEQ ID NO 285	YLR312C						-1.58
SEQ ID NO 287	YLR327C		-2.10	1.04	2.48		
SEQ ID NO 289	YLR346C				1.79		
SEQ ID NO 291	YLR390W	ECM19	2.77				
SEQ ID NO 293	YLR414C						-1.67
SEQ ID NO 295	YML053C			2.80			
SEQ ID NO 297	YML128C	COX14			1.81		
SEQ ID NO 299	YML132W	COS3			1.42		
SEQ ID NO 301	YMR009W				-2.17		
SEQ ID NO 303	YMR011W	HXT2			-1.86		
SEQ ID NO 305	YMR043W	MCM1	2.15	2.56	1.16		
SEQ ID NO 307	YMR099C				1.63		
SEQ ID NO 309	YMR107W		-6.48	5.88			
SEQ ID NO 311	YMR110C				1.53		
SEQ ID NO 313	YMR173W	DDR48	-3.32	1.58		-2.07	
SEQ ID NO 315	YMR173W-A		-1.78	1.58	1.47	-2.07	
SEQ ID NO 317	YMR251W		-64.41				
SEQ ID NO 319	YMR251W-A	HQR7	-64.41		-4.19		-3.18
SEQ ID NO 319	YMR256C	COX7		3.79	2.18		
SEQ ID NO 321	YMR273C	ZDS1	2.42				
SEQ ID NO 323	YNL030W	HHF2	-3.97				-1.56
SEQ ID NO 325	YNL031C	HHT2			-5.69		



Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 327	YNL112W	DBP2	2.82				
SEQ ID NO 329	YNL131W	TOM22	-9.70				
SEQ ID NO 331	YNL134C				1.52		
SEQ ID NO 333	YNL143C		1.12				
SEQ ID NO 335	YNL179C		2.88		-2.02		
SEQ ID NO 337	YNL338W		1.78	2.79	1.62	-2.87	
SEQ ID NO 339	YNA002C	FUN34			-1.87		
SEQ ID NO 709	YOL052C-A	DDR2				1.65	
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZEO1			-3.45		-1.87
SEQ ID NO 345	YOL126C	MDH2		1.91		-3.11	
SEQ ID NO 347	YOL139C	COC33			2.17		
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCY1			-1.46		
SEQ ID NO 355	YOR121C		1.54	3.40	1.63		
SEQ ID NO 357	YOR122C	PFY1			1.40		
SEQ ID NO 359	YOR131C		2.81				
SEQ ID NO 361	YOR261C	RPN8		2.59	1.54		
SEQ ID NO 363	YOR267C		1.78	1.07	-1.10		
SEQ ID NO 365	YOR285W		-2.15				-1.21
SEQ ID NO 367	YOR286W		-18.36				
SEQ ID NO 369	YOR327C	SNC2					-1.66
SEQ ID NO 371	YOR373C	NDD1	2.19	1.92			
SEQ ID NO 373	YOR374W	ALD4		-12.93			
SEQ ID NO 375	YOR382W		4.02				
SEQ ID NO 377	YPL037C	EGD1	-5.83				-2.17
SEQ ID NO 379	YPL078C	ATP4	-4.50		1.22		
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC18	2.28				
SEQ ID NO 385	YPL089C	RLM1	1.94	2.74	1.22		
SEQ ID NO 387	YPL190C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPL271W	ATP15			2.40		
SEQ ID NO 393	YPR028W	YIP2	-12.41				
SEQ ID NO 395	YPR035W	GLN1			-2.78		

TABLE 8

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's		
aa	codons	frequency, per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency, per thousand	total number
Ala	GCU	30.7	8686	x	6	21.1	118595
	GCC	12.7	3582		4	12.6	70785
	GCA	15.4	4367		2	18.2	91018
	GCG	2	578		1	6.1	34546
Arg	CGU	5.9	1682	x	1	6.5	36518
	CGC	0.7	204		1	2.6	14571
	CGA	3.5	989		3	3	16957
	CGG	0.8	220		3	1.7	9801
	AGA	23.6	6673		1	21.3	119672
	AGG	2.7	769		2	9.3	52057
Asn	AAU	37.9	10731	x	1	36	202351
	AAC	18.7	5293		2	24.9	140194
Asp	GAU	43.6	12323	x	5	37.3	212658
	GAC	14.7	4152		7	20.4	114451
Cys	UGU	9.7	2757	x	1	8	44797
	UGC	1.7	493		1	4.7	26357
Gln	CAA	35.2	9964	x	1	27.5	154629
	CAG	6.9	1948		8	12.2	89463
Glu	GAA	49.5	14001	x	3	45.9	257930
	GAG	11.5	3252		10	19.1	107568

TABLE 8 - continued

TABLE 6 - continued

C. albicans 522 CDS's					S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene		codons used in wt muBAX gene		total number
						wt	muBAX	
Gly	GGU	33.5	9492	x		2		134515
	GGC	4.5	1281			7		54629
	GGA	13.7	3874			2		61481
His	GGG	7.7	2182			8		33627
	CAU	14	3964					77260
	CAC	5.8	1642					43878
Ile	AUU	39.9	11281	x		3		169795
	AUC	14.2	4005			7		96126
	AUA	12.3	3478					100027
Leu	UUA	1	295	x				148133
	UUG	36.1	10204			2		152590
	CUU	9.8	2777			2		69479
	CUC	2.5	694			7		30218
	CUA	4	1133			1		75414
Lys	AAA	48.6	13760	x		2		236746
	AAG	19.4	5477			6		173174
Met	AUG	18.4	5219	x		8		117410
Phe	UUU	28.6	8100	x		4		146355
	UUC	15.9	4486			7		102389

TABLE 8 - continued

C. albicans 522 CDS's				S. cerevisiae 11645 CDS's		
aa	codons	frequency, per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	total number
Pro	CCU	13.2	3722		1	76366
	CCC	3.6	1027		5	38247
	CGA	26.6	7531	x		102277
	CCG	2.4	686		1	29758
Ser	CUG	3.1	875		9	58583
	UCU	23.3	6595	x	1	132608
	UCC	10.3	2928		4	79928
	UCA	24.6	6955			105570
	UCG	6.5	1836		1	48186
	AGU	23.6	6673			79648
	AGC	4.5	1269		5	54330
Thr	ACU	30.7	8889		1	113634
	ACC	13.9	3928	x	8	70777
	ACA	17.4	4928		5	99759
	ACG	3.6	1019		1	44817
Trp	UGG	11	3115	x	6	58092
Tyr	UAU	24	6782			105489
	UAC	11.6	3280	x	2	82483
Val	GUU	33.2	9391		1	123726
	GUC	10.3	2927	x	3	65203
	GUA	8	2265			66100
	GUG	10	2842		7	60033

**TABLE 9: Regulation of 23 selected "Bax-specific" functions**

<i>Cellular role: Amino-acid metabolism</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YOR302W	YOR302W	11541.92	26806.35	5595.74	2.32
<i>Cellular role: Cell stress</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YML028W	TSA1	12889.91	2168.45	11327.36	0.17
<i>Cellular role: Chromatin/chromosome structure</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBR009C	HHF1	2149.89	8855.43	2909.14	4.03
YDR224C	HTB1	13661.40	55656.34	18829.27	4.07
YNL030W	HHF2	8676.99	19603.93	4732.39	2.26
<i>Cellular role: Energy generation</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YBL099W	ATP1	2728.21	8786.71	1644.48	3.22
YGR183C	OCR9	23181.54	81865.40	24053.00	3.53
YJL186W	OCR8	5296.71	18093.93	5001.65	3.42
YLR038C	COX12	7336.65	19935.69	5118.43	2.72
<i>Cellular role: Signal transduction</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YHR135C	YCK1	3939.64	8358.11	3707.17	2.12
YOL100W	PKH2	2218.45	6088.96	2619.31	2.74
<i>Cellular role: Transcription factor</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR216W	ADR1	5925.91	18459.00	6434.43	3.11
<i>Cellular role: Unknown</i>					
ORF	Gene	Control	Bax	H2O2	B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62	2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89	2.68
YGR236C	SPG1	17717.80	64439.96	24134.29	3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50	2.38
YJL142C	YJL142C	6988.27	16006.02	6740.46	2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04	2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27	2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00	5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15	3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66	2.11
YJL060W	YJL060W	8798.50	2406.38	6356.11	0.27

## REFERENCES

- Altshul, S.F., Gish, W., Miller, W., Myers, E.W. and Lipman D.J. (1990). Basic local alignment search tool. *J. Mol. Biol.* **215**, 403-410.
- 5 Apte, S. S., M. G. Mattei M. F. Seldin and B. R. Olsen (1995). "The highly conserved defender against the death 1 (DAD1) gene maps to human chromosome 14q11-q12 and mouse chromosome 14 and has plant and nematode homologs." *FEBS Lett* **363**(3): 304-6.
- Bairoch, A. and Apweiler, R. (1998). The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. *Nucleic acids Res.* **26**, 38-42.
- 10 Bishop M.J., ed. (1994). Guide to Huge Computers, Academic Press, San Diego.
- Brown, A.J., G. Bertram, *et al.* (1991). "Codon utilisation in the pathogenic yeast, *Candida albicans*." *Nucleic Acids Res* **19**(15): 4298.
- Carillo, H. and Lipton, D. (1988). *SIAM J. Applied Math.* **48**, 1073.
- Casadaban, M.J., and Cohen, S.N. (1980). Analysis of gene control signals by DNA fusion and  
15 cloning in *Escherichia coli*. *J. Mol. Biol.* **138**, 179-207.
- Chen, C. T., Bartel, P.L., Sternglanz, R., and Fields, S. (1991). The 2-hybrid system - a method to identify and clone genes for proteins that interact with a protein of interest. *Proc. Natl. Acad Sci USA* **88**, 9578-9582.
- Cormack, B.P., G. Bertram, *et al.* (1997). "Yeast-enhanced green fluorescent protein (yEGFP) a  
20 reporter of gene expression in *Candida albicans*." *Microbiology* **143**(Pt 2): 303-11.
- Devereux, J., Haeberli, P. and Smithies, O. (1984). A comprehensive set of sequence analysis programs for the VAX. *Nucleic Acids Research* **12**, 387-395.
- Fonzi, W. A. and M. Y. Irwin (1993). "Isogenic strain construction and gene mapping in *Candida albicans*." *Genetics* **134**(3): 717-28.
- 25 Gatignol, A., Dassin, M. and Tiraby, G. (1990). Cloning of *Saccharomyces cerevisiae* promoters using a probe vector based on phleomycin resistance. *Gene* **91**, 35-41.
- Geysen, H.M., Rodda, S.J. and Mason, T.J. (1986). A priori delineation of a peptide which mimics a discontinuous antigenic determinant. *Mol. Immunol.* **23**, 709-715.
- Greenhalf, W., C. Stephan, and B. Chaudhuri (1996). "Role of mitochondria and C-terminal  
30 membrane anchor of Bcl-2 in Bax induced growth arrest and mortality in *Saccharomyces cerevisiae*." *FEBS Lett* **380**(1 2): 169-75.
- Herreros, E., M.I. Garcia-Saez, *et al.* (1992). "A reorganized *Candida albicans* DNA sequence promoting homologous non-integrative genetic transformation." *Mol Microbiol* **6**(23): 3567-74.

- Hirnebush, A.G. and Liebman, S.W., in : The Molecular Biology of the Yeast *Saccharomyces* (1991). Broach, J.R., Pringle, J.R. and Jones, E.W., eds., CSH Laboratory Press, NY.
- Ink, B., M. Zornig, B. Baum, N. Hajibagheri, C. James, T. Chittenden and G. Evan (1997). "Human Bak induces cell death in *Schizosaccharomyces pombe* with morphological changes similar to those with apoptosis in mammalian cells." *Mol Cell Biol* **17**(5): 2468-74.
- Jürgenmeier, J.M., Krajewski, S., Armstrong, R., Wilson, G.M., Oltersdorf, T., Fritz, L.C., Red, J.C., and Oltvie, S. (1997). Bax- and Bak-induced cell death in the fission yeast *Schizosaccharomyces pombe*. *Mol. Biol. Cell* **8**, 325-329.
- Knudson, C. M. and S. J. Korsmeyer (1997). "Bcl-2 and Bax function independently to regulate cell death." *Nat Genet* **16**(4): 358-63.
- Kohler, F. and Milstein, C. (1975). Continuous cultures of fused cells secreting antibody of predefined specificity. *Nature* **256**, 495-497.
- Kozak, M. (1981). "Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes." *Nucleic Acids Res* **9**(20): 5233-62.
- Ligr, M., Madeo, F., Froehlich, E., Hilt, W., Froehlich, K.-U. and Wolf, D.H. (1998). Mammalian Bax triggers apoptotic changes in yeast. *FEBS Lett*, **438**, 61-65.
- Lloyd, A.T. and P.M. Sharp (1992). "Evolution of codon usage patterns: the extent and nature of divergence between *Candida albicans* and *Saccharomyces cerevisiae*." *Nucleic Acids Res* **20**(20): 5289-95.
- Lockhart, D.J. Dong, H. Byrne, M.C., Follettie, M., Gallo, M.V., Choc, M.S., Mittman, M., Wang, C., Kobayashi, M., Horton, H and Brown, E.L. (1996). Expression monitoring by hybridisation to high density oligonucleotide arrays. *Nature Biotechnology* **14**, 1675-1680.
- Madeo, F., Frohlich, E., Ligr, M., Grey, M., Sigrist, S. J., Wolf, D.H., and Frohlich, K.U. (1999). Oxygen stress: a regulator of apoptosis in yeast. *J Cell Biol* **145**, 757-767.
- Muchmore, S. W., M. Sattler, H. Liang, R. P. Meadows, J. E. Harlan, H. S. Yoon, D. Oltvai, Z. N. and S. J. Korsmeyer (1994). "Checkpoints of dueling dimers foil death wishes [comment]." *Cell* **79**(2): 189-92.
- Reed, J. C., J. M. Jurgensmeier, and S. Matsuyama (1998). "Bcl-2 family proteins and mitochondria." *Biochim Biophys Acta* **1366**(1-2): 127-37.
- RiboGene Inc., Patent application (1995) PCT WO 95/11969.
- Rossanese, O.W., J. Soderholm, *et al.* (1999). "Golgi structure correlates with transitional endoplasmic reticulum organization in *Pichia pastoris* and *Saccharomyces cerevisiae*." *J Cell Biol* **145**(1): 69-81.
- Sambrook J., Fritsch E.F. and Maniatis, T. (1989). *Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup> Ed., CSH Laboratory Press, NY.

- Sambrook, J., E.F. Fritsch, *et al.* (1989). *Detection and Analysis of Proteins Expressed from Cloned Genes. Molecular Cloning: A Laboratory Manual*. New York, Cold Spring Harbor Laboratory Press. **3**: 18.35.
- Sandbaken, M.G., Lupisella, J.A., DiDomenico, B., and Chakraborty, K. (1990). Protein synthesis in yeast Structural and functional analysis of the gene encoding elongation factor III. *J. Biol. Chem.* **265**, 15838-15844.
- Sato, T., M. Hanada, S. Bodrug, S. Irie, N. Iwama, L. H. Boise, C. B. Thompson, E. Golemis, L. Fong, H. G. Wang and J. C. Reed (1994). "Interactions among members of the Bcl-2 protein family analyzed with a yeast two-hybrid system [published erratum appears in Proc Natl Acad Sci U S A 1995 Feb 28;92(5):2016]." *Proc Natl Acad Sci U S A* **91**(20): 9238-42.
- Sherman, F., Fink, G.R., and Hicks, J.B. (1979). *Methods in yeast genetics*, CSH Laboratory Press, NY.
- Schiestl, R.H., and Gietz, D.R. (1989). High efficiency transformation of intact yeast cells using single stranded nucleic acids as a carrier. *Curr. Genet.* **16**, 339-346.
- Schwartz, L. M., S. W. Smith, M. E. Jones and B. A. Osborne (1993). "Do all programmed cell deaths occur via apoptosis?" *Proc Natl Acad Sci U S A* **90**(3): 980-4.
- Stoesser, G., Moseley, M.A., Sleep, J., McGowran, M., Garcia-Pastor, M. and Sterk, P. (1998). *Nucleic Acids Res.* **26**, 8-15.
- Walsh, T.J. (1992). Invasive Fungal Infections: Problems and Challenges for Developing New Antifungal Compounds, in "Emerging Targets in Antibacterial and Antifungal Chemotherapy", J. A. Sutcliffe and N.H. Georgopapadakou, eds, Chapman and Hall, NY, pp 349-373.
- Zha, H., H. A. Fisk, M. P. Yaffe, N. Mahajan, B. Herman and J. C. Reed (1996).. "Structure-function comparisons of the proapoptotic protein Bax in yeast and mammalian cells." *Mol Cell Biol* **16**(11): 6494-508.
- Zhu, J. (1986). One step selection of a multicopy integrant based on yeast genomic transformation. In "Heterologous gene expression in *Saccharomyces cerevisiae* using a dominant selection and amplification system". Ghent University, doctoral dissertation, p 45.



**CLAIMS**

1. An isolated nucleic acid representing a synthetic *BAX*-gene selected from the group consisting of:
  - 5 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
  - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
  - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
  - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by  
10 SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
  - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,  
or a nucleic acid representing the complement of any of said nucleic acids as defined in (a)  
15 to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid  
20 sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
- 25 7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
- 30 10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
- a) providing (a) genetically modified yeast or fungi according to claim 11,
  - 5 b) treating said genetically modified yeast or fungi with a mutagen,
  - c) isolating resistant yeast or fungal cells, and,
  - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
- 10 14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
- 15 a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
  - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
  - 20 c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
- a) providing a genetically modified organism according to claim 10,
  - b) expressing a cDNA library in said genetically modified organism, and,
  - 25 c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
- 30 18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,
- b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,
- e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and
- f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),
20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.
22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.
23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.
24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
- 5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 28.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
- 10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428,
- 15 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
- 20 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of
- 25 the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540,
- 30 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- (d) a functional fragment of any of said polypeptides as defined in a) to c).

32. A polypeptide according to claim 31 for use as a medicament.
33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.
34. An antibody according to claim 33 for use as a medicament.
35. A pharmaceutical composition comprising an antibody of claim 33 or 34.
36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

- 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,

- (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,



- 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 5 (e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,
- 10 (f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- 15 (g) the complement of any of the nucleic acid molecule as specified in a) to f),
- 20 for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 25
- 30
- 35

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs

18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60,  
 5 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102,  
 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136,  
 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,  
 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204,  
 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238,  
 10 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,  
 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296,  
 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330,  
 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364,  
 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398,  
 15 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,  
 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466,  
 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500,  
 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534,  
 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568,  
 20 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592,  
 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626,  
 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660,  
 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708,  
 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a  
 25 functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar o any

of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24,  
 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68,  
 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108,  
 30 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142,  
 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,  
 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210,  
 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244,  
 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,  
 35 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302,

- 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 686, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in  
10 a pharmaceutically acceptable carrier.

40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically  
15 modified yeast or fungus.

41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

20 (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,

(b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells; wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said  
25 compound on a polypeptide in the same or a parallel pathway,

(c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said  
30 compound on a polypeptide in the same or a parallel pathway,

(d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,

(e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel
- 20 pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

25 43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

5 44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- 10 (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

15 45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in  
20 frame with a reporter gene,
- (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

25 46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide  
30 encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
- 5 59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
- 10 60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
- 15 63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating an/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 25 66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
- 30 67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.



68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
69. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 36 or a human homologue thereof or an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.
71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
72. An expression vector comprising a human homologue of a nucleic acid as defined in claim 36.
73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.
75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.
76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.
77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.
78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.
79. A polypeptide encoded by a nucleic acid of claim 77.

**Figure 1:**

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGGATATTAAGTAGTCATGTTGTAATCTCTGGCCTAAGTATACGTAACGAAAATGGTA  
GCACGTCGGGTTTATGGCCCCCAGGTTAATGTCTTCTCTGAAATTCCGCATCACTTTGAGA  
AATAATGGGAACACCTTAACGCGTGAGCTGTGCCCCACCGCTTCGCCTAATAAAGCGGTGTT  
CTCAAAATTTCTCCCCGTTTTTCACGATCAACGACCCCATCTAGTTCTGGTAAAATUGCGC  
TTACAAGAACAAGAAAAGAAACATCCCCGTAATGCAACAGTGAGACACTTGGCGTCATAT  
ATAAGGTTTTTGGATCAGTAACCGTTATTTCACCATAAACACAGGTTTTTAAATATATTATT  
ATATATCATGGTATATGTGTAAAATTTTTTTCTGCTGACTGGTTTTGTATTATTATTACCT  
TTTAAAAATTTTACTTTCTTCTGTAAATTTTTTCTGATTGGCTCTATACTCAAACCAAC  
AACAACCTTACTCTACAACATACTCTCTGCCCCGAAAAGAAACCAGCTTCCAAAGCTC  
CAGCTGAAAAGAAAGCCAGCTGCCAAGAAAACATCAACCTCCGTGGATGGTAAGAAGAGAT  
CTAAGGTTTGAAGGAGACACCTATCCCTCTTATATTTTACAAAGTTTGAAGCAACATCAC  
CAGACACTGCTATTTCOCAGAAAGTCTATGTCTATTTTGAAGTCTTTCGTCAACGATATCT  
TTGAAAGAATTGCTACTGAAGCTTCTAAATTCGGCGCTTATAACAGAAATCCACTATTT  
CTGCTAGAGAAATCCAAACAGCCCTTAGATTGATCTTACCTGGTGAATTGGCTAAACATC  
CCGTCCTCGAAGGTACTAGGCTCTTACCAAATACTCCTCCTCTACTCAAGCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

MSSAAEKKPKASKAPAEKKPAARETSTSVDGKKRSKVRKETYSSYIYKVLKQTHPDTGISQ  
KSMSILNSFVNDIFFRIATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTR  
AVTKYSSSTQA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAGAATTATGGGCATATTGACCTTCTCCGGTTTCCTCCCGC  
GCTCTCGTATCCCTCTGCATTTCACCTCCAGCAAGCGCTCCACTATCTCTATATCTTTAC  
CAGTAAAACCTTTAACCTTTTGTGATATTTTGAACCTTCAACCAATTCAGTATGGCTG  
TCTATATAAAGATATTTCTGATAGCACTATGTTTATCTTTATACAATATACAAAAGCTCA  
CCCAGGACGAGCAGCGCGGCTATTTTTCTATCATTTCCGTGAATAGCGACCAACGGTCCGC  
GCTATTTTATTTTGTGCAATTTTTTTCGGGATGGGTTCCTCCCAAAAGCTAGCCCCGGA  
GATTTTTTAATTACGTAAAGAAACAAGGGCCCGGATGTTCTGCTATTGGTATATAAAGAG  
AGAACGAGACATATAGAAAATTGTGCTTCTAGATTCTCGCAGTAGGATGAGATAAATTTT  
AAAGAAGCAGGAAGCAAGGATTTTGTAGTGAATTTGTAGCGCTCAATTAAAGAGGACGG  
CATGGACCTTTCTTAAGCAGGCTCACTTGCATCACAGACGATTAAACATTTGCCACAG  
CACCTATTCTGTGCAAACATTTCAAACAAAGTGATCAACCAAGACTAAGAATAAACTCTG  
ATGCTCTTAACTTTTATGCTGACACAAAGGTTGGTAAAATCAATTTTACGACTACTTGG  
GCGACTCTTGGGGGGTCTTGTTTTTCTACCCAGCAGATTTACCCCTGTCTGCACACCCG  
AAGTCAGCGCATTCGCCAATTGAAACCCCAATTCCGACAGAGAAATGTTAAATTTGATCG  
GGCTTTTCACTGGAAGATGTTGAGTCCACGAAAAATGGATTCAAGACATCAAGGAAATAG  
CAAAGGTTAAAATGTTTGGTTTCCCAATAATTGCTGACACTTTTAGAAACGTGGCATTTCC  
TATATGATATGCTAGATGCCGAGGATTCAAAAATATCAATGATGGGTCACTGAAGACCG  
TGAGGTCTGTCTTCGTCAATCGATCCCAAGAAAGATTAGACTGATTTTTACCTACCCCT  
CCACCGTCGGAAGAAACACTTCTGAAGTGTAAAGGGTAATCGACGCCCTTGAATTGACTC  
ACAAGCAAGGGCTAGTAACCTCAATTAATTGCGACCCAGCTGACGATGTCATTATTCCTC  
CCTCTCTCTCAATGATGAGGCGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCTT  
ATTTAAGATTCAACCAAGTGGAAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MPSRICSAQLKRTAWTLPEKAHLQSQTIKTFATAPILCKQFKQSDQFRLKNSDAPNFDA  
DTTVGKINFYDYLGDWSWGLFSHPADFTPVCTTEVSAFAKLKPEPDKRMVKLIGLSVEDV  
ESHEKNIQDIKRTAKVKNVGFPITGDTFRNVAFLYDMVDABGFKNINDGSLKTVRSVFVI  
DPKKKIRLIFTYPSTVGRNDSSEVLRLVIDALQLTDKEGVVTFPINWQPADUVCIIPPSVSNDE  
AKAKFGQFNEIKPYLRFLKSK

2/251

YBR089C-A, 800 bp, CDS: 501-800 (SEQ ID NO 47)

TTTTFTAGCTGGCGGGCAACTATAAAGTACAGCAAGTGAGGTTGAGGCAATACCTGGGAG  
 TTTACACTATGGGAGACAGCTCCTAACACCAAGCAGAAAAACGACTTTTTCGCAAGTAT  
 GTAAGGCGCTGGGTGAGUCCAGCGGACGAGGATGSEUTTAATAAGAAGGTACAGTTTAGC  
 ACAGCTAGAACAGCATAACCTAAGGGCAACTCTGCTTTTCCGAGAACTTAAAGAGGGG  
 TAGACAATGATGGTAATCTTATAAACCAGGCTACAAAGAAGGTTGTAGCAGCAAGGAAGAT  
 GATATTTTAAATACGCTTCAGGTGAAATGAATAGCCGCCCATACCGGCATGCTCAACTTG  
 TAACTCAGGACTCTAGCTTTCTACTGTACTATCCTCTAAAGGACTGCTGTCTGTGCAAC  
 CCTTCTCTTTGTTTATCATAGCGCACGACAAGAGTACTAACTAATTAACCTTAGAACAATA  
 ACATATATAAACTAGCGCTATGGCCGCAACTAAAGAAGCAAAAGCAACCAAGGAACCAA  
 AGAACAGGACCAACAGGAGAAAGAGCATCCTAACGCCCTTAGGACCCGGTTGTGAGCTT  
 ATATGTTCTTTGCTAATGAAAACAGAGACATTGTCCGTTCGAGAACTCTGACGTAACTT  
 TTGGCCAAAGTAGGCAGAAATATTGGGTGAGAGGTGGAAGGCCCTTAAGTGTGAAGAAAAGC  
 AACCTTATCAATCTAAGGCTCAACGACACAAGAGAGATACGAATCTGAAAAGGAATTGT  
 ACAATGCTACACGTGCTTGA

YBR089C-A, 99 aa (SEQ ID NO 48)

MAATKEAKQPKPKKRTTRKKLPNAPKRRLSAYMFFANENRDLVRSENPDVTFQGVCRZ  
 LGERWKALTAEEKQPYESKAQADKKRYSEKELYNATPA

YBR149W, 1535 bp, CDS: 501-1535 (SEQ ID NO 57)

TTGCGAAACATCAACTTCTCCTTAATCGACCAACTGACAATGAAGTTTCAGGTTCACAGAG  
 AGATCTGCCAATTTCCAGAAGGAAACAAATAGGTGGGTAAAGAATGATGCTACCAAGATAAG  
 GATAACTATATCAAAACACTGATGCAACATTTGAAGAAAAAGAGAGTACCAAGTTGATA  
 AAAGACAGCAAGAATGGCGCTCCACCTTAACATCTTAACAATTTGCTTTACTGAAAAATG  
 CTACTAGTATATAATCATTAAGTAICTAATCATCACTCAATAAAAATATTATAGATCGCT  
 TAAAAACTCCTTTATTCGGATTATAAATCCACCAAAAGCCGCTCTACCTTACCTCCGC  
 CTGCAAAAATTATATAATAAAGTGAGCCTCGTAATACAGGGCTAAAAAGGAAGAGGGG  
 GGATATCAAGCATCTGGACTTAATTCGCACTACTCTCCGCCCTCAATTGAATAAAGCCTCTT  
 GATTTTAAATCAACTGCTATCATGTCTCTTTCAGTAGCCTCAACCGAAAAACATAGTGGAAA  
 ATATGTTGCATCCAAAGACTACAGAAATATACTTTTCACTCAACAATCGTCTTTCCTATCC  
 CAGCACATGGGTTTGGGACAGCAAACTCTCAGCAAAAGTTAGCTGAAACAAAACAGCCCG  
 TAAAAGCTGCAATCAAGCTGGATAAAGGCACAATGATAUTGCTTGGGCTACGAGACAG  
 AGCCATTCGTAGGTGAAGCCATCAAGGAGTTAATTAGAAGATGGATUTATCAAAAGGCCACC  
 ATCTTTTCATAACCACAAAAGTGTGCGCGGTTCTATGGGACGAAGTGGACAGATCATTGA  
 ATGAATCTTTGAAAGCTTTAGGCTTGGAATACGTGACTTCTCTTGCACATTGCGCCGC  
 TATGTTTTGAAAAGATTAAAGACCCCTAAGGGGATCAGCGGACTGGTGAAACACTCCCTTTC  
 ATGATCTCTGAAAAACAATCTATGCTGCGGACGGTGACTATTTAGAAACTTACAAGCAAT  
 TGGAAAAAATTTACCTTGATTCCTAACCATCAATCGATGAGAGAGGATTTGGTGTCTCAAAAT  
 TTTCCATTGAGTATTTGCAAGCTCTCATTAAGGAATGCAGAGTTAAGCCCAACGGTGAACC  
 AAGTGGAAACTCACCTCACCTTACCACAAATCGAACTAAGAAAAGTTCTGCTTTATGCACG  
 ACATTCCTGTTAACAGCATACTCACCATTAGGTTCCCATGGCGCAACCAACTTGAAATCC  
 CACTAGTGAAAAAGCTTGCCGAAAAGTACAATGTCAAGGAAAATGACTTTGCTAATTCTTT  
 ACCATATTAGACAAGGCATCTCGTAATTCCGAGATCCTTGAAATCCAGTTAAGGATTTCTCT  
 CGAGTATTCGAATTCGCATCTTTGACCAAGGATGAATTACAAGAGTTGAACGACTTCGGTG  
 AAAAAATACCCAGTGAGATTCTCGATGAGCCATTTGCAGCCATCTTTCCAGAGTTTACTG  
 GAAACGGACCAAACTTGGACAATTTAAAGTATTAA

YBR149W, 344 aa (SEQ ID NO 58)

MSSSVASTENIVENMLHPKTTETVYFSLNNGVRIPALGLGTANPHEKLAETKQAVKAAIKA  
 GYRHIDTAWAYETEPFVGRAIKELLEDGSTKRECIETTKVWPVLWDEVDRSLNESKAL  
 CJFYVHLLQHWPLCFEKIRDPXGISGLVKTFVDESGKITMYAADGPLYETVKQLEKLYLD  
 PNDHRVRAIGVSNFSIEYLERLIKECKVKFVNVQVETHPHLPQMELEKFCFPHDILITAY  
 SPLGSHGAPNLRIPLVKKLABKYNVTGNLLISYHROGTTIVIPRSLNPVRYSSSIFAS  
 LTKDELQELNDFCEKYPVRFTDRPFAILPEFTGNNGPNLDNLKY

3/251

YBR289W, 3218 bp, CDS: 501-3218 (SEQ ID NO 63)

GATACGATCTATAGTCTCTAAAAAGGTAAAAACAATCAAGCGGGCTTTTGACTTCGAAGT  
GGAGGCTAAGCACCAATTAATTTGAGCTTATTTATAACTGAGAAATACTTATAGACCTCTAA  
ATCTCTTCCAAACCATTTGAATGGTCTAAATAATCATCACTACTGCTATCTTCGAGCAATTG  
AGGACATGTGGTACGAACCGGATTCACAGCTCCCTTGAAGGAGGAGCTGTTCACCTAA  
AAGATACTCGAAAATAAGTTTGTCTCTTTGTATCAGTGATATAGAAATGACAAATACATCTFA  
TTTTGGTTGGGTGGTAAGGTTTACAGCCTCTGTTGTTGCCCAAGTCCCTGTTATCGCCAA  
CTTTAAATAAATCTCTTCTTGTCTTTGACCAAAAATTTCAATTTTCGTCCGATTTAAAA  
GAAACTGAAATTTCAACATAAACACCAAAACAAAGCATCATCAAGGGAACATATAGTAA  
ACAACCTACACAAAAGCAACAATGAATAATCAGCCGAGGGTACCAACAGCGTTTCCAAATA  
GTATTGGAATATATTTAGCAACATTGGAACCTCCATCTTTTAACATGGCGCAAAATTCGCG  
AACAGCTGTATCAGAGCCTCACACCACAACAAATTCAGATGATTGAGCAACGACACCAAC  
ACTTACTCAGGAGTCTCTACACACACAAACAACAACAACAACAACAACAACTTCAACCGCCAC  
CGCAAAACCCATCAATCTCCACCCCTCTCTCCGCAACAATCTCAACCCATTGCTAATCAAT  
CAGCGACTTCTACCCCTCTCTCTCTCTCCAGCACCACTTACATCCCCAAATTTGGTC  
AAGTCCCTTAGCTCCAGCGCTTATTAATTTGCCTCCACAAATTCCTCAGTTACCTTTGG  
CTACACAGCAACAAGTTTTGAACAAGTTGAGGCAGCAGGCCATAGCAAAAAATAATCCAC  
AGGTTGTCAATGCAATTACTGTTGCACACACAAGTGCAACGCCAAATTCAGCAGCAAA  
ACGCACACCAAAACGGCACAACTCAGCTAGAACAGCAGAGGCAATTGCTGCTTCAGCAGC  
AACAGCAGCAGCAACTTAGAAACCAATACAGCTACAAACAGCAACAACAGTTTAGGCATC  
ATGTGCAAAATACAACAGCAGCAACAAAAGCAACAACAACAGCAGCAGCAGCATCAGCAAC  
ACAACAACAACAACAGCAACAGCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC  
AGCAACAACAACAACAACAGCAGCAGCAGCAGCAGCAGCAGCAAGGACAAATACCGCAAT  
CTCAGCAAGTTCTCAAGTTAGATCCATGAGTGGACAACTCCACCAATGTTTCAGCCCA  
CTATTTGGCCAACTTCTTCAATTTCCAAAATTAACCTTACCCAAAGTACCAAACTATTCAAAT  
ACGATCCACCAGAAACCAAGCTACCATATCCAACTTATTTGTCAGACAAAAGCAGATA  
CGGATACTTTGTTGTACGAACAAATATCCAGCGTGATAAAATTAACAAATATTCGCTAA  
TAAGAGAAACCAATGGTTACGATCCGTTTAGCATTTATGGATTTAGTAATAAAGAGTATA  
TTAGTAGACTGTGGCATACTGAAGTATTATCAAGATTTGAAGAACACTAGAATGAAT  
CTATCACAAGCACTTCTCAGAAGATTCCTTCGGCAAGTATTTGGGGAAATGGTTACTCAG  
GGTATGGTAATGGGATTACGAATACAACCTACCAGAGTTATTCACAACTAGAAGTTGGAA  
ATAGGAAGCATTACCTAGAGGATAAATTAACCTCTATTAACAGGCCATGAATGAGACAT  
CGGAACAGTTAGTTCCCATAGATTGGAGTTGGATCAAGATCGTGACAGATTCTTCTCTA  
GGGACACTTCTTATGCAACAAAATGACAAGCTTATTAANNTGACACTTTCTCCAGC  
ACATGTTGCGAGATTACCGATTTGAGGACGCTACGAGAGAGCAACACATTGATACTATTT  
GTCAATCTATACAAGAGCAGATTGAGGAGTTTCAAGGAAATCCATATATAGAGTTGAATC  
AGCACCGTCTAGCCGCTGATCACTTCACAAATTAGATCAAGCTGGATTTCTCTCTGGAC  
AAAACCAATTAATCGATCAATTTGAGTGGGAGATCTCTAATAGTGATAACTGTCCAGAAG  
AGTTTTCAGAGTCCATGTGTCAAGAATTAAGAATACAGGTTAGTTTGTGACTGUCATTG  
CTCACTTCATAAGAGAGCAAGTTCAATGTATCTAATCACTGGCAGTGTAGGTTACA  
ATTTTGAATGGATCAGCGATAGAAGATGATGACATTAGAAGCAGAATGCTCCCAACGATTA  
CTCTTGAATGATGTTTATAGGCCTGCAGCGGAAGCAAAATTTTACTCCAAACCTATTAC  
ACATTTCACTGTCAGACTTAGACAGATTGGATAAAGATAAGGACAGAGACACAAGAAGGA  
AAGAAGACAAAGGTAGATCTAATAGACGTGGTATGCTGUCATTGTCCGGCACATCTGCAG  
GTAATACATCTATGAACGGCGTTCAACAACACAGTAGCAGCAGCAATGCTTCATCGTTGC  
CACCAAGGAGAGATTTTACTGCCAGATATTGCAGATATTCCAAGCACTTTGAGGACTCCAG  
TACCTAGCACTTTAATGCTGGTGGTGTGTTGACGTAGGCTCTCTGTGGAATCGTACGAAT  
TGAGAAACACAAACCACTTATAAAGCAGGCGAGATAGACCTAAGCCAGTTTCACCTGCTT  
GTTATATTAATGACCATATTCGGGCTCATTTGCTACTACTTTCTATTAATTAATGCTTGA  
AAGTTAATACAAAAGAGAGTTTCGAGCAGCGCCCAATGACACAAGTAGTGGCACCAATG  
CAATGCTTCCCACTCCCAATCCCTGAAAACCTAGCTGAATACTAACATTCCGCGCTGGTG  
TGACGATACCTTCATTCCTAAACCGGATTGCCAATCACACTGTTACTAATTCACCCCAATC  
CCACACTGCAGCCAGTAATCCAGGTGGGGCAGCTAGTAAATCGGTACCTACACCTAGTC  
TTCCTATAGCACTCCAGTAGCACCAATGATAGCCAAAGCAGATTTGTTGACTAATAGCA  
ATAATGGTAGCAGTAACAATAACACACAGAAATACATAG

4/251

YBR289W, 905 aa (SEQ ID NO 64)

MNNQPPQGTNSVPNSIGNIFSNICTPSFNMAQIPQQLYQSLTFQQQLQMIQQRHQQLLSRL  
 QQQQQQQQQTSPPPQTHQSPPPPPQQSQPTANQSATSTPPPPPA7HKI,HPQTGGVPTA7A  
 PINLPPOIAQLPLATQQQVLNKLRRQQAIAKNFQVWNAITVAQQQVQRQIEQOKGQQTAAQ  
 TQLEQQRRQLLVQQQQQQQLRNQIQRQQQQQFRHHVQIQQQQQKQQQQQQHQQQQQQQQQ  
 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQGQIPQSQQVPQVRSMSGQPPTNVQPTIGQLPQ  
 LPKLNLPKYQTIQYDPPETKLPYPTYWSDKKADTDLTLLYEQIIRQDKINKYSLIRETNGY  
 DFFSIYGFSSNKEYISRLWHTLKYQDLKNTRMKSITSTSQKIPSASIWGNFYSGYNGGIT  
 NTTTRVIPQVEVCNRKHYLEDKLVYKQAMNETSEQLVPIRLEFDQDRDRFFLRDTILLWN  
 KNDKLIKIEDFVQDMLRDYRFEDATREQHIDTICQSIQEQIQETQGNPYIELNQDRLGGU  
 DLRIKIKLDIVVGQNLIDQFEWEISNSDNCPEEFAESMCQELPLPGEFVTAIAHSIREQ  
 VHMVYHKSALLCYNFDGSAIEDDDIRSRMLPTITLDDVYRPAAESXIPTENLLQISAAEL  
 ERLOKDKDRDTRRKRRQGRSNRRGMLALSGTSASNTSMNGVHINTVAAGNASSLPPEGILL  
 PDIAIDIPRTERTFVPSTLMPGGVDVGPVSVESEYELRNTTYKSRPDRPKPVSPPCYITDHT  
 PGHSLLLSISKLPQKVNTKEEFAAAPNDTSSGTKAMLPSPESLKTKLNSNIRAGVTIPSP  
 NPIANHTVTNSFNFTLQFVIPGGAASKSVPTPSLPIAPPVAPHDSEATLLTNSNNGSSNN  
 NTQNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

TTAAGAAAATGAACGTTACTATTTCCCTCCCTCGTTT7TAGTTACATAAAAATTTACTAATCG  
 TTGGAAAATTGCGGAAGCTATCACGCGATAACTAGGTACACACGCATTATTTTATAATC  
 CCATTATTAAATAAATCCCTTATGACCCCTTTTAGTAATAACTTATTAAAGAACCTCCGGTA  
 AAATACTGTACTGCGGGGAAAGAAGGCGCTTCCCTTCTTGGAACTTAATATAAATAATA  
 AATTTGCTTAAGGGCATTAGGUUTTACTGCTTTGGCTAGCGTAU7TTCGATTUATAC  
 AATTTGCACTATTCCGGCAGCTAGTTGATACTATAACATCCTACATTTTACTTGT7TTA  
 CGTTTCATTTTATT7GAAGTTTGTAACTTTATCAGAAAGAAAACAAGAAAGGAGAAAAG  
 GAAAAGAGGGGTCAGGTTAGTATCAATAAAAAAAGAGAGTAACAACAAATACAGAC  
 TCAATTGAAGCACTATAAGAAATGCTAAAGATTGCGATAAATTACTTACTCTACCTACGGGC  
 ACATAGACCTTTTAGCCCAAGCTGT7TAAGAAAGCTCTCGAGCCAGCTTGGTCCCTAAAGCTC  
 ATATATACAGGGTCGAGGAAC7TTACCTGATGAAGTCCCTCACCAGATGAACGCTCCTC  
 AGAAACCTGAAGATATTCC7GTTGCCACTGAGAAAAGCT7GCTCGAATATGACGCTTTT  
 TGT7TCGGTG7TCCAAC7TAGGTTTGGTAATT7TCCGGCTCAATGGTCCGCCCTT7TGGGATA  
 AAACCGGTGCAATTATGGGCCAAGGGCTCT7TGAACGGCAAAGCTGCGGGGATATTGCTTA  
 GTACT7TCCAGT7TACGGAGG7TGTCAAGAAAGTACCG7TAAAGCCCTG7T7GCT7TAT7TAG  
 CTCATCAUGGAATTATCTTTTACCAC7TGGGTTATAAGAATTCA7T7GCTGAGTTAGCCA  
 GTATAGAAGAGGTACACGG7TGGCTCTCCATGGGGTGCTGGTACCC7TGCAGGACCTGACG  
 GCTCAAGAACTGCGCTCTCCACT7GAAT7TGAGAA7TGCTGAAT7TCAAGG7TAAACAT7TCT  
 ACGAAACCGCCAAAAA7CTTTCCCTGCAAAAGAGCCAAGCCCTCCACTGAAAAGAAGA  
 CCACTAC7TCTGATCGGGCTAAGACACAACTAAACCTGCAGCACCTACAACTGCAGAA  
 AGAAGGAGGACAAAGGATTAT7TATCCTGCTGTACTGTCA7GTAA

YCR004C, 247 aa (SEQ ID NO 70)

MVKIAII7YSTYGHIDVLAQAVKKGVEAAGGKADIYRVEETLPDEVLT7KMNA7PQKPEDIP  
 VATEKTLLEYDAFLFGV7PTRFGNLP7AQWSAFWDKTGGLN7AKGSLNGKAAGIFVSTSSYGG  
 GQESTVKACLSYLAHHGII7FLPLGYKNSFAELASIEV7HGGSP7GAGTLAGPDGSR7ASP  
 LELRIAET7QKTFYETAKKLFPAKFAK7PSTEKKTTTSDAAKRQTKPAAAT7TAEKKEDKGL  
 LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATCAAGGCACATTGTTAATTGAAGAAGAAC7AAGAAGAAACAAAATTAA  
 AACCGATTGACCAATATATGTCTCTGAATGCCAAGGATGGAAATTAT7TGCAGAAGATTAG  
 ACTTTTTTTTGT7TGCAGTGGGATGAGCTTGGAGCAGGAAGAATACACTATACTGGATCTA  
 AACACTACAATAGATGCA7TAAGAATATTGGCAGCCGCAAAAAGGCTTCAAGCTTACACAAC  
 ACGGTTTATTTGAAATAATATCCTTCTCGAAAGCTTTAACGAAC7CAGAA7TTTTCGAGT  
 TATTAAACTTAAATACCGCTGAACCCGAACATAGAAATATCGAATGGGAAAAA7AACTG  
 CATAAAGGCATTAAAAGACGAGCGGA7TTTTTTTAA7TAA7AATCTTAATATCATTAA7

5/251

AGATAAATAAAGTCTATATATACGTATATAAATAAAAAATATTCAAAAAATAAAAATAAA  
 CTATPATTTTTAGCGTAAAGGATGGGGAAAGAGAAAAAATAATGATCTATCGATTTTC  
 AATTCAATTCAATTTATTTCTTTTTCGGATAAGAAAGCAACACCTGGCAATTCCCTTACCTT  
 CCAATTAATTCACAAGAGCCACCCACCCAGTAGAGACATGGGAGATCTTGTCTAGTGACAC  
 CGTACTTCTTAGCGACAGTGGCAGTGTCCACCACCACCAATGATCACCCTGTTACCGACGAG  
 CAGAGCTCTTGACAACCTTCGTCTAACAAGCCCTTAGTACCAGCAGCGAACTTTTCGAAATTC  
 CGAAAACACCTGGTGGACCGTTCCAGACAATGGTCTTAGCCTTTGCCAACAGTACCAGCAA  
 ACAACTTTCTAGATTCTGGACCATTGTCTCAACCCCTTGCCAGCCAGCTTGGAAATACCTTCCT  
 TGTCTAGTGACAGTCTTGGTGTCTGGCATCAGCAGAGAAAGCATCAGCAATGATGAAGTGA  
 CTGGCAAGACGACTTCGACACCCCTTGGCCCTTGGCCCTTTCCATCAACTTTTGGAACTATTT  
 CAGCACCCAGCCCTTGTGGAAGATGGAGTCACCGATTTTCACTGTTTTTCCAAAACCTTCTTGA  
 AGGCGAAAAGCCATACCACCACCAATGATGATAGAGTCCACCTTGTCCAAACAGTTGTCAA  
 TCAATTGA

YCR013C, 215 aa (SEQ ID NO 78)

MGKEKRKKLIYRFQNSIYFFSDKKATPGNSLPSNNSKEAPPEVETWEILSVTPYFLATV  
 AVSPPPMMTVLPAAELIUTSSNKALVPAANFNSKTPGGPFQTMVLAFATVAANNFLDSG  
 PLSNPCCPAGIPSLSVTVLVLASAEKASAMMKSTGKITSFPLALAFSINFGTISAPALSK  
 MESPISVFSKTFKVKAIPPPMMIESTLSNKLIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTGCTAAATTTACTTCGAAGACAGAAGCCAGTAAATTTTGTTTTCTTC  
 ATGGAAATAGTTTCCAAAAGTTCTTAGTAATTACCATATCTTCTTGTATCTGGCGCTGC  
 GAAAGAAAGGTTAGCCGACCGGCATCACCCATAATTTGTATATATAGCAATGAAGCAACT  
 TGTTCGAAGTTTCTTTAAAGTACTTATAGTATTGAATAATATCATGTTCACTTTGATAAAAT  
 TGGGTATTTTATTTGAUATTATATACCGCTTGGACACTAATGTCTTTCAAGTTGGTGTAC  
 CTCACCTGCTTTTCAATGTACTCGCGCAAAATTGATTAGAGGAAGCCACAGTTTGGCAAGG  
 GCACATATGATAGGAAGCAGTAACCGCAAGGAAGGATAAGAACATCATTTAGGGAGTCTG  
 TGGCAGTTTAGCACATGCTTTGGACCATTAAGGCTTACCTAGAGGAGAAGAGCATATTT  
 CAGGATAAACAGACAAAATAATGACGATACAAGCGAAGCCCACTTCGAGCATATCGTATG  
 ATTGACTACATACGGCACAGCACCCGCCCTTCCATATATAACACTTCCAAAATCATCGAAG  
 ATTGGAATGGAAGACCTGCCAGCGCTTGGTCCGTGCAGAGGATTTGCCCTTCTACAGTCCA  
 AGATGGAAAGGTAAAGGTACAATATTTACCACAATAATAAATATGGGAAGCACAACTTAT  
 UTAAAGCTGATACUAGGUATGCTCTCTATTGAGTTTGGTAAATACATTCCGGTATGATG  
 GTTGGCGAATGGATGTTATAGATGTTGAGGCCCGGGAGTGCCAGCCCTTCACCGCAGTAA  
 ATAAATGGAGAAAACAUCAACACTAGTGAGGTCAAGTATACAGTTGTGGCAGAAGCCCAAG  
 TAAAGGTTACCTTAAAGGATGGCACCAACACACAGTGTGGTGGGCTAGGTACAAATTACTT  
 TCTCTCCAGAGGTGAATGTTATAACAGGTTCGAAAAAGAGGCTGTAGGCGATGCGTTAA  
 AGAAGGCGTTATTGAGCTTTGAAAAAATCATACTCGATTAATGAGACTAAGATTACAAATA  
 ATTACTATGTGATGGCTTGTATGGCTCAAAAAAATTAATAATGAAGCTAACACCAATT  
 ACAACTTATGTTCACCGACTAATACCAAGCCGACTTTTATCAAAATTGGAGGATGCTAAAG  
 CCACGCATATCAAATAA

YDL059C, 238 aa (SEQ ID NO 84)

MPTQAKPSSSISYDSTTYGTAPGLDIKEFCIIIECWNGRPASAWSVQRIGLLQSKIERVTV  
 NIYHMNKYKHNLSKLIPGHALIQFANETFGYDGRMDVIDVARECQFFTAVINNGENTN  
 TSEVKYTVVAEAQVKVTLKDGNTNTCCGLGRITLSSRGECCYNRSKKEAVGDAIKKALLSF  
 EKIILDYEQKIITNNYYVDGLYCSKKIKNEANTNYNLLSATNSKPTPTKLRDAKGTHTK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTTACGAATGGCCCTTTTTTTTTTCTTCCAGCATCATACTCTTCGCTT  
 GTCTTTTGGAAATTCCTTTTATTCTTACTTTTGACGTTTGTCTTGACCTGTGAGTCCACGGG  
 CTTTCAAGGCGGCCCTTTAAATTCCTAAGTTTGTGAACCGGCCCATGTATTTGATCTTCCCTT  
 TTACTTTGCTTCTCAACTGTACTATTTACAGTAATAATTAGTCCAAACCTTCAGATTCCTTCT  
 CGCTAAATGCTCATCTCTAAATTATCATTTATTATTCCTAATAAAATCTTAAATTTTTCAC  
 TGGTTCNGTAUGGCTCATCGUCCAAATATTACCCGCTCTTGTATGTGATCTTTTGTACTTTT

6/251

TCGGTGCCAAATGCAAAAGGGAAATCCAAGGAAAAACCATACAGGACACTACATCAGAG  
 ATANTCTTCANTTAACAGASTAGACGAATATACTGCTGGGCTCACTACCATTTTGTTC  
 TAGAGTAAACGTAGAGAAAGATGTCTAGAGATGCACCAATTPAGGCTGACAAGGATTATA  
 GCCAAATTTTGAAGGAAGAGTTTCTTAAGATUGATTGCTCTGCTCAAAATGATTGTAAC  
 CTGCTTTAGACCAACTGTTAGTGTGGAGAGAAGAAACCAACACAGCTTCAGATCTGCCCT  
 CCTCGAAAGAAGTTTGGCCAAAGATTGTAGATCTGCTAGCATCAAGGAATAAGTGGGACG  
 ACCTAAATGAGCAATTGACTCTACTCTCAAAAAGCATGGTCAGTTGAAATGTCTAATTC  
 AGTATATCATACAAAAGGTTATCCAAATATTTCAAAAAGCTCGAAATCTTTGGATTTAAACA  
 CCAGAATTAGTGTCAATTGAAACTATCAGGGTGGTTACAGAGAACAAAATATTTGTAGAAG  
 TGGAAAGAGCTAGGGTCACCAAGAGATTGGTGGAAATTAAGAAGCAAGAGGGTAAGATTG  
 ATGAGCTGCAGACATCTTCTGTAGTTACAGCTTGACACCTATCCCTCCATCGAAATGT  
 CTGAGAAAATTCAGTTTATATTAGAGCAATGGAATTGAGTATATTAAAAAGGTGATTATT  
 CCCAAGCCACGGTGTCTTCAAGAAAAATCTGAAAAAACTTTTAAAAATCCAAAATACG  
 AGTCNTTGAAGCTAGAATAATTATAATCTTCTGCTAAAAATTAGTTTGCACAAGAGAGAA  
 ACTTAGAAGTTTGGCAGTATCTGCAAGAAATTTATCAACACAGACGCCAATTAAATCAGATG  
 AGGCTAAGTGGAAACCTGTCTTATGCGACATTGTATATTTCTTAGTCTTTTACCTTACG  
 CCAATTTACAAAATCATTTAATTCACAAAATCCAGAATGATAACAACCTGAAAAAATTAG  
 AAAGCCCAAGAATCTTTAGTAAAATTGTTTACTACGAATGAGTTGATGAGATGGCCAATTG  
 TTCAAAAAAUCTATGAGCCCGTCTTAAATGAGGATGATTGGCATTGGGTGGAGAAGCTA  
 ATAAGCATCACTGGGAAGATTTCAAAAAAGGGTCATCGAGCACAAATTTAACACTCAATT  
 CCGAATACTATTCCAGAATTACTTTACTAAGATTGAATGAATTGCTGGACCTAACGGAGA  
 GCCAGACGGAAACATACATCAGTGATTTGGTAAACCAGGGCATCATATACGCTAAAGTTA  
 ATCGCCAGCCAAAATCGTGAATTTTGAAAAACCAAAAAACTCAAGCCAATTATTGAACG  
 AATGGTCACATAATGTTGACGAATATTAGAACATATAGAAACAATAGGCCATTTAATTA  
 CAAAAGAGGAAATCATGCACGGTTTGCAGCTAAATGA

YDL147W, 445 aa (SEQ ID NO 88)

MSRDAPTKADKDYSQLKEEFPKIDSLAQNDNSALDQLLVLEKKTRQASDLASSKEVLA  
 KIVDLLASRNKWDLDLNEQLTLLSKKHGQLKLSIQYMLQKVM EY LKSSKSLDLNTRL SVLE  
 TIRVVTENKIFVEVERARVTKDLVEIKKEEGKIDEAADILCELVETVYGSMESEKIQFI  
 LEQMELSILKGDYSQATVLSRKILKKTFFKNPKYESLKLEYNLLVKISLHKREYLEVAQV  
 LQEIYQTD AIKSDEAKWKPVLSHIVYFLVLSFYGNLQNDLIHKIQNDNNLKKLESQESLV  
 KLFTTMELMRWPIVQKTYEPVINEEDLAFQGEAMKHHWEDIQKRVJEHNLRVISEYYSRI  
 TLLRLNELLDLTESQTEYISDLVNQGLIYAKVMRPAKIVNFEKPKNSSQLLNEWSHNVD  
 ELLEHLETCIQLITKEETMNGIQAQ

YDR253C, 1076 bp, CDS: 501-1076 (SEQ ID NO 113)

TTTCCCCGCTAAAATAAACCACAGATGCTTTCTATGCTTCTAATCTTTTACCAATTTACCTT  
 TGTTTATTTCAATATAAACTTTAATTTACAGTCCCTATCTATTGCUUGACTGGACTAACA  
 TGCACGTGACATTTTGTGATGTTTTTGGTCCCTTACTTAGTACGCTTAGTACGCCACAG  
 TTTATATTTCTTTGACAATAATAAAGAACCTGATTGTGGGTTACAACCTGCTACACTTTT  
 AGTTTAAAAATAAGCAGGAATTAATCTTCAGTTCTGTATCATTATTATAAATAAACTATA  
 TTTGTTCTCTTTGTGCGCCCTCGGAACCTTCTTCATTACATTGACGAGGTATATATAGATA  
 TAGTAGATATACATATCTATCCATGGTATATATGTATGCACCTCGATAATTGAATAGCGT  
 TTCATGTATATGCCAAGAAATTTGTTAATAATATAGTGGAAAAAGTCAAGAGGTATTAT  
 AAATTTCAAAAAAGTACCAATGGAGGATCAGGATGCTGCATTATCAAAACAGGCTACAG  
 AAGCAATAGTGGATGTATCACTAAATATAGATAACATAGATCCTATATAAAAGAGTTAT  
 TAGAAAGGGTAAGGAATAGGCCAAAACAGGTTACAAAATAAAAAACAGCACTCATACCGG  
 CAGAAAATCGTGTGTGATATAAATAGTCAAGGCGGTATACATAAAGGTTAAAAAGGAAAAAG  
 CATTACCAAAAACACCGAAGTCCAGCAAAAAGCAAAACUCAAAGATCGTAGAAATAGTACTG  
 CTGMAAAAAGCATTTAAATGTGCGAAATGTTCTGTTCGGAATTTTCAAGATCATCAGATTTGA  
 GAAGCCACGAAAAGACACACTTCGCCATATTGCCATAACATTTGTCTCAATGTGGCAAAG  
 STTTTGC AAGGAAAGATGCATTGAAAAGACATTATGATACACTGACATGTAGGAGAAACA  
 GGACTAAAATTACTAACTGCGGGTGGTGAGGGTATCAATGAATTACTGAAAAAAGTCAAGC  
 AATCCAACATCGTTTCACTCGTCAAGATAACAACCACAATGGTAGCAGTAATGGCTGA

7/251

YDR253c, 191 aa (SEQ ID NO 114)

MEDQDAAFIKQATEAIVDVSLNIDNIDPTIKELLERVRNRQNRLLQNKKPALIPAENGVDI  
 NSQGGNIKVKKENALPKPPKSSKSKPQDRNSTGEKRFKCAKCSLEFSRSSDLERHIEKTH  
 FALFENICPQCGKGFARKDALKRHYDITLCRRNRTKLLTAGGEGINELLKKVKQSNIVHR  
 QDNNHNGSSNG

YDR276C, 668 bp, CDS: 501-568 (SEQ ID NO 117)

ACCTTTAGTTCCTTAGCATCACCAATCGCAGACATCCAACGTATCCGTGCGCGTAATCCTT  
 CTCTTNGTAGTTCGAGCACAGCATACAGAAAGAAGCCGCGCGAAGCGGTAAATGTCTTTCC  
 TCCGGCCTTCTAACCAACCAAAACCGATCTCGGAACATGGGGGGGGGAAGGTCTCTGAAAT  
 CGAAAAACCCGAGACAGCGAGAGGGATTTCGAGAAATATTACAAAGATCACTATTTACTG  
 CTCCCTTCACCTTCGCGAGTCCCTTAATAGCCGAAGATGCAATGGGTGTGGGCTCTGGGTG  
 CCTTTAACCAGGCCCTCAAAGGGGGTCTTGTTATTTTGGCATGGGCGCTCTATAAA  
 TACAAAAGAGCAACTGAGTCTTTTCTTTTTCGCAAGAGCGAAAGCAAAAAAGAGCAAAAT  
 TTACTATTCGGTTCTTCTTTTTCGCGAGTATAATACAATTCATTATACATTTTGAATAAA  
 CAGCACAGCACAAATACAACAATGGATTCCTGCCAAGATCATTAAACATTATATTATCCCTTT  
 TCTTACCACCAGTCGCGCTTTTCTAGCCCGTGGGTGGGTAAGTACTGATAGTGGATA  
 TCATTTTGACCATTTTGGCTTGGTTCCAGGTATGCTATATGCCTTGTACATTGTCTAC  
 AAGACTAA

YDR276C, 55 aa (SEQ ID NO 118)

MDSAKIINIILSLFLPPVAVFLARGWGTDCIVDIIILTILAMFPGMLYALYIVLQD

YDR377W, 806 bp, CDS: 501-806 (SEQ ID NO 127)

AATACAAGACTTGGTGGTCAGCGGAGCGCTATCCTTAGAGAAATCTATCGACCTCTCTAA  
 TATCAAGCACACCACATGGAAAGATTGGGAAAGAATCAACAAGAAGGAATTGCTTCGGGG  
 CAAAACCGAACACAAAACCTCCCTCAAAGTTTTTAACTTTTGAAGAGTTGTGGAACGGTGT  
 AGAAGCGCATATAAAATAGATCTCTTAATATATTTCTAACATCTTCTTGTAAATGTAAATAT  
 TTTAAAAGCGTTTGATCTTATTCAGGAGAGAAACCAATCATATCGAAGGATTTCTCAATAGT  
 AAGTATCCCGCGCGTGGTCTCTCGGGGAAATAGAAACGAGAAACTTCAAGTACTTGATAGCA  
 AGAAAGTGAGTGCTTGGCTTCCCCATTTTGATTATATAAGAAAGGCATTATTTTCTAGGGC  
 AAGAAAAGACATTGTTGAAATTGTTCCAGAAACTTTCAATTTAAAGTCTTTTCGTGAACGA  
 GTGGACGTCAAAAAGAAATATGATTTTTAAACGTGCAGTATCTACATTGATTCTCTCAA  
 AAGTCTGTCTTCCAAGAAATATAGGTTCGGCACCAAAATGCCAAGCGCATTGCTAATGTTG  
 TTCACCTTTTATAAGTCTTGCCTCAAGGACCAAGCAACAGCCATCAAGGCTAACACTAGAT  
 TGGCCAGATACAAAGCCAAGTACTTTGATGGGGATAATGCTAGTGGTAAACCATTGTGGC  
 ATTTTGCTCTAGGTATAATTCCTTTGGCTATTCCATGGAATATTACTTTCAATTTGACAC  
 ATCATAAAGCTCCCGAAGAGCATTCG

YDR377W, 101 aa (SEQ ID NO 128)

MLPKRAVSTLIPPKVVSSKNICSA>NAKRIANVWHFYKSLPQCPAPATKANTRILARYKAK  
 YPDGDNASCKPLWHFALGIIAPGYSMEYYFHLRHHKCAEEH

YELC39C, 842 bp, CDS: 501-842 (SEQ ID NO 141)

AGTAATTTGCTCCCATTTTGGTATACGAGCTAGCAGGACCTTTTGGCCAACTGAACATTG  
 CATATTCATCCCACTCACCAACCGTCATCGTTGGTATTATTATTATCATTTCCGCTTGAAGA  
 AAAAGAAAACGAAAAAAGAAATGGATCAACAGCGGGTTATAGCGCCCCCTATTGAATTAT  
 TTTCTCTCGTGCCTTCTCTGAGAAGGCTCTGCAGTCCCCCGGAGGGTCTTTTCCAC  
 CTCTTCAAGCTAATAACGATAACAGCGAGGGCATTTAATCAAGTTCCAACCTACTATTAAG  
 TGGCCCCAAGGGGCAAGACAAAGGCACACACATATATATATATCGTGTGTGAAGCTC  
 GACAGATTTAGATCAGAAATAGTCTCTTTTGTGTGAGGTGAAACCAAAATCAAGACTTA  
 TACAAAGAGATCACATACAGCAATTAATTCACATTAATTTAAGTAAACTTCAGTAAACCA  
 CNTTACATCA:AAACAAAACATGGCTTAAAGAAAAGTACGGGATTCAAAACAGGCTCTGTAA  
 AAPAGGGTGTCAATTCTTTAAACAGAGGTGTCAAGCAGTGTATACAAATACAAAGAGGCTC  
 CTCCTAACAAAGTTGGACCTAATTTACATGGTATTTTTGGTAGACATTTCAGGTCAAGTAA  
 AGGGTATTTCTTAACAGATGCAAAACATCAACAGAAAGTCAAATGGATGAGGATAGTA



8/251

TGTCCGAGTACTTGACGAACCCAAAGAAATATATTCCTGGTACCAAGATGGCGTTTGCCG  
GGTTGAAGAAGGAAAAGGACAGAAACGATTTAATTACTTTATATGACAAAGGCTGCCAAAT  
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESTGFKPGSAKKGATLFKTRCQQCHTIEGGPNKVGPNLHGIFCRHSCQVKGYSYTD  
ANTINKNVKWBDSMSEYLTNPKKYIPGTKMAFAGLKKRKRNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTCTAAACCTACTGCCCTTTATATTTTACGGCTTTAAATAAACCATGGACA  
ACGTGAATTGGGTAGCAATCTTTTTPAATAGAAAGTTTATTTATGTATAAUAATAATTTA  
AAGATATTCATAGTGATAAGTAATTTTAAATGAGTTTAAAGTACTACTTTTTCCTTTACCG  
CCACTTTCCCTGTACTATCAAAAAGCCAAATTCGCCATTTGTAGCCGCCACACGCATTTTG  
ATCATCAATTTACGAAATTTGCCGCACACGTCGTACCGTGATAAGCACTCTTACTATCATGT  
TTTACGGGAGTAGCAATGATGTTCAAATTTATTCGACGCTTTCTTTTCGTGAAATCGTAGTATCA  
TAGACCTTCTCTAAATGATGGAAAGCCGTAAAGAAGGAAATTCGTAAAAGTAAATTAACGAAGT  
AGTATTTAGTAAAACAGAGTTTGA AAAACCTGATAAAATCTTCAAACTCGAAGTGA AAAAGAAACA  
CAATAGAAATATTTTTCCTCAATGCTACCTTTATATCTTTTAACAAATGCGAAGGGACAAAC  
AAATGCAAATAGAAATGCAAAAACCGTGAAATTATACAAGGGATATTGACCAACGTAGATA  
ACTGAGATGAACCTTACTTTTATCTAATGTAAACCGAATATAGTGAAGAAAGCGCAATTAATT  
CAGAAGACAAATGCTGAGAGCAGTAAAGCCGTAAAATTTGAACGAAATTTTATATTAGAGGGA  
CTTTTATCAAGTTTATCAAAATGCAAGATAATATAATTGACAACGTCACGACGCAAAATTA  
ACTCCAAACAAATAACTCTATAGTAAACCGCCCTCCGCCATAAAACATACTACAACCAATAGGG  
ATTCAAACCAACAAATAGAGGTAACTACAAACAGAAAGATAATAATAACCGGCAACAGCAACC  
GCCGTCCATACCTCTCAAAAACCTGCAATTAUAAACAAACAGCAACAGCAGTAAACATTAACAACA  
GTATCAACAGTATCAATAGCAACCAACCAAAATATGAACAATGGTTTAGGTGGGTCCGTCC  
AACATCATTTTAAACAGCTCTTCTCCACAAAAGGTCCGAATTTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLVLLTNAKGQGMQIELKNGELIQGILFNVDNWMNLTLNVTEYSEPSAUNSEDNAES  
SKAVKLNELIYTRGTFKFKIKLDNIIDKVKQIINSNMNSNSNGPGHKRYYNMRDSNNNRG  
NYNPRNDNNKGNRRRYPYQNRQYNNNSNSSLNMSINSINSNNQNTNGLGGSVQIHFNSS  
SPQKVEF

>YPR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAATATTTCAACGGTGGTGCTTAATGGTTPCCCATGATATCTCTGTTATTGACTCTGT  
TCTTAAGACAGTTTTCGCTTTTCAGACCAAGGTAAGTGTCAAGAGGTTGGAAGGTACAATTTA  
CGACTATAGAGATTACATCTTGCAGTCTGCTGATGCTGCCAGGTGTGGTTA AAAAGCATTG  
ATTTATTTTAGGAAGCACCTCAGAATATATTTTCCATAGAAGCCTAAATTTAAGTATGCATT  
ATAGCCCCATGATACTTTTTPPIGACTACTTGTATTGCAATCTAATTGAACCTAAGTGG  
GCATCTCGGTCATTGGTATATGTATCACTTTTACGTAAAAAAGTAGTGGCTAATATAA  
AACATAAAATCTACAAGAAGGGTGAAGTGCTTTTCCGANTTTTGGCACTGCAAGTAATTGG  
TGCAATTTGAAATACGAGATTTTCGTTCTCTAGAGCATATAAAAATAAGGAATTAGCCCT  
ACCTATCCTTCTGTTAAATATGAGCGGAGAAACGTTTGAGTTCAACATTAGACATTTCTG  
GTAAAGTTTACCCAAATACACTTTTCCACTGATGCTACTTCAGCAGACTTGAAAAGCAAG  
CAGAGCAATTGACCCAAGTCCCAAGTGCCCGCCAAAATACATGGTTAAAGCTGGCTTGT  
CTGGCGAAGAGTCCATTA AAAATATATCCCTTAATCAACCCAGCATCCACAGTAATGCTAC  
TGGCGACTCCAGATGCTAACCTGATTTCTAAACCAAGCCAAAAGATAATTTCAATTGAAG  
ACCTTGGCGCTTGAGGCAACAAGTCAAAACATTTCTCAATTTGCTGCTTGGTTTCAAGAACTA  
TGGGCAACACCTGTTATCTGAATGCTACCTACAGGCTTTATACAGAGTGACGATTTTAA  
GGGATATGATTCTTAATTTATAACCCCTTCTCAACCTCTCTCTAACAGTGGTGCACAAGATG  
AAGAGATTCACAAACAAATCGTTATTGAAATGAAGCGTTTGTTTGA AAAATTTACAGAACTA  
AAAGTTTCAAGAGTGTMTTGGCAATTTGTTTATTA AAACACCGCTAAGAAAGCTGTATCCAC  
AATTTGCTGAACCTGATTCACAAGGTTGGCTTCTATTA AAACAAACCAAGACGCTGAGAGTGT  
TTACACAACTATTTCCATAGTATGAGTATTTGTTTGGGTGACAAATTTTCCGAAGATTTCA  
GGATTCAATTTAAACATCCATCAAAAGACACAGCTAATGATTAACGATATTACTGTAAAG

9/251

AAAATGAAAGCGATTCTAAATTACAATGTCTATATTTCTCGTACTACAAATTTTCATGAGAA  
 ATGGGCTCCTGGGAAGGTTTGAATGAGAAANTTGAAAAAGATCAGACTTGACTGGCGCCA  
 ATTCCATCTATAGCGTCGAAAAGAAAATATCAAGATTAACCAAGTTTTTTAACTGTTCACT  
 ACGTTAGATTTTTCTGGAAAAGGTCAACCAACAAAAATCTAAAATATTGCGTAACCTCG  
 TTTTCCCATTTTCAATTAGATGTTGCAGACBTGTTTACCCUCASAATACGCAGCAGAGAAGG  
 TAAAAGTTGCTGACGAACCTGAGAAAAGTTGAAAAGGAGAAAAATGAAAAGGAAAGACAGA  
 TCAAAAGGCGTAAATTTGACCCATCATCCAGTGAAAATGTCATGACACCAAGAGAACAAAT  
 ATGAGACACAAGTGGCTCTTAACGMAAGTGMAAAAGATCAATCCCTCGAAGACTATAAGA  
 AACATTTTCCCTCCAAACTTGGAAAAGGTGAAAACCCATCTTGTTGTTTATAACTTGATCG  
 GTGTCATTACACATCAAGGTGCCAATTTCTGACTCTCGACACTATTAAGCTTTTCATAAGCG  
 ACGAAGTGGACGAAAAATAATGGTACAAATTTAATGATGATAAAGTTAGCGTTGTTGAAA  
 AGGAAAAAATTGAATCTTAGCCGGTGGGGGCGAAAGTGATAGTGCACTGATCTTAATGT  
 ATAAAGGATTTGGTCTGTA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGETFEFNIRHSGKVYPITLSTDATSADLKSKEELTQVPSARQKYMVKGGUSGEESIK  
 IYPLIKPGSTVMLLGTPLEANLISKPAKKNFIEDLAPEQQVQQAQLPVGFKNMGNTCYL  
 NATLQALYRVNDLRDMILNYPNSQGVNSGAQDEEIERQIVIEMKRCFENLQNKSTKSVL  
 PIVLLNLTLRKCYPOFAERDSQCCFYKQQAEELEFTQLFHSMSIVFGDKFSZDFRQFKTT  
 IKDTANDNDITVKENESDSKLQCHISGTFNFMNGLLEGLNEXIEKRSDLTGANSIYSVR  
 KKISRLPKFLTVOYVRRFFWKRSTNKKSKILRKVVFPPQLDVAJMLTPEYAAAEVVKVDEL  
 RKVEKEKNEKEREIKRRKFDPSSEENVMTFREQYETQVALNESEKDWLEEVYKHFPPNL  
 EKGENFSCVYNLIGVITHQGANSESGHYQAFTRDFELDENKWKFNDDKVSVVEKEKIBSL  
 AGGGESDSALILMYKGFGL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTTTAATCAAGTGATGAGGCGGAAACGTGCAAGATCCATAATGAAGGAT  
 AAAAAGAGTTCCTAAAAGGGAAGTAAGGAATAACAGAGTGAAGAAACCGAAAAGACAAC  
 TTAACAAATTCGGCAACACTTTTATGGGGCCCCGCTCGCCTGTGTGCAAGTAGTATTCGAC  
 CTGGAACACGCATTTACCACGAGAAGACAGCAATAGTCCGTACAACATTAAATTAAGTTTCG  
 ACAATTCCTCGCCCTTTATAAGCCATGCTAGTGCCCAATCAACACCTTTACTTGCCCTGAA  
 GTTCCTTTTTTTCGCTAGCCCTGTAACCTTAAATAAGCCATCTAACCTTTTTTTTTCTAAAAAT  
 TTTCTTTATTACCTGTGCGCTTATTTCTTATTTCTACACATTATTTGCCACCCCATTTGAAA  
 TTGTAGCTTGTATTAAATAGCGAAACCCCAAGTATAACCGGTGGAAGTACCTATTGAAG  
 TGAGATAAGAAGCCATCGCTATGCCCCGTGTTAGCCGAATTGACCAAGTCGTTAAGCATAG  
 CCTTTGAAAACGGCGATTATGCCGCGTGTGAGAAGCTCTTGCCCCCTATCAAGATCGAAC  
 TTATCAAGAATAACCTTTTAAATACCTGACTTATCCATTCAAAATGACATCTTATTGAATG  
 ATTTGATGATTACTAAAAGGATCCTGGAAGTAGGTGCCCTTGCTAGCAACCAAACTTTTCA  
 ATTTTGACAGCTTCGAGAATTACTTCAACCAATTGAAGCTTACTACTTTAGCAACAAATC  
 ATPAATTATCTGAATCTGACRAGAATCGAAGCTGATAAGCTCTGTATTTGTTGAACCTTAT  
 TGTCTCAGAATAACACAACCAAGTTTCACTCGGAATTGCAGTATCTAGATAAACCATATCA  
 AGAAGCTTGGGAAGCGATTCACTTTTGTCTTACCCNTCAAACCTAGACAGATGGCTCATGG  
 AAGGCTCGTACCAAGAAAGCATGGGATCTTCTGCAATCTGCGTCCCAAGATATATATCAGAAAT  
 TCGACTCTTTTACCGATAACCTAAAATCAGCTATAAGAGACGAAATTGCTAAAAATACCG  
 AGCTATCCTACGACTTTCTCCCTCTCTCCAACATAAAGGCTTTGCTCTTTTTCACAACCG  
 AAAAGAAACTGAAAAATTTGCACTAGAGAGAACTGGGCTATTGTCAACTCGAAACTTT  
 ACTTCAATAACCAATCAAGGAGAAAGCTGATTACGAAGATGAATGATGCATGAAAGAAG  
 ACCAAAGACAAACATTATCGAAAAGCAATGCGATTATGCCATAAGTATTGAAAAATATTG  
 TGTA

>YFR052W, 274 aa (SEQ ID NO 158)

MFSLAEITKSLSIATFENGDYAAACEKLLPPIKIELIKNNLLIPDSIQNDIYINDLMTKR  
 ILEVGAASIQTFNFDSPENYFNQLKPYFYSNNHKLSESEKKSKEITSLYIANTTSQNNTT  
 KPHSELQYLDKHIKNLEDDSLSPYIKLDRWLMESYQKAWDIIQSGSQNISEFDSFTDI  
 LKSAIRDEIAKNTELSDYDFLPLSNIKALLFPNNEKETEKFALEARNWPVNSKVYFNNQSK  
 EKADYSEDEMMHEEDQXTNIIKAMDYAIISIENIV

10/251

&gt;YGL072C, 860 bp, CDS: 501-860 (SEQ ID NO 159)

ACTCTTTTGTCTAGGGAGTTTCTGTGCTAAGAGGTTTGTCAATGACACCGAAAAGAGGAT  
 AATAGGTAATACTTTTTGTAAGTGTAAAGAATATTAAATCGTTTTACGGGAATTGGCCCTC  
 TTCCCTATATTCTATCCGAGGTTGTGTACTGTAGCGGTTTATACTTCAACCTGTGAAAGT  
 TATCTAATATGCGAATTCTGTTTCTGCTTGATAATCTCAAGAATATACTCTCGAGCACGC  
 GATGGAGCAGAAAGGGGAGCAATGAATACTGATGAGCTTAACGATGAGGAGGCCGTTTCC  
 GTTCTCTTGATTACCCCTTTCATCCAACACTCAATATAAGTACGCCAACTTCCCTTAAAA  
 CGGCCAATGTGACACCAGTTCACCTCGGCAAGCCCTTCTCAGGCTCTCACTAGCTCGAATA  
 ACGAGAATCTTCACGACTCATCTACTTGGCATTTCCTGGGTGCAGTTCAACCTCACTCG  
 CGTCCGGCGGTGTGAGGTGCATGGGTGCCGGTATTTTTTTTAGTTCGCTCTCGGCCTTAC  
 GCGATCAGCTTCGAGAACATACTATATTAAATGATTATATACGCTATTTAATGACCTTGC  
 CCTGTGACTATTTCTTAGCTCGTTTGGGACGGCGGTGATCGTTGTACTTGTCTGGGTCC  
 TGTATTTGACTATAGCCGGTTCGGGTATTTCTCCACAAATCTTTTCTTAGCGTTCTCG  
 GCGCGGTGTCCGGCTGGGTGGAATAACTGTGCTCATTAAAGCTTGGCAGGTTATCACTC  
 ACTTTAGTGTCTTTCAGTGGCGCTGAACCTTATATCGGGGGAACUUCTTGTACTTCCCTCA  
 CTAGTGTATTGTGCTTTAG

&gt;YGL072C, 119 aa (SEQ ID NO 160)

MGAGIFFSSLCALRDQLREHTILNDYIRYLMTLPCVLFLLSSFGQAVIVVLCRVLYFDYSR  
 FRYPLHKSFLSVLCRRVGLGCITVVIKAWQVITHFSVFSOAELYIGCHPCTSIH/SVIVV

&gt;YGL080W, 803 bp, CDS: 501-893 (SEQ ID NO 161)

GAAGAAAAAGAGAAGGGGATGATCAGGAAGGAGAAATAGAACTTGAAATTATTAGAGTA  
 AAAAGAATAAAGGACAGGACGAAGATAAAGAAGACGCTTACTTGCTTCTCGAAAAACAAG  
 AAAATTATTACCCCTCAGCACTCCAATAGTATGTGGTTACTACTAATAGTAATCTTGATT  
 TTTGACCGCCTACTATCGAATTAAATATAATTTTATAACCCAGTTCTATATTGCTGGGTG  
 GTATTATAGCTTCATGGCTACTCAAATAAGTGGAGTTTCTTCTCTGGACGTGGCCTGTA  
 AASTTCTCTTTTGGGACGGGCCCCCGCTTTTAAACCGAGGCGAAATGACAAGTGCTTTCTGG  
 CAAAGAAGGAATAGCCACTACAACCTGCGGTCTCCACCTTTCTCCACCGATAATCTATT  
 AAACACTCACTTTGCCAATCAGCAAAACGTCAATACATCTACATATATACGTATAGATTTTA  
 TTGCACTGTGATCAAAAAGAATGTCTCAACCGGTTCAACGCGCTGCACACGCTCATTTCC  
 TTCAAAAATACATCAATAAAGAAACTTTGAAATATATTTTCACAACACACTTCTCGGGTC  
 CCGTAATCAATTTCCGATATCCAAATTTGCTGCTATATATGATCTGAAAAAGACCTTACAC  
 TAATCTCTGGCCCAATGACTTTTGGCTTTAGTTACCTATTTCAGGTGTTTTTCATGAAGTATG  
 CTCTTTTCAGTATCACCAAAACTACTTACTGTTGGATGCCACCTTATTAATGAAACTG  
 CGCAATTAGCTTCAAGGCTATAGGTTTCTCAAAATACACGTATTTTACAACAGATGAGGAGA  
 AGAAAGCTCTAGATAAGGAATGGAAAGAGAAAGAAAAAACTGGTAACAGTAA

&gt;YGL080W, 130 aa (SEQ ID NO 162)

MSQPVQRAARSFLQKYINKETLKYLFTTHFWGPVSNFGIPIAALYDLKKDPTLISGFMT  
 FALVTYSGVFMKYALSVSPKNYLLFGCHLINETAQLAQDYRFLKYTYFTTDEEKKALDKR  
 WKEKFKTGKQ

&gt;YGR008C, 755 bp, CDS: 501-755 (SEQ ID NO 165)

CCCAATAGTTATGAACTTAACCGAGCTCAAATAATTTAAAGATAAAAGATAAAAGATAAA  
 AGATAAAGACAAAAAGAAAATTCATAGCCCATGTTGAAGTATCCAGCGGCAAAATGTTGC  
 TATCCAACAGAAAGTACCAAGCCAGTTTCAAAAAGGTACAGAAATTAAGTGATGCTATCCG  
 TCCCACAACATAATTTTCTCCAGCGGACCAATATACGCCGACGGGGGAGGAAAACTCT  
 CAGTAAGCAATGAAGGGATAGATAATGGGGGCGCGGCTGCTAGCTTAGGCTAAGAAAAT  
 CCTTCGAAAAACAGGCGGCTTCGAGCGCAGAAAGCGAACACTTGTCAATTTGTATAGAACGAC  
 TATTTATAAGTTTGGCTTTTGTGCACTCTCTTGGCCCTAATTACCCATACCTATTGTAACTA  
 TTCTTCTGTAACTCAATTATACAAATAAAGCAACATCAACAGTAACAAACCGCTCAAG  
 TGTACAAACCAATCAGAAAAAATGACGAGAAACAAACAAGTGGACCGAACCTGAAGGAAAGG  
 CTGATCCAAAGTACTTTTCGCACACTGGTAACCTACGGTGAATCTCCAAATCACTCAACA  
 AGCAAGCTTCCGGCAAGGGTAATTTGGGGTAAGCCAGGCGATGAGATTGATGACTTAATTG  
 ATAAATGGTGAATTAACCCUAGTGTTCAGAAAGATAGAAAGAGGCTCAAAATTTGCAATCGC

11/251

ATGAACAAAAGTTTGAAAACGTCCAAAAGGAATGA

&gt;YGR008C, 84 aa (SEQ ID NO 166)

MPRTNKWTEREGKADPKYFSHTGNYGESPNHIKKQSSGKGNWGXPGDEIDDLIDNGEIPP  
VFKKDRRG5NLQSHQKFEENVQKE

&gt;YGR023W, 2156 bp, CDS: 501-2156 (SEQ ID NO 167)

TTAGATCATGGCTAGGGGATCTGGGAAGTACAATGATGTGCTCTCCCCCTCTCAAAACACA  
ACACCAGCATGAACCTAAGCCCTCATCTCGAAAGTCGAAGGTGCTCTCATTCAGCTTAATTAG  
TGGTGCCCTGTTGTCTCTCCATGAACAAGGAGCACTTAATTAATTCCTTGTTCATGAGAT  
ATCATTCTTTTCTTCCCTCTTCTTGGGCTCTTGACAGTCATCAAATCGAAGTTTCTAG  
TTTTCTCTCTTCCGCAACATCAATTTTACCTAGAAAAGTGTAGATGAAAACCGAAGGATA  
CTGCTATTTTACGTAGTAAGTACTCTTCGGTCCATATTGGGAAGACCAAGGCATAATAAGGATA  
TATTCCSAGGABATAATTGGGATATAATCTTCCATTGCTTCCGAAATTTGTTTAAACACT  
TCTAGTTTCATTTCCGGGTTCGTTTCGATCTTCGTTTCCACTTTTAACTTACTCCCACTTAGT  
ATAATATAAGTAGTTAAGGTATGGCAAGCTGCAATCCGACCAGGAAGAAGAGCTCTGCTT  
CAAGCCCTATCTATGTGGAGAACGATTTCTCATGGCGTTAACAACACTACCGCTAAGTGTTC  
TTTCCGACGAGTTGGTTCCAGCTAATAGCACAAACATCGAGCACAGCTCTCTCCATCACTT  
CGCTTTTCCGAGTTGAGTCATTTACGTCCAGTACCGATGCAACGAGCAGCGCAAGTCTTA  
CAACGCGGAGTATAGCTTCAGTATCCTTTACTTCCCTTCCGACAAAGTTCTTCACTGCTTA  
CTCTTTTCTGCAACATTATCCTCAGAACTTTTCTCTCTGTCCTATGCAAGTTTCCGCTCTT  
CAACATCGTCTGCTCTTCTTCCGAGGTTACGTCATCATCTGTCATCATCAATATCTCTCTT  
CCTCTTTCATCATCAACAATAATATCATCTCATCACTGCTCCGACATTCAGTGTGGCAT  
CAACATCTTTCGACAGTTGCTTCTTCTCACTTTCTCACTAGCTCATCTGTTGGTTATCTCTA  
CGTCTTCTCTCAACGTTTACGTTTAGTTCCGAAAGTTCAAGCTCTTTGATTTCTCTCTCAA  
TTTCAACATCCGTTTTCGACTTCTTCAGTGTACGTTCCCTCTCTTCAACTTCATCTCCAC  
CTTCTCTCTCATCCGAATTGACATCACTCTGTACTCACTCACTCTCTCTCTCTCTCTCTCT  
TCTTTTCTCTACT  
CATCTCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCT  
CATCCATATACTCGTCTTCTGTCATATCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCACTCACT  
ATTTGGCAAAAACCATTAAGTATTAATAGAAGGCCAGACCATCTCTCTTAAGTACTATA  
CCACATAAAGTATTCACCGACAGCATCCGCTCTCTCAGGAAAAAATTCACATCACTCTAG  
GCTTATCAAAAAAGAATCGTAATATTAATCATCTGTTTGTGTTGTTGTTGTTGTTGTTGTTG  
TCATCTCTAATCTCTCTAATATTTGATTTACATGTTTTGTGTTGAGCTAAAAAACGGATT  
TCATTCACTCTCTGACCGTAAAAATCTCTACAGCTTATCGTAGTAACTTTTCAACAAAATAT  
GGTATTTCTTGTCTGGGTAAAAAATTTGGTGATATCGATCCAGAGATATACTTAAACATG  
ACAACCCCTACACCCCTAAACACACTAATCTTCAAGCCCTACCAAGCAAGCAAGCAAGCAAG  
ACGCTAATGATGAAAACCTATCATCCAACTTCCATAACAGAGGCATAGATGATCAATGCT  
CACCTACTAAATCTGATCATATTTCAATGTCGATAGTAAATAGTCAAGATTAACAAGCAAG  
CAGATGAAGTAATGCACGATGAAAACATTCATCGTGTTTATGATGACAGCGAAGCTAGCA  
TCGACGAGAACTATTACACGAAACCAACCAACGGCTTAAATATCACGAAGTATTAA

&gt;YGR023W, 551 aa (SEQ ID NO 168)

MASCPNTRKKSSASSLSMWRPILMALTTLPISVLSQELVPANSTTSSTAPSTLSLAVES  
PTSTSDATSSASLSTPSTASVSFTSPFQSSSLTLLSSTLSSELSSSSMQVSSSSTSSSSS  
EVTSSSSSSSSLSFSSSSSTLSSSSSLPTFTVASTSSTVASSTLSSTSSSLVISTSSSTFT  
FSSESSSSSLISSSISTSVSTSSVYVPSSTSSPPSSSELSSSYSSSSSSSTLFSYSSS  
FSSSSSSSSSSSSSSSSSSSSSSSYFTLSTSSSSSTVSSSSYPSPSSSSGNPTSSITST  
SASSSITPASEYSNLAKTILSILEGQTLLSNYYTFTITYSFTASASSGKNSHHSGLSKKNR  
NIIIGCVVGIGAPLILILLILTYMFCVQPKKTDFTDSGKTVTAYRSNIFTKIWFLLGK  
KIGETERFSSDSPICSNNIQNFGUIDPNDLNNNNPYTFKHTNVEGYDDDDDDDDANDENL  
SSNFHNRGIDDQYSFTKSASYSMKNSMSQDYNDADVMHEDENIHRVYDSEASIDENYYT  
KPNNGLNITNY

12/251

>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2:  
880-1244 (SEQ ID NO 169)

TATAAAAAAATTCCTTSTA3ACAATAAAATAAGAAATGCCCATTTTGTAACTTAGCGAAA  
GATGCCAGTACATCCCTTTTACACCCGTCGATTAAAGGTGTTTGGGTTTAATAGGAGCT  
TTATCATATCTCTTTGATTTTTTTTCTGCTGTCTCCGGCTTGAGGGACTCACAGAGATCT  
GGAAATTTTCAGATTGTCASTGCTTAGGATGGGTGTTCAGTAGACGGTGGCCGCCGTGGA  
TGCGAAATCTCATACGTTTACACACATAGTGTTTGGAAATTAATAGTAGCAATAGCTATC  
TGCTTACTGTTTTTAAAGTAITAGCCCGTTCTCAGTGCTTCTTTTTTAAGCAATAACAACG  
GCAAGACCAAAGATATATCAAATATGGCTAAGCAATCTCTAGGTATGTTTGGAGGATACG  
AATAACGATAGAAAACATGAGTGAATTTCCGTCCACGAAAAAATGTTAACATAAAATGCA  
ACAGAACAATTAATCGAATAATGTTAAATTATTTGTAAAACAATGCTATCATCAGCAGCA  
ATGTACCTAAGCCAAAAAAGAAAAAAAAAAAAAAAAAAAAAAGAAACAGCTTTTGCAT  
ATTCAATCCAGGCATAGGGCGACTATTTAGCACTCAACGATTTTTAAGCTTCTCTATTGC  
TGACATAAATTCGGCTTTAGAATCCAATATTEAAAAACGTGAGTACCGCAGACACATAG  
AAGAAAAGTAGGAAGTTACCGTTTATATTTGATTTGTGAAATGCATACTCCGTTCGGATGTG  
GGCCAAACATAGATTTAAGTGTGGATGAAAATTTATGTGCTCATTTGTGAAAAAAGTTTGTG  
CTTTTACTAAACAAATTTTTTTATTMTTGTTTTCAATAGACGTTTCTCTCACACAGAA  
AGGCCAGAAAGGCTTATTTCACTGCTCCATCTCTGAACGTCGTGTTTTGTTATCTGCTC  
CATTATCCAAGGAATTGAGAGCTCAATATGGTATCAAGGCTTTGCCAATCAGAAGCAGACG  
ATCAACTCTTGGTTGTTTCGTGTTCCAGAAGCGTCAAGAAGGTAACATTTTCATCTGTTT  
ACAGATTCAAGTTTGTCTGTTCAAGTTGACAAGGTCACCAAGGAAAAGGTCACCGGTGCTT  
CCGTTCCAATTAACCTGCACCCATCCAAGCTTGTTATCACTAAGTTACACTTGGACAAGG  
ACAGAAAGGCTTTTGATCCAAAGAAAGGCTGCTAAATTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKIMYVSSDRNKARKAYFTAPSSSERVLLSAPLSKELRAQYGIKALPIRMDEVLLV  
VRGSKKQCEKISSVYRLKPAVQVDKVTKEKVNCAASVPINLHPSKLVITKLHLDKDRKAL  
IQPKCKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTCGAATTTATTTTGTGAAAACAGGGCTCGAAAGTGATCTCTTGCTTAGAAATATTGCGT  
TGCCGCTGGTGTCCATATCTTGGTTGCTTGTACTGCGACCGCTACTACTGTTATGTTGAT  
TTTTCCGCAATTCCCCACCGACTAAACATCCCTTTTGAAGAAACCAATAAGTTGTCC  
AATAGCATTCGAAATCTTACGCTTTTCCCTTAACCTAGACTTGCCAAACTACTGCTATTCT  
TCTTATATCGGCCAACTTGCAAAAACCCCAATTTGAATCTCCCTACCAATCTCAGCGAAA  
TTTTCTTTCACACCGATCTCATTTTTCACGTGAAATCACTAAGTTTCCTGATAAAGGTATAG  
ACGACAGTTTCCAACGGTGACCCCTTGGATCAAAATCACTGTCCTGTACGGGGAGTTTATTC  
TAATATCAAAATAACTTATTCCTCTCTCTTTCTCTCTGCTCCGAATGCCACCGCTGCTAG  
ATAGCGAATAAGTGAAACATGGTCTTGCTTCACCCCTACTCTCGCCGAGAGCTGTACAA  
GATATTTTTTACTTTTGCCATCTTATACTCATCTAATCACTGTTTCATTTTCTCTCTA  
TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTTTTCCAAAGAACTCCCTTTTTA  
CAATTCGTAAGACGAACTGAAGTATTCAGCACTATATTATACATAACATACAAAGCAAG  
ACAAAGAAACATTTTAGATCTAACATTTTACTTCAATTGTTTTTGTATTCCCTTATAATA  
AGAAAGACCTCTCTGTTAATGTGGGAGTAATCCGTCCCCTACTCGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPIILASSCTRYFLLPSYTHPNHLHFHFSISFFFFFFFFFFFFSFRRNCLFRIVKDEV  
KYSGVVYYIHTKQDKETFLDLTFYFNCFCIPYNKKDLLFNVGIVIRPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTTAGATCTAACATTTTACTTCAATTGTTTTGTATTCCCTATAATAAGA  
AAGACCTGCTGTTTAAATGTGGGAGTAATCCGTCCCTACTCGATCTTCAATAAATTGTCA  
TCTTGTATCTAAAGGAGCGCTCCAGTACTCCAATTAAGCACCACCAAGTGGGTCTAGTGT  
CGATTTTTTTTTCACGCATACGTTTGTATGTTTCTTAAATTTCCCATGATTTTTTGTGTC  
CAATGTCATATCTACAAACTCTATACGAAAGTAAAGCACTTCATCTTTTTTGCCCTAAA  
ACGGCAATATTTTAGACATTAATATAAGGGGCCCAAGGGAGAAATUGCTTAATTTTAAACTTTT

13/251

CTTTGCTCTTGAATGAAAAAGTAAATAAATAAAACTAAATCAAAAAGAAACGCCACGT  
TTGAATTTTAAAGCAAAAATTTTGTGGATTAGTAATGATATAAAATAAACCAAGTCGTT  
GGTAAGAAATTTGGTTAGGTTATGAATAGTAATGAACTGGATCTAAGAAATAAATATTTTT  
ATGAGATATTTCCGTAAGAAAAGAAAATCAGATACTTCAACCCCTACTCAGTTGTTCTCCG  
CCTCCAAAGTTCAGACAAACATCAATGAAATTTCTATCACTAACGATCAGGATGAAGATA  
GTACTGAAGATGAAAAATAGGCTTCATTGAAGGATTATACACTAGGGCAGGACACCCGCTG  
CACGGTATAGGATAGCACCCGACTGTTCTTCCCAACCAATTAAGGCATCTCCTGTCTCTAC  
ATATTTCAACCAACCTTAATTCAAGTCCACAACTCCTTCACAGGGCATCAGATTTCACCTA  
CTAATAAAAAAATTTCAATAAAATGATCGACCAGACAAGATAGAGGTAAACAGTTGCACTA  
CCACTTCATCACCCTTCCTCAAAAAGATCGAATGTFTTGGCTTCCTCAGCTAAGAAAACATT  
CATCTCCTTCACATATTATCATTTTCCAAAAACAGTGGCAGTCATATGGGGATCCAAACC  
AGCTATCTACGCCCTCCACCTCCCAAAAAGTGCAGGTCACACGATGGAGTTACACAGTTTCAT  
TCAATGSAAAACATAGTTCTTCTAGCACCTCTTCTTTATTTGCATTAGAGTCACTGAAAA  
CCCAAAATAGACGCTCATCAAACTCTTCCAAATCATCTAGTCAATATCGACGCCACTACTA  
ATCAACACCAACGTCATUATTCAAGGTCCAAATCAAGTCCCTGCTCTCTGAAUGGAATAT  
CCATGATCAAAAGGCACGCCCTTTGGTTTATCTGCACTTTTATCACTAATAGCAATTAAT  
TCAABACAGACCATCAAAATTGAGCACGCATAAAAAAGATGGGCTTACTTTACAGAGATTCTT  
TTACAGSAAACCAAGCAATTGATACTTTATGCTTGAICATAGGAAGCTTAGATCGTAAT  
TGGGCATGTTGATCGGAAAAATCGCTGCAAGCTCAAAAATTGTTCCATGACGTACTTTATG  
ACCATCGGCTTAAGACATTTCTGTAAGGATTTACAGATTTACAGATTTATCTCAGAAATCAA  
TTTAA  
TGGCAGATCAGTCGCAGAGTTCTACTTCAATTGCCAACACATTTTCTTCATCATCTTCTT  
CAGTTAATTCGCTCCGTACTTAAACTGAAATATATGGTGTFTTTTGTCCCATTTGACACAT  
GTTATTCCTCTACATGCTCTCTCGAAAAACTTTTGTACTCTATTTCTTGGCCCAATCGTT  
TGCAACACAGGCTAATTTACATTTTAAATTAGGTGGTGGTCTTAAGAGAAATATTTTCGT  
TAGCACTCGATTAAGGAGGATGATGAACGAATTTCTTGGACAAATTTCTGTACCAAGAGCG  
TATGGGAATCATTTATCCAAACACAAATCAAAAGGCAGGAGGCAATATATGAGTTGTTTA  
CTACAGAAAAGAAGTTTGTAAATCTTTTGGAAATCATCCGAGATACTTTTCATGAAGAAAT  
TATTAGAAACGAATATTATTCATCTGATGTAGGATAAAATTTGTAAAGCACGCTTTTCG  
CAGATATCAATGAATTAATTTCTGTCATAGAGAAATTTTAAAGGCTTTAGCACAAAGGC  
AATCATTAAGCCCAATTTGTCTCGAATTGCGAGATATATTTTGCAGTATCTTCTCTTCT  
TTGATCCTTTTCTGTCTATACATAGCATCAAGACCATACGCAAGTATCTAATTGAAACCC  
AAAGATCAGTTAATCCCAATTTTGTCTGTTTGTGACGATGAAGTGTCTAATTCTTCCCTCA  
GGCATGGGATCGAATTTCTTCTTATCTCAGGGTGTTTCAAGAUCTGATAGATATTTCACTGT  
TGGTAAGAGAAATAATACACTTTCTCGGACCCAGTAAACAGACAAAGATGATCTACAAATGC  
TAATGAAGTCCAAGATCTTTTAAAGGATCTAATGAAAAGGATTGATAGAGCAAGCGGTG  
CAGCACAGATCGTTATGAAGTTAAAGTGTAAAGCAGAAAAATTTCTATTCAAAATGAAT  
ACGTTAATCTGGGTTTGAATAACGAAAAAAGGAAAAATCAAGCATGAAGGTTTACTCTCJA  
GGAGGAGCTGAACAAAACAGATGGGTCTTTTTCAGGAGACATTCAAATTTTACCTACTCG  
ACAAATATGCTAATTAATTTTGAATCAAAAGCTGTAACAAAGTGGCAACACACACTGTAT  
TTACAGAGACCAATTTCCACTCCCTTTTACTGTTTATTTGTCTGGGCTGAGGATATGCCACCCA  
TAAAAAGATNTGTACACAAAACCCAAATTCCTCAGCCGGTCTGCTCTTAACCCCAATATC  
AAACGAGCAATCCCAAGAATGCTATTCTATTCGCCTATTACGGTACGAAACCAACATATC  
AAGTTACTTTGTACGCGCCGCGAGCCGGATTACAGACATTAATAGAAAAGCTGAAAC  
AAGAGCAAAAGGCTCTCTTGTATGAATAAATTAACATATTACTTTTAAAGCAAAATCGTACGTC  
AATCTTTTCACTCATACATAAATACTAATCGCGTCAACGATGTCTAATCTGTCTATGCTG  
GTAAATTTTATTTGGTTGCAACAAATATGGGACTCTTTGTCTTAAATTAATGCTACATCGA  
TCAATCAAAAACAGTGCACCTTCTGCACAAAATATCAATTTACACAGATCTCTGTATTGG  
AAGATNTAAAGTTATGATCTTCTAATTTGACAAAACCTGTACGGCTGTCTTTTAGAGG  
TAATCGACGATGCAGAAAAATCCAGATTTTCTTTTCGAAAAAAATCTTAAAGTGTATTTA  
AATATGTTGCAATGTTCAAAGACGGTTTCTGTAATGGTAAAGAAATCATTATGATTGCAAC  
ATCATTTTGTGACGCCGCACAAATTAATGATTTGTAAATCCTTTGATATTTGATTTTAAAT  
GGGTAATTTTAAAAAAAACCTAAAGGCAGGCTTGGTAGATTTTAGCGTTGATTCTGAAC  
CTCTGTCTTTTCTTTTGGAGAAATAGATCTGCAATTTGGTTGTAAAAAAATATCAAAA  
TATTAAACGTACCGGAAGTGTGTGATAAAATGGATTTAAATGAGGGAGCTTTTAAATC  
TACATGATAACAAAGTTTATAGCGAACATGTATAAAGAGACGTTCAAAGTAGTTTCCATGT  
TTCUGATAAAAAATTCAACTTTTGCATGTTTTCAGAACTCTGCTTTTTTCTCAATTAAGC

14/251

AAGGGAAGAGGGGAGGAGACAAACGGGATGTTTTCATTGCGAGGGGCAACCAGAACAGTTTCG  
CGTGTTCCTACCCCTTATATTGTGGCAATTAATAGTAACCTTATTGAAATTAGACATATAG  
AAAATGGAGAACCTGTCCGCTGTGTACTTTGGAAACAAGATAAGTATGTTAAATCATATG  
CCAAGAAGATCTTATATTGTTATGAGGATCCTCAAGGATTTGAAATTATCGAACTGTTAA  
ATTTTPTGA

>YGRG70W, 1155 aa (SEQ ID NO 174)

MNSNELDLRNKYFYEIFGKKRKSSTSTPTQLFSGSEVQTNINELISITNDEDEDSTEDENK  
ASLKDYTLGHDTGARYRIAPDCSSHQKASPVHLISTNLNSSPQSFTGQDISPTNKKISL  
NDSTRQDKGNSTTTSSPSQKRSNVLLPHVRKHSSPSLLSPSKNSGSHMGDPNQISTPPT  
FKSAGHTMBLEHSSFNKGKSSSTSSLPALSLKTQNRSSNSSMSSQYRHTNQHQHH  
SRKSSPVSLTEISMIKGTPLVYPALLSLIAIKFKQTIKLSTHKKMGLLYRDSFTGKQAT  
DTLCLIGSLDRNLCLIGKSLEAQKLPFDVLYDHCVRDSVLEIYELSSSIPMAHQSSQS  
STSIANTFSSSSSVNSLRTKTEIYGVTVPLTHCYSSSTCSLEKLCYSSISCPNRLQQQANL  
HLKLGGLKRNISLALDKEEDERISWTSNVPKSVWESLSKQQIKRQEAIVEIPTTEKKFV  
KSLEIIRDTFMKLLLETNIIIPSDVRINFVKHVFABINEIYSVNRPEPLKALAQHQSLSPIC  
PGIADIFLQYLPFFDFFLSYIASRPYAKYLIETQRSVMPNPFARFDDEVSNSSLRHGIDSF  
LSQGVSRPGRYSLLVREIHFSDPVTOKDOLQMLMKVQDLLKDLMKRIDRASGAAQDRYD  
VKVLKQKILPKNEYVNLGLNNEKRKIKHECLLSRQVNTDASPSGDIQFYLLDNMLLF  
KSKAVNKWHQHTVFQRFIFLPLLFICPAEDMPPIKRYVTENPNCSAGVLLPQYQTSNPKN  
AIVFAYYGTQQYQVTLYAPQAPAGLQTLIEKVQEQKRLIDETKHITFKQMVGGQFHSYL  
NPNRVNDVLIHAGKILLVATNMGLFVFLNYATSINQKPVHLLHKISISQISVLEEYKVMY  
LLIDKRLYGCPLDVLDCAFNADFLFRKNSKVI.FKYVAMFKDGFONCKRIIMIAHPLHAA  
QLLIVNPLIFDFNSGNFKKLNKAGLVDFSVDSFPLSFSELENKICIGCKKNIKILNVPEV  
CDKNGFKMRELLNLHDNKVLNMYKEIFKQVSMFPLKNSTFACFPELCFFLNKQGGKREET  
KGCPHWEGEPEGFACSYPIVAINSNFIEIRHIENCLVRCVLGNKIRMLKSYAKKILYC  
YRDPQGFETTELNF

>YGR132C, 1364 bp, CDS: 501-1364 (SEQ ID NO 177)

CATACATGTATCAGACGTATAGCTCCACGATTCTCAAGAATCCAGAAGCTTGGCATATT  
ATGCTATAAACCCGATGATTATGTATATTTTATGTTGTCTCCAGTAAGTGGCAGCATAAACC  
CGCCCACTCTGCCCTGCATGCTGTGAAGCAGTAATATGCCATATATACCACATATATTCC  
GCTTCCGTTTCAGGATTTCCGAAAGAGAAACTTCAGTGAATGACTATGACTACATAGTTGG  
AGTCTTAGACCATTCGAANTGACTTATTCAAGTATCAGAGATCAACACTGATGAGAATAA  
ACTCGTCTTCATGATGATACGGGTAACCGCAATGTATGCCATCAATAAATTTACAGGAAA  
GGGAGTTTGACGATCTCATGGATGCAACGGTTGAGGCTATATAATATTAAGCAGAAAGAAG  
AGGAAAAAATAAANTCCCTAAACCAACCATCAACCCCTACCAAACTTACATTCABAATCA  
ATAATTTACTTTTAGAAAAAGATGTCTAATTCTGCCAAACTTATCGATGTATCATCAACCAAGG  
TGGCGTTGCCCATTKGTATAATTGCTASCGGGATTTCAGTACTCCATGTATGATGTGAAGG  
GTGGTTCCTCGTGGTGTTATTTTCGACAGAAATCAATGGTGTAAACCAACAGGTTGTGGGTG  
AAGCCACTTCATTTCTTGGTGCTTGGCTACAGAAGGGGATCATATACCATGTGAGGACGA  
AACCAAGAGCATTTGCTACCAATACTGGTACGAAGGATTTGCCAATGGTGTCAATTGACCT  
TGAGAGTCTTACATAGACCAGAGGTCCTTACAGCTACCCGCAATATACCAAAATTTGGGTCT  
TCCATTACGACCAAAAGAGTGTACCAATCTATCGGCAATGAGGTTTAAAGTCTATAGTAG  
CTCAATTTGATGCTGCTGAGTTAATTACTCAGAGAGAAATTAATCTCAAAAAATCAGAA  
AAGAGCTTTCTACGAGGGCCAAACGAATTCGGTATTAAGTTGGAAGATGTCTCTATCACTC  
ATATGACGTTTGGTCCCGAATTCACGAAAGCAGTTGAGCAGMCCAGATTGCCACACCNAC  
ATGCCCAAGAGGCCAAATTCCTTGTCCGAAAGGCAGAGCAAGAGAGACAAGCTTCTGTTA  
TCAGAGCTGAAGGTGAAGCAGAAAGTGTGGAATTCATTTCAAAAGCCTTAGCTAAAGTTG  
CTCATGCTCTCTTATTGATTAGAAGATTAGAAGCTTCTAAGGACATCGCTCAAACATTAG  
CAAACTCATCTAACCTCTCTATTTACCAAGTCAACATTCCTGGTGGTGGTAACAGCGAGT  
CTTCGGGATGACCAAAATTCCTTGTCTTTGAACATTTGGCCGTAA

>YGR132C, 287 aa (SEQ ID NO 178)

MSKSAKLIDVITKVALFGLIASGIQYSMDVKGGSRGVI7DRINGVKQQVVGEETHFLV  
PWLQKAIIDVRTKPKSTATWGTDLQMSUTLRLVIRHPEVLQLPAIYQNLGLDYDERV

15/251

LPSIGNEVLKSIVAQFDRAELITORELISQKLRKELSTRANEFGIKLEDVSLTHMTFGPE  
 FTKAVEQKQIAQQDAERAKFLVEKAEQERQASVIRAEGEAFSAEPISKALAKVGDGLLLI  
 RRLEASKDIAQTLANSSNVVYLPQHSGGGNSSESSGS?NSLLLNIGR

>YGR135W, 1277 bp, CDS: 501-1277 (SEQ ID NO 179)

TTCTGAAC TGAATCTGAAATGTGTTAAACCTGTTTCCTC TAAAGCCTGC AAAACAAAGACGA  
 TAGTTCCCTTATTACACCTTGCTTAGT TTTATCGCTGATTACTCCTTCGACACCCAGCT  
 GAACCCCTCCAGGAAGAAGGGTGGTGTTC TACCGATGGTAAGATTTTCCCATTGCCCAAAGC  
 CGATAAGCCCTATCCCAC TTCATGAATATATAACACTCCGAGAGCTCGATGTTGGAGACAG  
 TGAGTGAGCAGTGAAT TGC TCA TGT TTTCTCTGCA TCCCTCATTTAATGACAA TTAGCCAT  
 GTAATAACATCTTTGAGGCAGTTAAATATTGCTTACCCCTGCAGGTGCGCAAAAAATTTATAG  
 AATAAAAGCATAAAAAAGATGGATATCTATGTAAATAAGGAAACATTGGCAGAGCGAAGAGA  
 ACAGACTGCTTTCTATATAAAAGTTTTTCGATCAGTCTCTATTTTAAATAATTGATTATTGGA  
 TATAGTTAGTAGTGTTAAACATGGGTTCCAGAAGATACGATTCCAGGACAACAATTTTCT  
 CUUCTGAGGGACCTTATATATCAGGT TGAATACGUCU TAGAATCCAT TCAUATGCAGGTA  
 CCGCAAT TGGGATTATGGCATCTGATGGGATTGTTC TPGCAGCAGAAACGCAAGTCACAA  
 GTACTTTACTAGAACAAGACACCTCTACCGAAAACTTTATAAGTTAAAACGATAAATTTG  
 CGGCTGGCGTTGCTGGACTGACTGCAGATGCAGAAAT TCTAATAAATAACGGCTAGAATTC  
 ACGCTCAAAATTACCTTAAAACCTATAATGAAGATATACCACTAGAAATTTTGGTGAGAA  
 GCGTAAC TATATA TAAAACAAGCTTACACCGCAACATGCTGCTTAAAGACCAT TTTGGTGTCT  
 CCTTTATCTACGCCGCTATAGACGATAGATACGGTTACCAATTGTATACATCTAATCCAC  
 CGGGAAACTATACAGGGTGGAAAGGCTATTAGTGT TGGCGCTAACACATCAGCAGCACAAA  
 CCGTACTTCAAATGGACTACAAAGGATGATATGAAAGTCGATGATGCCATTGAACTGGCTT  
 TAAAAAGCTTATCCAAACTTACCGACAGTAGCGCGCTGACTTATGACAGGTTGGAAATTTG  
 CTACTATCAGAAAGGGTGCTAATGACGGAGAAAGTGATCAGAAAGATTTTCAAGCCTCAAG  
 AGATAAAGGATATATTGGTAAAGACTGGTATTACCAAGAGGATGAAGACGAAGAAGCTG  
 ATCAAGATATGAATAA

>YGR135W, 258 aa (SEQ ID NO 180)

MGRRYDSRTITFSPEGRLYQVEYALESI SHAGTAIGIMASDGIVLAAERKVTSTLLSDQ  
 TSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKY NEDIPVEILVRRLSDIKQ  
 GYTQHGLRPFQVSVFIYAGYEDRYGYQLYTSNPSGN YTGWKALSVGANTSAAQTLQMDY  
 KUDMKYDDAIELALKK IISK ITHSSALTYDRLEFAPLRKGANDGEVYQKIFKPQEIKDILV  
 KTGITKKDEDEADEDMK

>YGR155W, 2024 bp, CDS: 501-2024 (SEQ ID NO 181)

GTGTTCTCATCCGACCCCTCTGATTCA TTTGGTGGCCATTACATTTTCCCTCAATGACACA  
 TCCCTTATTTCATAACTGATTAAAAATGGTAATGGCAGGTGATAGTAGTGGCTCACAAAA  
 CAAAATTTCTTTCTCAGUGCTGACAAAGCTTCAT TTAGCAT TCTAACTTATTCACAAACAA  
 CTTCAACTTCACCCAAGTAAGGATAATCAGCTCTGTCG TGACTGATAAAATGCTATATCCG  
 GCATATGCAGTCCACACGGCATTTACCGTTTTCACTAATTTATTGCCATNTTCTCTCCACAGT  
 TTTGCAACCGAAGCGAAGAAAAAGAAACCAACACCGAAAAATTTTTTCTCCTAAAGGTTAAA  
 GTAAAACGCAAGGCACCTCACCAGGCTTGATATATATAAACTGCTGATGCTCTTATGCCAA  
 AGTAAAAGGCAACACTTGAAGATTTTCGTTGTAGGCCACTTGCTCAAAGGACATCTAGATA  
 AATACGACGTAAGAATAAAATGACTAAATCTGAGCAGCAAGCCGATTCAAGACATAAAG  
 TTATCGACTTAGTTGGTAACACCCCATTTGATCGCACTGAAAAAATTCCTTAAGGCTTTGG  
 GTATCAAACACAAATTTATGCTAAGCTGGAACTATACAATCCAGGTGGTTCCATCAAG  
 ACAGAATTGCCAAGTCTATGGTGGAAAGACTGAAGCTTCCCGTAGAATTCATCTCTTCCA  
 GACTACTCTGATCGAACCTACTTCTGGTAACACCGGTATCGGTCTAGCTTTAATTCGGCG  
 CCATCAAAGGTATACAGAACTATCAATCACTTCCCGGAAAAAATGTCTAACGAGAAAGTTT  
 CTCTCTTAAAGGCTCTGGGTGCTGAAA TCATCAGAACTCCAACCTGCTGCTGCCTGGGATT  
 CTCCACAATCACATATGGTGTTCCTAAGAAGTTGGAAAAAGAGATTCTCTGGTGTCTGTTA  
 TACTTGACCAATATAACAAATATGATGAACCCAGAAGCTCAT TACTTTGGTACTGGTGGCG  
 AAATCCAAAGACAGCTAGAAGACTTGAATTTATTTGATAATCTACGCGCTGTTGTTGCTC  
 GTCTGTGTACTGGTGGGACTATTAGCGGTATTTCCAAGTACTTGAAAGAACAGAAATGATA  
 AGATCCAAATCGTTGGTGC TGAACCATTCGGTTCAATTTTAGCCCAACCTGAAAACCTTGA



16/251

ATAAGACTGATATCACTGACTACAAAGTTGAGGGTATTGGTTATGATTTTGTTCCTCAGG  
 TTTTCGACAGAAATTAATTGATCTTTTCGTATAAGACAGACGACAAGCCTTCTTTCAAAT  
 ACGCCAGACAATTGATTTCTAACGAAGGTGTCTTGGTGGGTGGTCTTCCGGTCTTGCCCT  
 TCACTTCGGGTCGTGAAATACGTGTGAAGACCAACCTGAAGTGAAGATGATGTTCATTG  
 TTGCCATATTTCCAGATTCCATCAGGTCCGTACCTAACCAATTCGTCCATGACGATGCT  
 TCAAAAAGAACAAATTTGTGGGATGATGACGTGTTGGCCCGTTTGAAGCTCTTCAAGCTGG  
 AGGCTTCGACGACAAATACGCTGATGTGTTTGGTAACGCTACTGTAAAGGATCTTCACT  
 TGAACCCGGTCTTTCCGTTAAGGAAACCGCTAAGGTCACTGATGTATCAACATATTAA  
 AAGACAATGGCTTTGACCAATTGCTGTGTTGACTGAAGACGGCAAGTTGTCTEGTTTAG  
 TTACTCTCTCTGAGCTTCTAAGAAACTATCAATCAATAATTCAAACAACGACAACACTA  
 TAAAGGGTAAATACTTGGACTTCAAGAAATTAAACAATTTCAATGATGTTTCTCTTACA  
 ACGAAAATAAATCCGGTAAGAAGAAGTTTATTAAATTCGATGAAAACCTCAAAGCTATCTG  
 ACCTGAATCTGTTCTTTGAAAAAACTCATCTGCCGTTATCACTGATGGCTTGAABCCAA  
 TCCATATCGTTACTAAGATGGATTACTGAGCTACTTAGCATAA

>YGR155W, 507 aa (SEQ ID NO 182)

MTKSEQQADSRINVIDLVGNTPLIALKGLPKALGIKQTIYAKLELYNPGSSIKDRIAKSM  
 VEEAEASGRHHFSRSTLIEPTSGNTGIGLALIGAIGYRTIITLPEKMSNEKVSVLKALG  
 AEIRPTAAAWDSPESHIGVAKKLEKMI PGAVILDQYNNMMNPEAHYFGTGREIQROLE  
 ELNLFONLRAVVAGAGTGSTISGISKYLKEQNDRIQIVGADPFSGSILAOPENLNKTDITD  
 YKVEGTGYDFVTQVLDFKLIDVWYKTDKPSFKYARQLISNEGVLVGGSSGSAPTAVVKY  
 CEDHIFELTEDDIVAIFPDSIRSYLTKFVDDDEWLKKNLWDDQVLAERFDSKLEASTTKY  
 ADVFGNAIVYKDLHLKPVVSVKETAKVTDVILKLLKNGFDQLPVLTEDGKLSGLVTLSELL  
 RKLSTNNNNNDNTTKGKYLKPKKIMNFNDVSSYNENKSGKKKPTKFDENSKISDINRFFF  
 KNSSAVITDGLKPIHIVTKMDLLSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEQ ID NO 207)

GACACCTTTTCCGGTGTTCGAGGGGCAACGGCGGGCTTGCAGTGAAGCTTTCACTTAAAGTT  
 GTCGTGAAAACTTTTCATTTTACCTTCTGAGTATTCATGGCTTTGAACGACCAGATTC  
 CAATTCATATGAGTTGGATGAATTGGATTCTCGAGGAGATATTAGATCGGGAGTTGAATT  
 CATCATTTTACGTATATCAACTAGTTGACGATTATGATATCTTTATAGATTTTAAGGTGG  
 CGAAACAAACATGAGACCCAGATGGAATTGATTATGGGGACATTGTTGCCCTTATATATA  
 ATTTCAATATACTAATTCAAATGATTAAAAACGTGAGGGGACACGCAACTTCGGGTGTT  
 AAGAAATATTTTGCTACATTAGATAATGGTGGAGTTTCTTGGCTTGTGGGATAAAAGCCA  
 TCAATGTGCGAGCAGCTCATCTTTACGTTTCTGTCTTCTCCCCACCTCATATGAGTGG  
 TATCTTTCTATCAGCACTTGATGAATATTCTTPTTCTCATATATCTGAAGACAAAAGAT  
 CGGCACGGCAATGCCCTGCAGCAATTTCTTCTAGTTTTTTCCGAATTTCCATTACGTATTG  
 GATCTTGTGCGCATATTTGTCACTCCTTCACGGAAAAAAGAGCACTCCGTCAGTT  
 CGGAAAAACCTTTTGACTCAATGCAACAGTGTCAATACTCTTTGCGCTGTCTCTTCAAGA  
 AAAATCAGGAGTGCAAGATATCGATTAAATCTTGGAGTTATGATGGTTAGTCTTAGTT  
 TAACTCTCTTGAAGAAGGGTTTTTTTCAAGTTGGTCAACACTCTTTAGAGGTAAAAA  
 AAAAAAAAAAAAAAGAGAATTCTTCATGTAATTTACCATGATTCTACCTTTTGCAG  
 CAAAAATGAAGATAATCCGAGCGCATGCCAAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MMILFLIYLKDKRSARQCPAFLPSFSEFPLRIGSCAHICQSFTKKEHWVTSEKLLTQ  
 CMSEVILCAVSLKKNQECKISINSLEVMMVSLSLTLKKGFFSWSFLFRGKKKKKKKKR  
 ILHVIYHDSFLQAKMKIIRAHAK

>YHR138C, 845 bp, CDS: 501-845 (SEQ ID NO 209)

CTACGAAATTAAGCAAAAAATTAATAAAATAAAAACAAAAACAAAAACAAAAAC  
 AAAAAACAAACCAAAACACATATTCTTATGATGACTCCACCAAGAGATCGTGGTGA  
 CTPTCTAATTGTTTGTCTTCAGTACAGTTACTATCAGTGTCTCTTCTTTTATATG  
 ACTATGTGATGTTACTGATACATCACGGCGCTTCCTTTATGTTTCTTTTATGTTCCG  
 TACAGGATTTATAGTTTTTACACTATATTGACTTCAATAATTTCTAATATTCAGTTCCCA  
 TTAAATTTGATTATTCCGATTAGATCGGTCCGCGCTACCAAAAGAGGCGAAGAAAAGAG

17/251

GAAAAACGCAAGTGGATAAAAGGGGTGGGGGGCAAAAGTATTTAAGAAAAAGCGATGCGATG  
 GAGAGAACAANTGGATAAGTTGCGTTTCCTCGTTATATTACAACATTTAAATCTATTGTG  
 TAACAGACTATAGCATATATATGAAGGCCAGTTACTTAGTTTTGATTTTCAATTAGCATAT  
 TCTCCATGGACAGGCATCTTCCTTATCATCATACATCGTAACTTTCCCCAAGACCGATA  
 ATATGGCTACCGAACAGAATAGCATTATGAAGATGTCAAAAAATATGTGGTGGACATAG  
 GGGTTAAAAATAACACACGAATATAGCTTGATAAAGGGCTTTACAGTGGACTTAUCTGATA  
 CCGACCAATTTTGGACGGTCTGAAAGAACCTTTGAGCTATATTGAAAGCGAGTACGGTG  
 CTAATGCAATTTGGAAAAGGATTCAAGAAGTTCATGCTCTAAACCGTGACCATTIAGTTG  
 CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)  
 MKASYLVLIPLSIFEMAQASSLSSYIVTFPKIDNMATDQNSILEDVKKYVVDIGGKIHE  
 YSTIKCFTVQLPDSQILDCLKERLSYTESYGAACNLEKDSFVHAINRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)  
 ATATCTTACGTAATCAACTTCCGTAATCAACTTCCGTAATCAAGATCTCTTAGCATCTC  
 TTGTTCAATCTTCAGACTCTACTAAGTGTTCTTACCAACCATTGGATGCTCATTACAAAT  
 GAATGAATATATTGCACGGGAACGGAAGCGGCATGCTTTTCCGTCCTCGTGCTTAGTAA  
 AGCAAAACGGAGTAGAATCGGTAAGAACTTCCTTTTGGGGTGGAAAATCATTGCCATTG  
 TTTTGGACACCTTTTCTTTTTCCTGTTATGTTTCGAGCACCGCGTTTCCTTTTGGGTACTTGAT  
 GAGGTAGCAGATTCTCTGGAACGTGCTTTCTCTCGAGGTAACCTGCCCTTGTCTCTCTGGT  
 GACTTTCTTAAAAATATAAAAGGAAAAGCATATCTCTAGTTTCGAGTTTTTTCTTCATACTT  
 TATTTCTCTTATCTTAAACCGTCCAGATATAGAATAAATCATCATATTAAGCTAAATATAG  
 ACGATAATATAGTATCGATAATGCCATTGTGTTAAGGACTTTAAGCCACAAGCTTTGGGTG  
 ACACCAACTTATTCAAACCAATCAAAATGGTAACAATGAACCTTCTACACCGTGCTGTCA  
 TTCTCTCCATTGACTAGAAATGAGAGCCCAACATCCAGGTAATATTCCAAACAGAGACTGGG  
 CCGTTGAATACTACGCTCAACGTGCTCAAAGACCAGGAACCTTGATTATCACTGAAGGTA  
 CCTTTCCCTCTCCACATCTGCGGGTTACGACAATGCTCCAGGTATCTGGTCCGAAGAAC  
 AAAATTAAAGAAATGGACCPAGATTTTCAAGGCTAATTCATGAGAATAAATCGTTTCGCATGGG  
 TCCAATTAATGGGTCTAGGTTGGGCTGCTTTTCCAGACACCCCTTGCTAGGGATGGTTTGC  
 GTTACGACTCCCGCTTCTGACAACTCTATATCAATCCAGAAACAACAACAAAAGCCTAACA  
 AGCCTAACCAACCCACAACACAGTATTAACAAGGATGAATTAAGCAATACCTCAAGAAT  
 ACGTCAAGCTGCCAAAACTCCATTGCTGCTGGTGGCGATGGTGTGAAATCCACAGCG  
 CTACCGGTTACTTCTTCAACCACTTCTTGGACCCACACTCCAATAACAGAACCGATCACT  
 ATGTTGATCCATCGAAAAACAGAGCCCGTTTCACCTTGGAAAGTGGTTGATGCAGTTGTGG  
 ATGCTACTTGGCCCTGAAAAAGTCGGTTTGAGATTGTCTCCATATGGTGTCTTCAACAGTA  
 TGTCTCTCTGCTGCTGAACCCGTATTTGTTGCTCAATATGCTTATGCTTTAGGTGAACCTAC  
 AAAGAAGAGCTAAAGCTGGCAAGCGTTTGGCTTTTCGTCCATCTAGTTGAACCTCGTGCTCA  
 CCAACCCAAATTTTAACTGAAGGTGAAGGTGAATACAAATGGAGGTAGCAACAAATTTGCTT  
 ATTCTAATCTGGAAGGGUCCAATTATTAGAGCTGGTAACCTTGGCTCTGCACCCAGAAGTTG  
 TCACAGAAGAGCTCAAGCATCTCTAGAACATCGATCGCTTACCGTAGATTTTTTATCTCTA  
 ATCCAGATTTGGTTGATCGTTTGGAAAAAGGTTACCATTAAACAAATATGACAGAGACA  
 CTTTCTACAAAAATGTCAGCTGACGGATACATGACTACCTTACGTACGAAGAAGCTCTAA  
 AACTCGGTTGGCACAAAAATTAA

>YHR179W, 400 aa (SEQ ID NO 216)  
 MPFVKDPKPKQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRAQHFGNIPNRDWAWEYYAQ  
 RAQRPCITLIITEGTFPSPQSGGYDNAPGIWSEEQIKEWTKIFKATHENKSPAUVQIMVIG  
 WAAFPDITLARDGLRYDSASDNVYMNACQEEKAKKANNPOHSLTKDELKQYVKEYVQAAKN  
 SIAAGADGVEIHSANGYLLKQFLDPHSNNRTDEYGGSIENRARFTLEVVDAAVDAIGPEK  
 VGIRLSPYGVFNMSGGAGETGIVAQYAYVLGRIFERRAKAGKRLAFVHILVEPRVTNPFLTE  
 GEGEYNGGSKFAYSIWKGPILRAGNFALHPEVVRREEVKDFRTUIGYGRFFISNPDLVDR  
 LEXGLPLNLYDRDTFYKMSAEGYIEYFTYEEALKLGNLKN

>YIL074C, 1910 bp, CDS: 501-1910 (SEQ ID NO 219)  
 TGGGAGTCTTTAGCAAGTTCCGCAAAATATCGATATCAATAGTATTGCTAAATAAACCTTT

18/251

TTTATTCOCATTEACTGTCCCTTTTATACCTGGCTGACCCCTTAATTCCCTAGCAATCTTTGCCT  
 GCACCCCGTACCAGGAAGCGTGATAGAATCGGTAGCTACAAAATTTTATGATAGTTAATA  
 AGTGCCTATTCGTTTTCATAATGTCCAGTGCACCTATCAATAATATTACACTCTTGTTCTTG  
 CCAAACTATACACAAAATGCCACATTTTTTTTCTTTACACCGAAGAATTTGGCCGTCAGCCG  
 GACAGCGCTCAGATTAAATGTGCGGCTAGATTCCTTCACCGCTGGAAACGAGTCAACCGTTATG  
 AAAACTAATGGAATCTCCGAGGTTTAATACATTAAGAAGGTTACGAGCTACTACATTAAAA  
 AATACTTTTGTCTGTTTATGCTGTAGATTATTCTAACATTAAAACTAACAAACACTGATT  
 TCGGGTATTTCCCTCCCTAACATGTCTTATTTCAGCTGCGCGATAATTTACAAGATTGATTCC  
 AACGTGCCATGAACTTTCTGCGCTCTCCTGCTGCGAGTCTCAACCTCAOCAAACCTCAGTCAT  
 TTATCAACACACTACCTCCTCGTCTAAGCATTAACAAAGCAACCAAGGCTTTAAACCTTT  
 TTTCTACTGGTGACATGAATATTCTACTGTGCGAAAATGTCAATGCAACTGCAATCAAAA  
 TCTTCAAGGATCAGGGTTACCAAGTAGAGTTCACACAAGTCTTCTCTACCTGAGGATGAAT  
 TGATTCAAAATAACAAAGACGTACACGCTATCGGTATAAGATCCAAAACCTAGATTGACTG  
 AAAAAATACTACAGCATGCCAGGAATCTAGTTTGTATTGGTTGTTTTTGCATAGGTACCA  
 ATCAAGTAGACCTAAAAATATGCCGCTAGTAAAGGTATTGCTGTTTTCAATTCCGCATTCT  
 CCAATTCGAATCCCTTACCAGAAATCGGTAAATGCTGAGATTCATTAGTTTAGCAACACAAT  
 TAGGTGAATAGATCCATTGAACCTGCATACAGGTACATGGAATAAAGTCGCTGCTAGGTGTT  
 GCGAAGTAAGAGGAAAAACTCTCCGTATTATTGCGTATGCTCACATTGGTTCCGAATTAT  
 CAGTTCTTGCAGAAGCTATGGGCCGTCATGTGCTATACTATGATATCGTGACAATTATGC  
 CCTTAGGTACTGCCAGACAAGTTTCTACATTAGATGAATTGTTGAATAAATCTGATTTTG  
 TAACACTACATGTACCAGCTACTCCAGAACTGAAAAAATGTTATCTGCTCCACAAATTCG  
 CTGCTATGAAGGACGGGGTTATGTTTATTAATGCTTCAAGAGGTAAGTCTGCTGGAACATTC  
 CACTCTGTATCCAAGCGTCAAGGCCAACAATAATGCAAGGTGCTGCTTTAGATGTTTATC  
 CACATGAACCAAGCTAAGAACCGTGAAGGTTCAATTAACGATGAACCTTAACAGCTGGACTT  
 CTGAGTTGTTTTCATTAACCAAAATATAATCTGACACCACATATTGGTGGCTCTACAGAAG  
 AAGCTCAAAGTTCAATCGGTATTGAGGTGGCTACTGCATTGTCCAAATACATCAATGAAG  
 GTAACCTCTGTCGGTTCTGTGAACCTTCCCAGAAGTCAGTTTGAAGTCTTTGGACTACGATC  
 AAGAGAACACAGTACGTGTCTTGTATATTTCATCGTAAGCTTCTGCTGTTTGAAGACCG  
 TTAATTGATATCTTATCCGATCATAATATCGAGAAACAGTCTCTGTGATTCTTCACGGGAGAG  
 TCGCTTATCTAATGGGAGACATCTCTCTGTGTTAATCAAAGTGAAATCAAGGATATATATG  
 AAAAGTTGAACCAAACTTCTGCCAAGTTTCCATCAGCTTATTTATACTAA

>Y1L074C, 469 aa (SEQ ID NO 220)

MSYEAADNLQDSFQRAMNFSQSPGAVETSEPTQSEFMNTLPRRVSTIKQPKALXFFSTGDMN  
 ILLLENVNATAIKIFKQGGYQVEFFKESLPEDELIEKIKDVHAIGIRSKRLTERILQHA  
 RNLVCIGCFICIGTNQVDLKYAASKGIAVFNSPFSNSRSVAELVIGSII SLARQLGDRSIE  
 LHTCTWNKVAARCWEVRCKFLGIIIGYCHICSQLSVLAEMGLHVLVYDIVTIMALCTARQ  
 VSTLDFVJNKSDFTLHVPATPETEKMLGAPQFAAMKDGAYVTNASRGTVVVDIPSLIQAV  
 KANKLAGAALDVYPHEPAKNGEGSFNDELNSWTSSELVSLPNILTPHIGGSTEEAQSISG  
 IEVATALSKYINEGNSVGSVNFPEVSLKSLDYDQENTVRVLYIHRNVPGVLKTVNDELSD  
 HNIEKQFSDSHGEIAYLMADISSVNGSEIKDIYEKLNQTSARVSTRLLY

>YJR037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTTCATGCTTTTTCGCGGAATTTTCCTCCACCAACGCTTCCATTCGAGACCTGTCCCGTGA  
 TGTCGAGGACACGATAGACAAATTTCTCTGCACCGTATTCTCTTTGCAAAAGACTGCAGAC  
 CAGCTTCCGTTCTTTCCTACGCCGTAGACGATGCATTTCATCGTCTCTCTTCGATAACAGATT  
 TCACCAATTGCAGGCCAATCCCACGGGAGGCACCTGTAATCAAATAACCTTGCCCATAT  
 CCGTTCTTTGACAGATTATAAGTTGTTTTCTCTCTGTTGCTGTTCCGGACAGCCCTTATTTCT  
 CTGTATTCCCTTCTTTCTTTTCTGCAATTATCGTTTCTAGCCACTTACGAAAAAGGTCAAA  
 AAGTGAAAAAAAGAGGGAAAAAACCATGAGGAACAGTATGCTCCCTTAATATCGGAAAAG  
 CAATAGTAATAAAAAACAGCATCAGAGCTTTCCACGTCTCTCTCTTCCAGCTCTCATCTC  
 GTAAAGTATTCAAGTTTATCATGTGAGAATTCTATAAGCTAGCACCTGTTGACAAGAAAG  
 GCCAACCATCCCCCTTCACCAATTAAGGGGAAAAGTGGTGCCTTATCGTTAATGTTGCCCT  
 CCAATCTGTCACCTCACTCCCTCAATACAAAGAAGTAGAGGCCCTTGTCAAAACCTTATAAGC  
 ACGAAGCATTTACCATCATCGGGTTCCCATGCAACCAAGTTTGGCCACCAAGAACCTGCGCT  
 CTGATGAAGAAATTGCCCAAGTTCTGCCAACTGAACATATGGCGTGACTTTCCCCCATTTATGA

19/251

AAAAAATTGACCTTAATCGCTGGCAATCAGGACCCTGTTTACAAGTTTTTGAAGAGCCAAA  
AATCCGGTATGTTGGGCTTGAGAGGTATCAATGGAAATTTTGAAAAATCTTAGTCGATA  
AAAAGGGTAAAGTGTACGAAAGATACTCTTCACTAACCAAACCTTCTTCGTTGTCCGAAA  
CCATCGAAGAACCTTTTGAAAGAGGTGGAATAG

>YIR037W, 163 aa (SEQ ID NO 222)

MSEFYKLAPVDKKGQPPFFDQLKSKYVLIVNVASKCG\*TPQYKELEALYKRYKDEGPTII  
GFFPCNQFGHIEPGSDEEIAQFCQLNYGVTFPIKKKIDVNGGKEDPVYKFLKSQKSGMLGL  
RGIKWNFEKFLVDKKKGKVVYERYSSLTKPSSLSSETLEELLKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATAAAGTCTGCGGGGTATTCCCTTGACACAATTTTCATATCTTCCCATATGAATACCTG  
TTAGTCCGTATCACCAAGTGTAACTGTTCTTTACCAATGAGAACATCTAGAGTCTTTCTG  
ATATGCGTAACITCTGCCTCATTAAATTTAAAAATTTCTTCATAGTAAATAGCTTATTGCT  
TTGGAGCAGATGATCGACATGTATTTTAGGAACATAAACTGCCATAAATATAATAGATCA  
GCC\*AAAAATAAGCAATGCCAATCAACAAAGTTGTATTTCCCTATCTTCCGATATTCCGAGT  
CCACCATTCAGACCTCTGGTGAGATAGTTTGCCCTGCTTTTGGCTCCCTTCCAAAGTGTGTA  
TAAAAACCTCCCTGATTTTTTTGAATACTCCCTGAATGTCTATTTTAAGTATATTTATAAA  
ATTAGTTTTAAGTTGGTGCGGATAACGAAAACCTTGATGCAAGGTAAATAAATCAAGTATAT  
CATAGAGTTCTTTTCAATTCATATGCTATACACAAGGTTTGTTACGTCACAACCTCACAAATCA  
CCAAGTTTTTCAGGCACATCGCCCAATCTTGGCTCAAAACCTTTATTTTCTGAAGGGTAATT  
TGTACACTAGTCTTTTATGACAACTGTATGGGACAGGTC\*TCGCATGCCATATATCTTAG  
AATCAAATAGCTTGAATAAGTCCAAAGAGCAAGAAGATCCCCATGCCATCGCAGAGAGCG  
ACATTGTAAATATAGTCCATGACGCTCCCAATAGAATATTCAGGCCAGCACTTGATACCT  
ATCAAGAGAAAAGAGCTTGACTTACAAAAGAGTGACCTCCATAAAGTACTTCAATCTTTGA  
CGTACAGTGATCTCTCTCAATTTTCCATTGTTTGGGGGTTTCTCATTCAACTTTTCGAGCC  
TAATAGGCAATTCACCTTAGGCAAAAAATCCATTCTTTATAAGGGGAAGTGTCTGTTAGTG  
TTTTAGGGT\*TCACCCTGTTGATTTATATGGCACTTAAACTTAGGATGAACAGCTCGAAA  
AAGCTGGAGTGCGCTTTGAGTAA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYIRLLNHSQPTK\*SGTSPNLGSKPLPSKCNLYTELLVTTLYGTGLACLYLESNSLNK  
SKEQEDPHAIADDIVNIVHDAPNRIFKPALDITYQEKELDLQKSDLHKVLHSLTYSVDSQ  
PSIVWCFLIQLSSLICNSTLSEKKSILYKGSVSVVLGFPPLIYMALKLRMKQLEKAGVRF

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

CTATATTTCAACAAGCAATGACACACCCAAAACCCAAAGCCATTAAAGTAGATGATGAACCAATG  
GGACTACAAAATGAAATATAGAAAAAATAGAAATAGGCTAGAAGATCAATTTATTATTCGC  
CCTATTCTTCCCTTATTACCTACACAAAAATAAAGCAGCAACA\*AAAGAAACRAAAACAAAAAT  
GPAACCAACCAATAAATCTATGTAAACATACTCATTTCAATTGATATTCAATTACTTG  
ACTTTTTTGTCCCTTATTTGAGGCTCCATAAGCGCGCCCATTTT\*TCCTACTCCCTTTTTTC  
GTAAATAGTAATAATGTGCTGAAAAGAACAATGAAGTAGTTATCATACATATTTCCGTCGT  
GTCCATATGAGGGGAGGTG\*CTCT\*TTCT\*TTCCATCCCTTGTCGCAACCTCCAATATATAAG  
AGCA\*TAAGCAAC\*TGATC\*TTACT\*TTAGTAATTAACCTTAOCATACCTAGCCCGAAGGAAGAA  
AAZAAATTCACCTCAACAAACATGGTTCCCTAAGTTT\*ACAAACTTTCAAACGGCTTCAAA  
TCCCCAAGCATTGCTTTTGGGAACCTACGATATTTCCAAGATCGCAAACAGCCGAATTTGTGT  
ATGAAGGTGTCAAGTGCGGCTACCGTCATTTCCGATACTGCTGTTCTTTATGGTAATGAGA  
AGGAAGTTTGGCGATGGTATCATTTAAATGGTTGAACGAAGATCCAGGGAACCATAAACGTG  
AGGAAAT\*TT\*TTACACTAC\*TAAT\*TTATGGAATTCGCAAAACGGATATAAAAGAGCTAAAG  
CTGCCATTCGGCAATGTTGAATGAAGTCTCGGGCTTGCAATACATCGATCTTCTTTTGA  
TTCAATTCGCCACTCGAAGGTTCTAAATTAAGGTTGGAACTTTGGCGCGCCATGCAAGAAG  
CGGTTGATGAAGCATTGCTTAAGTCTATAGGGGTTTCCAACATATGGGAAAAAGCACATTG  
ATGAACTTTTGAAC\*TGCCAGAACTGAAGCACAAAGCCAGTGGTCAACCAAAATCGACATAT  
CACC\*TTGGATTATGAGAC\*AGCAATTAGCACATTACTGTAAATCTAAAGGCTCTCGTCGTG  
AAGCC\*TT\*TGCCCCAT\*TTGT\*TCACGGCTACAAAATGACTAATCCAGATT\*TA\*TTAAAGTTT  
GCAAGAGGTTGGACCGTAATCCAGGTCAAATTTTGATTGCTTGGTCTTTACAACACGGTT

20/251

ATTTACCACTACCGAAGACTAAAACITGTGAAGAGGTTAGAAGGTAACCTTGCAGCCTACA  
 ACTTTGAACCTGTCAGACGAACAGATGAAATTTCTTGATCATCCTGATGCTTATCAGCCTA  
 CCGATTGGGAATGCACAGACGGCCATAA

>YJR096W, 282 aa (SEQ ID NO 234)

MVPKFYKLSNGFKIPSIALGTYDIPRSQTAEIVYEGVKCGYRHFDTAVLYGNEKEVGDGI  
 IKWLINEDPGNHKREEIFYTTKLWNSQNGYKRAKAAIRQCINEVSGEQYIDLLLIHSPLEG  
 SKLRLETWRAMQEAVDEGLVKSIGVSNYCKKHIDELLNWPCLKHKPVVNQIETSPWIMRQ  
 ELADYCKSKGLVVEAFAPLCHGYKMTNPDLLKVCKEVDNRNFGQVLIIRWSLQBGYLEPLPKT  
 KTVKRLEGNLAAYNPELSDEQMKFLDHPDAYEPTDWECTDA?

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTTCACATATCAAAAAGAASTTATGGCTTATGTGCTCTTTCTAAGTTTGA  
 CTTTATGCCAATAATTTCTCCCTAGATCGCCGCCCGTTGAAGCAGCAGAATATTTTAAGT  
 GCGCCATAAAAACCCTAGATAGAAAAGAAAGGAGAGAAACATAAACGCAGAACACCACTACT  
 TTTAAGGCGTACGCAAACTGTTGGGCTTATCTATATTGTACTATCTACCTACTTGCAACG  
 TCCTTTTACCTCCTCGATACCTACTGCTTATGCCCCGAACAATTTACATGTAACCCGCAAC  
 TGCATGCTATATACAGGATACGTTAACATAAAGGGGGCGCTACTAAACCCCTCTGGCGCA  
 GTGCAAAAATAGAAATATATGCCAAGTGGGACCTTGTATAGTTTCTGGTTTAAAGCTACT  
 CCTTCATGCCAACGCTCCTTTCTGCTATCCTTTTCGCAAAGTGGCAAGTACTGAAAACCGA  
 GAAGAATAAATAATATATGCGATGAGTTTATACTTTACGACATTATTTTATTGCTCACTG  
 TTGAGGTGGTAATGCTCTTCATCTTCGTTTTCGCCCTTGCCATTCCCGATCCGTAGGGGTA  
 TTTTATAGCACTTATACCAATTGACAGCGAAGCAGCAATATAAATCTATAATCTTTATAA  
 CCGGTTGTCTGTGTTGGGCTGTTGTTTATTGATTCATGCAAAAGCTCTCAAATTCGTGTTT  
 CATTATACCACAACGACAACAGTGGCTCAATCGGGTCATCTGCTGTAACTCCAAATACAGG  
 CACTAGCATCAAGAGCGTACAATCAAAGAAATATGTATATTTCCGGGTTTCAATTGTACT  
 TTTCTATCTCTATCCCACTCTCATGCTTNTCTCAAGACACTGCTCAAAATACCAAGGCT  
 TAATCAACGAACAGAAAACCAAAAATTGAACAAACCTTCTCTAACACCAAGAAAGACT  
 CAAATGAAGCTGATTCCACCAACCTCAAGAGGAACTAAGGAAAAAGCAAATTTCTCTGG  
 AGGGCCTACAAAAGCAAGTCAAAAACCTTGAGAAATATTTTATGAGAAGAAATCAACCTG  
 GAAATGTAGCAGCTGCTGAAGCTTCCAAGAAAGGAAACTAA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTLFLLLTVEVVMLEFVLEPLPFRIIRRGIFSTYNQLTAKQIQIKTIISTTGCLVGL  
 LFTDSWKRSGIRVSTVHNDNSGSSICSSAVTPIQALASRAVNRNMYISGFILYFSJCTPT  
 VMGIYKRLVQYQGLINEQEKQKLNKESNSKKDSEADSTKLQZELRKKQISLEGLQKQV  
 KNLEKYFDEKNQPGNVAAAASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGCTTCCTATTAGGAGCAATAAAATATAAAGCACCAGCCATAGAAAGAATCCCCA  
 TTATAAAGCCUGCTGTTTTTTCTTGATTTGGAGTTCTTACCGAACTGAGGGGAGGACGCCA  
 TGAGACGCTCTTGTGTTGGTGTGCGGCATAACCCCTTCCACTTGAATTGACGGCCTGTTTC  
 TGCACGCATTCCCTGACGACTAAGTTGCGAAGCATTTTACTGATAATATACACTCTTTGGA  
 TCGAGCCTACTTCCAGTTGGTAATTGGTGTTCACAAATTTACGCAATTATATGTTTTTAAA  
 CCAAATTCGGCTCCTTTCCCTTTTTTCTTATTGCGTGGCGTGCCGTACAGAAAGATT  
 GGCTTGGTGTGAAATCAAGAGCAAGCACANTAGATATCAACATGAACAATATACAAAAGT  
 CTCTGGCACAGTTTGAAGTGGCTTAGACAGGCTAGGGCAATTTCTGAAGCTTTACGATATCA  
 CTAGAGAAGTTATTTTGGCAATGAGAATCTACTACATCGGTGATTTTCCGCTCTGGAGGAG  
 AAAAGGCTCTAGAGTTGAGTGAAGTTAAAGACTTCTACAAATTTGGTTTCTTTGAAAGGT  
 CTAGTGTGTGGCCAGTTTATGACTTTTTTTGCTGAAACGGTCCGCTCTAGAACCTGGTCCAG  
 GACAAAGACAAAGCTATAGAAAGAGGCAACTATATTGCCACGCTTATGCTAGGAGTGAGG  
 GCATATGTGGTGTTTGATCACCGACAAACAATATCTGTGAGACAGCATACACACTAT  
 TAAACAAAATCTGGAATCAATATTTAGTCCGACATCTTAAGCAAGAGTGGGCGAGATGTGA  
 CTCAGACCAATGATGCATTGAAAAATGAAGCAACTGGACACTTACATTAGCAAAATATCAAG  
 ATCCTTTCACAGGCTGACCTATCATGAAGCTTCAACAAGAACTGGATGAGACGAAATCTG  
 TTTTGCACAAAACGATTGAGAAATGTTTTACAAAGAGGTGAAAAGTTGGATTAATTTGGTGG

21/251

ACAAATCGGAGTCATTAACGGCAAGTTCCAAAATGTTTTATAAGCAAGCTAAAAAATCCA  
ATTCCTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRIVYIGVFRSGGEKALELSFVKDLSPQGFPERSSVCGQFMFFFAETVASRTGACQQRQSIE  
FGNYIGHVVARSEGIQGVLTIDKEYPVRPAYTLLNKILDEYLVVHPKKEWADVTTNDAL  
KNKQLDITYISKYQDFSQADALMKVQQELDETAKIVLHKTIEWVLQRGEKLDNLVDKSESILT  
ASSKMFYKQAKKNSCCIIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCCTGCAATCTGTCAAGAAGGGTATGTGTATGAACATGCAAAAT  
CACACTGTAAAAATGATTCATTACCCCTGATTATGGAGTGATTTTCTTTCTCTTTTCTTTT  
ACATTTTAGTTTCATTTATTAATGCAAAATFAGAGGGGTATACAGTTGAGATTTTAACACTTTGA  
ATTAAAAAAGTGTACAGAGGAAACCGACGCAAAAAGGCTTGGTGACGCAAACTTTTCCATC  
TTTATTTTACCTCTTCAGACGGTCTTAAGACCTTTTGAACGTATCAATATAGTTTCAATCA  
TCTGTTCTCTGTTGTTCTCTCGTTACTAAGATATTAGTCAGCTCTTGAAATTTTCAACCCCC  
TATTTTATTTGTTCTTAGCGTCCAACCCCTCTCAACCCCTTTTCCATTTCTTGTATAAAGCTA  
GTTAATTTAGGTAACGCTGCTCTTACCATCACTACAGTGCTTACGAGAATTTACCCAAACC  
CTGCGCAAGATAAAATAAGAAATGTCGAAACAGTGCGCGAGTGTTACAAACGGAGCTTTCA  
AAAGACAGGTTTCTGCTCTTCAGAGAAACAATCTCTAAGCAACACCCCAATTTATAAGCCAG  
CAZACCCGAAGATATTGGTTGTATGTTTCACTTTGCATGCCCATGGGCCCATAGAACACTAA  
TTACGAGGGCTTTTGAAGGGATTACCTCTGTTATAGGATGTAGCGTAGTCCATTGGCACC  
TTGACGAGAAAGGATGGAGATTTTTCGACATGGAAAAGCAATTGGAGGACAGTGGAAGATT  
TTTTGCAACATTGCCACGATGTTGCACTGTGTTATTAGAACTGCTAAAGAGGATTCCAGCA  
AGAGCTTCGCCGAGATCAAGAATGACAGTCAAAGATTTCATGGTTGATGCTACCAATGAGC  
CTCACTATGGATACAAGAGAATCAGTGACTTATATTACAAGAGCGATCTTCAATTACTCGG  
CAAGGTTTCACTGTCCTGCTGTGGACTTAGAAACCCAAACAATTTGTTAAACAACGAAA  
GTAGCGAAATTAAGGATTTTGAATCTTACTGCGTTGATGCAATTTGTCCACGACGATC  
ACAAAGAAAACCGACCTTTGTTTCTGCTTACGTTTGAAGAACACAGATCGATGACTTTCAATTTCT  
GGGTTTACGACAGCATCAACAATGGTGTATACAAAGACUGGATTTCGAGAGAAAGCAGAAG  
TTTACGAAAGTGAAGTCAAACAAGCTATTTGAACATTTTGGACAAAGTGAGAGAAATCTTGA  
GTGACAAATATTCCAAATTCAGGCCAAATACCGTGAAGAAGATAGACAAAAAATCTTGG  
GTGAGTTCTTCACTGTGGGTGATCAATTAACAGAAAGCTGACATTAGATTGTATACAAACCG  
TCAATAAGATTGATCTGTGTACGTCCAACATTTCAAATGCAATTTTACCTCTATTAGAG  
CCGGATATCCATTTATTCATTTGTGGGTAAAGAAATTTATACTGGAATTATGATGCCTTCA  
GGTACACAACAGATTTTGACCATATCAAGTTTACACTACACGCGTTTCCACACAAGGATCA  
AACCCTTGGGAATTACGCCCTTGGGACCCAAAGCCAGATATTTCCTCTTTTATAA

>YKR076W, 370 aa (SEQ ID NO 260)

MSKQWASGTNGAFKRQVSSFRETISKQHPYKPAKGRYWLTVSLACPWAHRTLITRALKG  
LTSVIGCSVVIWHLDEKQWRFLDMKQLEDSEDFLEHWEVAVGGIRTAKEDSSKSFAEIK  
NDSQRFMVDATNEPHYGYKRISCLYKSDPQYSARFTVPVLWDLETQTIVNNESSEIIRI  
LNSSAFDEPVDHDKTDLVFAQLKQTQIDDFNSWVYDSINNGVYKTFAEKAEVYESEVN  
NVFEHLDEXVEKILSDKYSKLKAKYGEEDRQKILGHEFFTVGDQLTEADIRLYTTVIRFDPV  
YVQHFKCNFTSIRAGYDFIHLWVRNLYWNYDAPRYTTDFDHIKLYTRSHTRINPLGITP  
LCPKPDIRPL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

TCAAGGATACCTCTTGTATTCTACGTCTCTCTTCACTTTGGTTAAATCACCTTTGCCC  
TTTCACTTTGTGGTGTGCGGGETGTGTGAGTCATTAATCTTCTTTATCCCGAGAGGGGGTCT  
ACATAAATCTTGTCTTTTCACTCCAAATAAGCCAGTTAAGTCAATTTCTTTTATTACAGAA  
GGTGTACCTTCTGTTGAGTTATTTTACTCTTGTTTTGTAGTTTGTACATCTCTTTATGCT  
CTTGAATCAAAACGATAATTCCGAAGCTTATTGCAATTTAGTTCTCTTACCCATTTCTTTTAC  
AACGGGCCCGAGAAAAAGTGGAGTTGGTCCGAGGAAGCTTTCAACGGCAAGAGGAAAAAAC  
CTTCCCATCCCTCCAGCATACAATTTTTTTTTTTTCAATGCAGGCTGAAAAAATAATTT  
CACTTGATGATGTAAGAACTCATCCACITTTTATACAAAGCAAGAAAGAAACCCCAAGTCCGAG

[illegible][illegible]

AGACAAGTCTTTTCAACGACAACTCTAAGATCAGAATGATTGAAATCATGTTGCCAGTCTTT  
UGATGCTCCACAAAACCTGGCTTGAACAGCTAAGTTGACTGCTGCTACCAACGCTAAGCA  
ATAAGCGATTTTAATCTCTAAATTATTACTTAAACTTTTATAAGCATTTTTATGTAACGAAA  
AATAAATTGGTTCATATTATTACTGCACCTGTCACCTTACCATGGAAAGACCAGACAGAAG  
TTGCCGACAGTCTGTTGAATTGGCCTGGTTAGGCTTAAGTCTGGGTCCGCTTCTTTACAA  
ATTTGGAGAAATTTCTCTTAACGATATGTATATCTTTTCGTTGGAAAAGATGTCTTCCA  
AAAAAAAAAACCGATGAATTAGTGGAACTAAGGAAAAAAAAAAGAGGTATCTTGATTAAGG  
AACACTGTTTAAACAGTGTGGTTTCCAAAACCTGAAAAGTGCATTAGTGTAATAGAAGAC  
TACACACCTCGATACAAATAATGGTTACTCAATTCAAAAAGTCCAGCGAAATCGACTCTG  
CAATPCTCAAGACAAGCTAGTTTGTCTGATGATTTCTACGCCACTTGGTGGCGTCCATGTA  
AAATGATTGCTCCAATGATTGAAATTTCTCTGAACAATACCCACAAGCTGATTTCTATA  
AATTGGAATGCTGATGAATTGGGTGATTTTTCUACAAAAGAATGAAGTTTCCGCTATGCCAA  
CTTTGTTCTATATTCAAGACCGGTAAAGGAAGTGCAAAAGGTTCTTGGTGCCAACCCACCCG  
CTATTAAAGCAAGCCATTGCCCTGCTAAGCTTAA

MVTQFKTASEFDSAIAQDKLVVVDYFATWCGPCKMTAPMIIEKFSRQYPQADPYKLDVDEL  
GDVAOKNEVSAMPTLSLEKNGKEVAKVVGANPAAIKCAIAANA

AACTACTGGGGATATATTTTGAGATTTACCACTAGTAGATACGGTGGTGTAGATACGTATGAT  
TCCATCTTGACGGACCAATCCACGATCATGGAACCTTTTAGATAAACGGTGTGCCATTTCA  
CTTCCAGTACTGTTTCGATATATGACCGCTAAAGAACGTGATCATCATCCCGATTCTTATCAA  
GATTAACAATCACGAACCACTGGAGTCAATTAATATTAAAAAATATGTTGATTGT/ATAA

23/251

AGGGGTGGGATCGCGGAAATTCATGCUCTACAGTAGAAGCGGTTGTTGCACAAATGAATT  
 AAATCTTTTATCTCCAACTCAAACTATCCGATAGATGCATAAATATCTCCAGCTTCTA  
 AACAGCACGGAGTGATGATRAATAAGGCATATATGTATATATATATCTATGTGCATATGCA  
 CGTCCTTTTAAACTCAAATACAAATTCCTAGTAAATCCTTTGTTGACACACGTCGG  
 AACAACTCAGGACGGACTTAATGGATATGCTTCATAATAAATGTAGTGAATGCTATCAAAA  
 GCACCTCCAAATAGCAATTGAGTAATGAGGTAGACAAACAAAATTCGAATACCATGACC  
 TCGGGAACACCGGATTTCTGAACTATTTGAGATGGAATCTCAAGATAATAATGATAGCA  
 TAGAGGATTTCTTGTCTTTAATATAAATTTAACCCAGGAGGTTCAGTTTCGAGAACCAAA  
 GACAATAAGACACACGAAAAACACAAAGAAGCATAACCCATTCTATGTACCGTCAGAGG  
 TAGTCCGAGAGATGGTCAAGAAACAGCATTGAATGGCAGAATATAG

>YLR053C, 1GB aa (SEQ ID NO 272)

MDMLHNKCSDAIKSTSNLSNEVDKQKLQYDDLGNITGFSELFEMESQDWNDSIEEFLFF  
 NINLTQEVFENQRQYEHKKTKKHNFYVPSFVVRVMYKHHALNGRT

>YLR390W, 839 bp, CDS: 501-839 (SEQ ID NO 291)

CTGAATTCAGACTCATAGCTCAGACGTCACCAATTGAGTGAGGAGTGGTTTAGTTACA  
 AATGCGAGAAGAAGAAGCTAAAAGAGATACGCCCATACAGAGCAATATCAAAATGAGCAAG  
 AATGAGGTCCTCCGAATGGTTGGTTCTGACTTACTATTTGATTTCACTTCTCTGATTCA  
 CTCACCAACGAAAGCCCGAAGTCTCTGAATGAAAATTTCAACATCATTAACAGACCGGC  
 GCGCGCCTTTACAATTTAGTATGTACGCCACCAATAAAGCTGCTTAAACATTAAGCTAG  
 AAAGCCCAAGGGTGTTAAATAGTACAGCGAACCCCTTCAGCAACGGTACATCAACACACC  
 CTTGAAAAGAATAGAGACAATACAGCTACAGTCATCCCTTCCTTTGTAATTTTGGCCAC  
 AATTGATTTGATTACATCATATTTGCTCTGTGCGCTTCTCTCATTTTTTCCGCATAAAT  
 AGGGGAAACGGGATGAAGAAATGCGATTGGCTGAAAAATACAACAATTTAGTGTATTCA  
 GTCATTTCAACTGACAAAAGTAACAAACACAAGAAACGTCAGTCCAGTGCAATATGCGAA  
 AGAACACTTTAGATATGCTCACTATACCTATCCCATGCTTGTGGGACTCTACACGGCCA  
 CGAGATTTTTTCGAGCCCATGTTTATCGATAGATTCGCTAAGGATGCAAACTTCAGAACCC  
 ACATTCCTCATCCCGAATACGACGAGGACCGGAAATCTGTTAAAGGTACCGCCCTTTTAT  
 CATCCACACCAGCTGCACCACTTACACCACTTACACCTCTACTCCACCACACACAGTAA

>YLR390W, 112 aa (SEQ ID NO 292)

MZWLDKNITIVVLFSSHSIDKSNKHKRQVQXNMRKNITLDMVTIGIACLVGVYTGTRFFBPI  
 VIDRLRKDGNLKRTDIFIPHYDEDGNLLKVTPSLSSSTPAAPPTPPTPTPTPPQQ

>YMR251W, 1601 bp, CDS: 501-1601 (SEQ ID NO 315)

ACTCCAGAGCGCAAGAGTTCGTTTCATCTACGAAATGTTGCTGCGCATTCGCACAA  
 CATGACATCCCAACCCCGGATGAAATCGAAAAGAAAAATAAGCTAAAGGAAAACAACAACG  
 AGAAACTATAGAGGAACATGTTGAGTTGAAAAGGTCATCCATATACCGCCCCCTATATG  
 TATGTACCTTTACCTTTTATTTAAGTACTAGTGCTGTTTASITTAGGTTATGTGAAGGCAC  
 GGGTTTTGTCTTTTTTTTTTTTTTTTTTACTATTACTTTCTTTTTCAAGCTTTTAAGCG  
 CCGAATGATATTTAAGCSAACATGACTAAAGGGACAGCGACGAGCATTCAGCCTGGACA  
 GTGATAGAAAAGTTATGCGGGAATACGTATATATAGTTGTATAAATGTGTTTATAGAAC  
 ATCGCAGCGCCTTTAAATATATTGTCCTTTTATTTCAATCTTATTCCATCTCTCTCTTGCA  
 ACCACGGCAAGGCTGGAGCTATGTCTGAAAAATCAGCTAGCAATAACAAAGCTGAATTCOA  
 AAAGGCAGTCATCGCCATTCAGAGAAATCATCTCTGCGGATCACCCCAATTTATAPACCTG  
 CTAAGGGGAAGCTACTGCTGTATATGTTGGCGTACCATGCCCCATGGGACACAAAGAACCTTGA  
 TCACCAGGGCCCTGAAAGGGCTAGCGCCTATAATCGGGTGCAGTGTAGCGCATTTGGCACC  
 TGGATGACAAAGGCTGGCGATTCCCTGAAGAAGGAGATGGGAAAACCAATGAAGGCACT  
 GGTTTTGACATTTGACGGCGGAATTAGCTCAGTAAATTTAAATACCACTACCTCTGTGCTTA  
 ACATACCCAAATAACGGCATCGGTTCTTGGTCCAGCGAACAGATGAACCGCATTTACGGGT  
 ACAAGAGACTAAGCGACTTCTATTTTCAAAACAAAGCCAGACTATAAGGGGAAGATTACCG  
 TACCTGTCTTTTGGGACTTGGAAACATGCACTATAGTAAACAAATGAAGGCAGTGATATCA  
 TCGGAATATGAATTCGGCTCGGTTTGTATGAGTTTGTGCGGGAAGAAATACCGTCAAGTCC  
 GTCTGGTACCTCGGTCTCTAGAGGCAAGATTAACAGATTCAACTCTTGGGTGTACGATA  
 AAATCAAAACGGTGTATACAAGGUCCGTTTTGCAGAAATGTGCASAGGTATACGAGAGGGG



24/251

ACGTAACAAGCCTTTTTCATATCTTGACAAATTGGAAATCTTCTGGACAAGAGGTACA  
 CAGATTTGGAGGCGGAGTATGGTAAGAACACACAGGACAAGATACTAGATCCCTACTTTG  
 CCATCGGAGACACTCTGACCGAGGCGGAGGTGAGACTCTACCCACGATAGTAAGGTTCCG  
 ACGTGGTATACCATCAACACTTCAAATGCAATCTGGCCACCATCAGAGATGATATATPCCC  
 GTATACACACGTGGCTCARGAATATATACATGGCGCCACCAAGCCTTCCAGCGCACACCGG  
 ACTTTACCCACATAAACTCGGATATACTCGCTCGCAGCCACGGGTCAACCCGATTGGGA  
 TCACCCCACTGGGGCCCAAGCCTGATATCCGACCTCCATGA

>YMR251W, 365 aa (SEQ ID NO 316)

MSEKSAANNAEFTKQSSPFREIISADHPIYKPAKGRYWLIVLPCPWAQRTLITRALKG  
 LAPLIIGCSVAHWLDDKGWRFLEEGDGKTNERHWFDIAGGTSVNLNTSTPVANIPNNAH  
 RLLVDGTDEPHYGYKRLSDFYFKTKPDYKGRITVTVLWDLCTIVNNESDIIGIMNSA  
 AFDEFVGEYRQVRLVPRSLAQITEFNSWVYDKINNGVYKAGFAECAEVYEREVTSLFQ  
 YLDKLENLLDKKYTDLEAEYGGWKKDKILDYFAIGDTLLEADVRLYPTIVRFDVVYHQH  
 PKCNLATIRDDYSRIHTWLXNIYWRHEAFQRTTDFTHIKLGYTRSQPRVNPILITPLGPK  
 PDIRPF

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTGGTCTCAATCTGSAATAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCC  
 CTGAAGGATACCTTACAACTCTGGTAGGAACCTCTGGTTATAGAAATACCCTTTAGCCT  
 TTTTACGTACTTGTATACCGTTTAAATTTCCCTATGTACTATAACCTTTTTTCACTACT  
 ATTATCGAATTCTATCGAGCGACCGGCTTTTGTACGGAAGAGTGAAAAATCGAGTTT  
 TCGTCTTTTGGTGAAGAATTTGGAGGACTATAAAGTACCTATACTTTGTATTACGGACT  
 CAATAACAAGTCGTTTCGTGTCAGTGGTATTGAAGTTCGTACATCTAAGAGTAGAGAGAAG  
 GTGGCATCTAATAGGTTTCGACGTTTTTCTTTTTTCAAGGTTTTTATTTGGTCTCCTAGA  
 ATTTAAGGTTCTAGTTAGTTTTGGTTTGTITTTGTGGGTTACATAATTTCAATTCAAAGGA  
 GAATTTAGCTGTCTTTTATAATGTCCAATAGAGATAACGAGAGCATGCTCCGTACTACAT  
 CAAGCGATAAGGGGATCGCTAGTCAAGGGGATAAACCGAAGCTCTGAAGTTTTGATTCTCTG  
 CACAGTCCCTTGACAATGAATTCUGGACGCTAAAAAACCTAAAAAGATTGTCGATTGGGT  
 CAATGCCATTACTTTATGTATCCAGAATTAGATATAAAATTCGGTGGGGAATCTAGTGGGA  
 GACGATCATGGTCTGGCACGACATCCAGTTCTCGGTCAATGCCAAGTGACACAACCACCG  
 TTAATAACACACGATATACCGATCCAACTCCGCTAGAGAACTTGCAATGGGAGGGGTAAC  
 CAGGGATAGAATCCCTCAATAAGACTAAACAAGGTAACTACTTAGGTAATAAAAAAGGTG  
 TTTCACTCTCCATTCAGGAATTTAATGCTAACGTATTAAAGAAAAACTTATTATCGGTTT  
 CCGCCAATCAACACCCCTAACCTTAAGCCTGATAATTTCTAGAGCTTGTACAAGATACTT  
 TACAAAAATATACAATAAGCCACAATGGTGAAGATAATGATGGGAATAGCAATGAAAAA  
 ACGATATTTCAGGATAAATCCGGAACATAAAGCAATCACAAATCATATGAAAAAAGGAGA  
 AACTATCAACTTCGAACAGGGGGCTTCTAAGGCATGGAAACGGCTCACTAATACGAAGCC  
 CTTCAACATTGCGGAGGTCATATACAGAGTTTGATGATAACGAAGATGACGATAAATAAGG  
 GACACAGTGGCTCTGAAACACTAAATAAAGTGAAGAAAGATCTCCAAAAATAAAGAGA  
 GACCACTGTCTGTTAAGAGATATAACTGAAGAACTGACAAACATCTCAATAGTGCCAGGAC  
 TAACCGACATGATGCCATTACATTAGCCAGAACTCTTAGTATGGCTGGTTTCATATTCAG  
 ATAAAAAGATCAACACACACCGGAAGGGCATTATGATGAAGGAGATATTGGTTTTTCAA  
 CTTACACAGCGAATACTTTGGATGATGCTGAATTTCCCTCCMATATGCCCATCAATAATA  
 CCATGACATGGCCTGAACGATCGTCACTGAGAAGGAGTAGATTCAACACTTATCGAATCA  
 CGTCACAAGACCAAGAAAAAGAGTGAAGACAAAGTGTGGATGAAATGAAAAACGACGACG  
 AAGAACGCTCTAAATTTGACCAAGAATACAATAAAGGTGAAATAGATCCGACAAATCCC  
 CTTTTAGACAGCAAGATGAGGACTCTGAGAATATGAGTTCCCTCGGTCAATTCGGTGATT  
 TTCAAGACATTTTATATCTATTTACAGACAGTCTAGTGGCGAGTGGAACAAGAAATGGGAA  
 TAGAGAAAGAAAGCCGAGAGGTACCCGTCAGGTTGAAATGACACAGTAGAACAAGACT  
 TACACTTAAGAGAGGGAAACAACAGACATGCTAAAGCCAAAGCGCAACGGATGACAAACAAG  
 AAACGAAGCGACATCTCGAAGAAACGATCGACATGGTTGAACATATAAATGAGCAGAG  
 AACACGATAACGAAGAAACCAAGGGGACGATGAAAAATGAAGAAAAAGTGGATTACAAA  
 GAATCGAGCTCGACAAATTCAAAAACATTTATATTTCTCTATTTAATGGCGGTGAGAAGA  
 CGGAGGTGTCAAATAAAGAAAGAAATGAACAAATTCAGTACTTCCACCGCCACATTCACGA  
 CAAGACAGAAATTCAGAGAAACTTTTTGGCAACCTATTCAGAAGAAAGCCACACCAAGC

25/251

ATGATGCATCATCATCACCCCTCGTCGTCACCATCATCGTCACCATCAATACCAAATAACG  
 ATGCCGTGCACGTTTCGCTGAGGAAAAGCAAAAAGCTTGGTAACAAAAGTGGAAAGGAGC  
 CGGTTCAAACCCATTGTGTTGCGCAATCGCCCTCGTCTCTACCGTCACCATCACAGCCGTC  
 ATGGTTCCCAAAAAATAAGCGTAAAAACCCCTTAAAGATTCTCAGCCGCAGCAGCAGATAC  
 CATTACAACCACAATTGGAAGGGCGCAATAGAGATAGAAAAGAAAGAGGAAAGCGATTCCG  
 AGAGCTTGCCCCCACTACAGCCGGCCGTTAGTGTAAAGTAGTACCAAAAGTAACCTCTAGAG  
 ACAGAGAAGAAGACGAGGCAAAAGAAAAGAAACAAGAAAGAGGAGCAATACGACAGAAATTT  
 CCAACCAACAACACTCCAAACACGTCCAAAAAGGAGAATAACCGATGAGCAAAAAGCTCAAC  
 TACAAGCTCCAGCTCAAGAACAACTCCAAACTTCAGTCCCAAGTTCAAGCTTCAGCCCCAG  
 TCCAAAATTCAGCCCCAGTCCAAACTTCAGCCCCAGTTGAAGCTTCAGCTCAAACTCAGG  
 CTCCAGCGGCACCCATTGAAACATACCTCCATATTGCCCCCAAGAAAGCTTACATTTG  
 CAGACGTCAAAAAACCTGACAAACCAAACTCCCCGTTCAATTCACACACACTGCCCTTG  
 GGTTCACCTGCCCCGTGTGACAGTGTCTACGTTTATCATGTTTCGACCACCGTCTACCAA  
 TTAACGTCGAAAGGGCCATATACCGGCTGAGTCACTTGAAATTGAGCAATTGGAAGAGCG  
 GACTGCGGAGCAGGTATTACTAAGTAACCTTCATGTATGCTTATCTGAACTTGGCTAATC  
 ACACTCTGTACATGGAGCAGGTAGCCACCACAAGAACAAACAACAACAACAACAAC  
 ACCCCGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRUNESMLRRTSSDKALASQRDKRKSEVLIAAQSLDNEIRSVKLNKRLSIGSMDDLID  
 PELDIKFCGESSGRRSWSCITSSASMPSDTTVNTRYSDPTPLENLHGRGNSGIESSN  
 KTKQCNLYGIIKKGVHSPSRKLNANVLKKNLLWVPANQHPNVKPDNFLELVQDTLQNIQLS  
 DNGEDNDGNSNENNDIEDNGEDKESQSYENKENNTINLNRGLSRHGNASLIRRPSTLRS  
 YTEFDDNEDDDNKCDASSETVNVKVEERISKIKERPVSLLDITEELTKISNSAGLTDNDAL  
 TLARTLSMAGSYSDKKDQPPRGHYDEGDTGFSTSQANTLDDGEFASNMPTNNPTWPPER  
 SSLRRSRFNTYRIRSQEQEKEVEQSVCEMKNDDEERLKLTKNTIKVEIDFIKSPFRQQDE  
 DSENMSPPGSLGDFQDIYNHYRQSSGEWEQEMGIEKEABEVPVKVRNDTVEQDLERGT  
 TDMVKPSATDDNKETKRHRRRNGTFLNKNMSREDDNEENQDDSENEENVDSQRMELDNS  
 KKHYISLFNCKEKTVEVSNKEEMNNSSTSTATSQTROKLEKTFANLFRKXPHKCHDASSP  
 SSSPSSSPSPINNDVAVHVVRKSKKLGNKSGREPVEPIVLFNRERPHRHHHSRHGSQKIS  
 VKTLKDSQPQQQIPLOPQLEGATEIEKKEESDSESLPQLQPAVSVSSTKSNRDRREEEEA  
 KKKNKRRSNTTETISNQQHSKHVQKENTDFQKAQIQAPAQEQVQTSVPVQASAPVQNSAPV  
 QTSAPVEASAQTQAPAAPFLKHTSIIPERKLTFAADVKKPDKPNSPVQFTDSAPGFPLPL  
 TVSTVIMFDHRLPIINVERAIFYRLSHLKLSSNKRGLREQVLLSNFMVAYLNLVNHTLYMEQ  
 VAHDKEQQQQQQQQP

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTATCTGACGTTGTAGAATCTAAGTTTACTGAAAAAATCAAGAGCATGTA  
 GATGTTACGGATCGACTCAAGACCCCTGTCTACTCTGAAATCTCTAATAATTATGCACA  
 CCACGCTAGTADAGATACAGCTTGATTGTGTATCCCGTTTATAGTCGTGCTATTTAAAA  
 TCTATGTATAATATAACCAGATAAAAAATACACCTTCGTACAGGTGCTAATAATGTTGAG  
 AATTCCGAATTCCTTTTTTAAGGCGTATCCGTATTGAATGATTGAAAAATTTATTTCTT  
 TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATGCTCATC3CAGAAAAT  
 TTTTCTTTCAGTTTATTTGTCTTATAAAAAGACTGTCTTACGCTCAAATAACTTATACTT  
 TTCTGTATCTCATTCAAATTATTTCTTGTCAACAACCTGTAACAGAAATTAAGCACTATT  
 AAGGCAAAATTTAGAGCAAAATATGACTTACGGTGGTAGAGATCAGCAATATAACAAGACTA  
 ACTACAAGTCTAGAGGTGGCGAATTCGGCGGTGGAAGAACTCTGATAGAACTCTTACA  
 ATGACAGACCACAAGGCGGTAACCTACCGTGGTGGTTTCGGTGGTCTTCCAATTACAACC  
 AACCCACAGGAATTGATCAAAACCAAACTGGGATGAAGAAATTACCCAAATTGCCAACTTTTG  
 AAAAGAAATTTCTATGTTGAACACCAAGTGTTCGGACAGATCTGACAGTGAAGATTGCTC  
 AGTTTCAGAAAGGAAAATGAATGACTATTTCCGGACACCAATATTCCAAAGCCAAATACCA  
 CTTTTCGATGAAGCTGGTTTCCACAGACTACGTTTCTGAATGAAGTGAAGGCTGAAGGATTG  
 ACAAACCAACTGGCAATTCATGTTCAGGGTTCGGCAATGGCTTTATCTGGTAGGGACATGG  
 TTGGTATTGCTGCCACTGGTTCGGGTAAAGACTTTGTCTTATTGTTTACCAGGTATTGTTC  
 ATATCAACGCTCAACCATTAATGGCTCCAGGCGATGACCAATTGTTTTGGTTTTGGCTC

[illegible]

MFYGGRDQQYKNTYKSRGGDFGGRKNSDRMSYNDPRPQGGNYRGGFGGRSNYNQFQELIK  
PNWDEELPKLPTFEKNFYVEHESVRCRSDSEIAQFRKENEMTISGHDIKPKPITCFDEAGF  
POYVLNEVKAEGFDKPTCIGCQCGWPMALSGRDMVGIAATGSGKTLSCYCLPGIVHINAQPL  
LAPGDGFIVLVLAPTRELAVQICQTECSKFGHSSRIANTCVYGGVPKQSQIRDLRSGSEIV  
IATPGRLIDMLBEGKTNLKRVTYLVLEADRMMDMGSEFQIRKIVDQIRPDRQTLMWSAF  
WFKEVKQLAADYVNDPIQVQVGSLELSASHNITQIVEVVSDFEKRDRNLNKYLETASQDNE  
YKTLIFASIKRMCDDITKYLRREDGWFALEIFGDKDQHRDWWLQGEFRNGRSPKVAIVVA  
ARGIDVKGINIVVINYDMPGNIEDYVHRIGRTGRAGATGTALSFFTEQNKGGLGAKLISIMR  
EANKNIPFELLKYDRRSYGGEGHPRYGGGRGGRGYGRGQYGGGRGGYGGNRQRDGGWGN  
RCRSNY

CAAAAAGAGCTAATCAACTCCTTGAACCTTAGATAAAATACGCCATAAATGATAACAGTGAG  
GAATGGCCTGTAATCTCAAAAATCTTTAGAAATACCTGCCAAGGCCAAGGCCGTCTCAGT  
TTAAAAACCTGGTTAAAAAGAGAACGACTGAAAAAGCCTGAAGATACTATAGACAAGAGATG  
AAAGCTATGAAAAAACCAAGAAAGTCTAAAAAGCTGCAAAATTAAGCGTTCTACTCTTTG  
TCAAAACCCCTTTTATAGCTAAACGCTTTACTTAATTTGTACAATAATATAGAATAGAAACAT  
AGTTGAATGTTTGAACCTTTACATATTCCTTTCAATCGTGTCGAGCGATATAAGTATTACG  
ATTATGCCCGCGAAACNGAACCCGCTTTAGACAATTTCAATCAACATACTCCACTCCGT

27/251

AGTGAGTAACCTTTTGGAGTAATACGAAGTAACCAAGAGGTCAAAACGGAACTATATACC  
 CCARAATAAGCAATCATTCAAATGGTCGAATTAACGAAATTAAGACGATGTCTGTTCAAT  
 TAGACGAACCAAAATTTTCAGAAATCAGGCCATCTGGGAAGAAAAGGCTTCTGCAACAA  
 ACAACGACGTTGTUGATGATGAAGATGACCTUGAAGATGATTTGAAGATCAATTTGATG  
 AAAATGAAACATTTGTTGGACAGAAATCGTTGCTTTAAAAGACATGTCCCCCAGGTAAGA  
 GACAAACAATCTCTAATTTTTTTTGGTTTACTAGCTCTTTTGTGAGAAATGCTTTTCACAA  
 AATCCCGAAACCTTGCCTGGACTTTGACCCACCCTGCTTTGTTACTCGGTGTGCCACTAT  
 CCTTATCTATACTTGCCGAAACAACAGCTAATCUGAAATGGAAGACATTTTGATTTACAAA  
 GTGATGCTAACAAACATATTGCCCCAAGGTGAAAAAATGCTGTCAGCAACAGCCAATTA

>YNL131W, 152 aa (SEQ ID NO 330)

MVELTEIKDDVVQLDEPQFSRNQAIVEEKA SATNNDVVDDEDDSDSDFEDEFDENETLLD  
 RIVALKDIVPPGKRQTI SNFFGFTESFVRNATKSNLAWTLTTTALILGVPI SLSTLAR  
 QQLIEMEXTFDLQSDANNILAQGEKDAAATAN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAAAATACACACCGCGCGCAAGCCATCATCCAGGCCCAAAGCAAGGATAAAGCATGCTTTTT  
 CCTGGATAAACCAGAATATAATAAACCCTACCTCGGACCATAATCCACACACCTGCTGA  
 AGCCACACCGATCCATCCCATGTTGGCCAAAGTCAAAATGTGTATTCAAATCTGTGTGCAA  
 CGAGTTACCAACCCGCTTCCTTCGCCTGTAGGCGTACCTGTAAAATTGTAAGACATTGTTGA  
 TATTGTATTGTAATATATTAAGTATGATATATTACAAAACATAAATCTTTTCAAAGCTCT  
 GTCCACACTTATTATTCAAGAAGGATATTTAAATTTGAAAGGACGTGAAAGCACGAATGAT  
 TACTACCCACTGATGTTTGGTTAGCACATGTGTAACCTACTGCTTATATATGTTGCGAGAAA  
 AGTGGUTUGGAATGAACAUCCTCTTTGTAUTGAATACCTTCATTTGATAAGGCACAGGGCTTTC  
 ACGCCGCTTACTATTCTTCGATCCGTCACCAATTGAAGCTTTTTACGAGGGGAATAGTCG  
 ATTTTACATTTCTTATCTCATCTGGCTTTGACTATTACCAGACACTCTTGATAAGCAGTA  
 ACACCAAGTAAGAAGAGACCGAAGGATCTCTCTTTGTTATCGGAAAAAAGAAAAA  
 AAAAAAAGAAAAAGATGTCTTATCTTCTTATCTTTCTTATCTTAAAGACCTACCATTTGTTC  
 CTTTTCTATTTTGGCAGCCCGGGTATTCGCAAGGGGAAAAAAGCCCAAGACAGCATTCCT  
 TGTTTATTATGACTATTACAAAGCCAGGAATGATTTTCGATGGCCGACATGAATTACGTCG  
 TTTTCAAGAACAGAAGCTTAAACCGTCCCTGCTGAGCGGGGGCGGTAATCCGCTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MREQLKLFTR EIVDFPFLILSGFDYVQTL LLISSNSKKRFKDSLLSEKKKKKKKKKKDV  
 LSYLSYLKDLFVVF LFWQPGYSQRKRNPRQHSLFIMPTTKPGMISHADMNIVVSKNRSL  
 NRPAERGCNR

>YNL179C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGGTTAATTTCAAATACCTAATCGGAGGTCTTATCTTATTTTCAAGGGCPAGGC  
 TCTCCACATCGGTAAGTGAAGACAGATAATGGAAAGTAGCAGAATTTTATTTATGTGCC  
 ATACAAGCCCCGGAGAAACAGAGTAGCTAAAAAATTAAGGCTGTGCAAAAGTGGTTTGTTC  
 CCGGACGCCCCGGGCTTTCTCTCCCTGAATCTTTTCGTTCCGGCCCCCTCTCTCAATA  
 CCAGATCTGCATCTATACTAAAGCTGCAGTGAGAGTAAACCGGAAAAATTAATCCGCGTGT  
 TTGCTTCCGTCTTAGCTTTTACTTGGGTATCGGAGAACCTCTAAGAGCTTAGACCGGTCT  
 TCTTCCCTAAAAAGGAAATTTATAAAAGGTTATTAATCTGCACTAAAGCAAAAAAACA  
 CGTTTTCGGCGTCCGCTCAAAATTTTCATTACGCTTCTTGGTCAAATCAGTTACGTAACGG  
 GTTATGACGAATACGATGAGATGAGTAATTGCACAGGCTCTATGCACACACCTAAGCA  
 GTGCTTACTTTGAATTAUPTTCCCTTTTAAATTCCTTGATATATGTCCTTTTTCCTCTCATC  
 TTAGTTCTTGGGAGTACTGGCAATCAAGCTTCTCCTTTTTTTTTTCTTTTTTTTTTATTTT  
 TTTTTTTTTTTTTTACTTTTCAGTTTCTCCTACCTTTTCTTATTTTCTTATTTAAAGTAA  
 GTTTAAATAGTACCTTCACTAAACACGTACGCGGATCCACCAACGAACAAAAGCACGAT  
 CCTTGACCCATCATTTGATTCCAAAGGTTTGAACATTCATTTTTTTTTCCTGTTCTAT  
 TGCACAAGACAATATCCAGATATTTCAGTTGATAGGAATACAAGACAGGTGGCACCCA  
 CAAAGCACACGCGGAAATATTTATTAAATACAAATATAG

>YNLE19C, 145 aa (SEQ ID NO 336)  
MSNCRRLLCRQLSSAYENYLPFFYFLTYRPFSLYLSSCEYWQSCPSFFFLFFLFFFFFFTF  
QFLVAFPLLFLPKVSLNSTLTKEHVRPIHORKARSLTHHCIPKRWNIHFFPSGLLHKTISR  
IESWIGNTROVAPTKHTPKYLLNTI

>Y01150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)  
TTCCCATTTTCCACTGCTATTECTGTGTGCTATTGTGCAGAACCATTTGTTTACTTGAATGTTA  
TTACTACCATTTTGTGAATCAAAAATATCTACTTCTTGTGGGGAGACGGGTAGAAGATTT  
GTATTTTTCGAGACGTCCTCTCAAAATATATGCCCCAACACCTTGATATTCTAGTTTATTTC  
CATTCGTGCTTCCTTTGAAGTCCCATTATACAGTGACGCATGTGGTGTGTGAAAAGTAGT  
TGCTTTTATTTTGGATCGTATCTCCCAATAACGTTGAAATTCAAGCTTTTCTATAGAAT  
TCTAACTGTGTGGCAGAGTTTCTGCTGCAGTTGCTGCTCCGGTCATTGTGCACAGCTTT  
TCTTGTGATGCTTGTGCAAGATAAATGCTTATCTGAACGTTCTCTATTGTTTTTTCGTC  
AATTTTCTTTCTTTCTTCTGCTTCCGCTTTTCCACATATTAAGCTGTATATAGAAGAGAAA  
AATGCGCAGAGATGTACTAGAAGATAAAAAATAATTTGTAATAACGTTAATATATATAAT  
ATTATCTATTTTCATTTAAAGTTTATATTCTGCCCTCAAAATTTTAAAAATTGGGAGGCAG  
TGTCGTCAATGGTCTCTTTCAAGTTCCTGAACCTTGAAACCTAACAAATCTTACTCTTTT  
TATTATCAAGAGTAGCACCAAGGGTGTATGCGGTAGCACCCAGAACCTGGTTTCCCCACTG  
GAATATTGCCCTTTTAGAACAGGGAATCTCTCGTTAAGGATATCGAGAACAATCTGCAATAG  
TAAATCTGGGCTTCCGATACCACTACTCTTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)  
MIKNNNCNNVNIYKYYLESPKVIYILPSNFKIWEAVSSMVSFKFLMLKPNFLFLSRVAP  
RVLAVAPPEPGEPTGLIFERTKSSLRISPTSCVNLASDT(SI

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)  
GCGTGAACCTATGTCATATTTGCGATTTTACCTACAAATAAATATCATCAFTATTATATFTAT  
GTTTGCATGTAGGTTTCTACAAATACATTGTTGTACCGCTATAGTTCCCTTTCAAAAGTAGA  
AAGAAATTCGTAAACAAAATAATCTCCAATAATTTTATAGCACCTTATCAATATCAATGCTGC  
AATACCTTCTCATTTCAACCAATTGGCCCCACCTCTTTTGTACAAAAAACGTCGCCATT  
ATAAAATAAGTAAGGAAGCATATAATTTGCAATTGTCCATTACGTAAGAAAAAAAATCATGT  
TCTACATATTACGTAATAAGTAATACGGAATTTCTCGCGGAAGTAGACTTCCCTGCAAAA  
AAGGGAAMAGTTCGATCAATATTCGAAAAAGGATCTTTAGTTTCCCAACTATATAAGGA  
GGAAAAGTCTATCTCTCTGACGTTGATATAACGTGTACGATTTTCAACCAACAGATAGC  
AGTATCACACGCCCGTAAATATGTCAGTTTTCGTTTTCAAGTGTAAACGGGTTCAATCCCC  
AACACATTTGTGATCTCTCTGTTGAAGGAAGACTATAAGGTCAATCGGTTCTGCCAGAAGTC  
AAGAAAGGCCGAGAAATTTAACGGAGGCCCTTTGGTAACAACCCAAAATTTCTCCATGGAAG  
TTGTCGCCAGACATATCTAAGCTGGACCGATTTCACCATGTTTTCCAAAAGCACGGCAAGG  
ATATCAAGATAGTTCTACATAACGCCCTCTCCATTCTGCTTTGATATCACTGACAGTGAAC  
GCGATTTATTAATTCCTGCTGTGAACGGTGTAAAGGGAATTTCTCCACTCAATTAAAAAAT  
ACGCCCTCTATTCTCTAGAACGTTGATTTCTCACTTCTTCTTATGCACTGTGTGATGATA  
TGGCAAAAGAAAACGATAAGTCTTTTACATTTAAACGAAGAATCTGGAACCCAGTCACTCT  
GGGAGAGTTTGCCAAAGTAGACCCAGTTAACGCCCTACTGTGGTTCTAAGAAGTTTGCTGAAA  
AAGCAGCTTCGGAAATTTCTAGAGGAGAATAGAGACTCTGTAAAATTTCGAATTAATGCGG  
TTAAACCCAGTTTACGTTTTTTGGTCCGCAAAATGTTTGACAAAGATGTGAAAAAACACTTCA  
ACACATCTTGCGAACTCGTCAACAGCTTGATGCATTTATCACCAGAGGACAAGATACCGG  
AACTATTTGCTGGATACATTTGATGTTGCTGATGTTGCAAAAGGTCATTTAGTTGCCCTTCC  
AAAAGAGGGAACAATTTGCTCAAGAGCTAATCGTATCGGAGGCCAGATTTACTATGCAGG  
ATGTTCTCGATATCTTAAACGAAGACTTCCCTGTTCTAAAAGGCAATAATCCAGTGGGGA  
AACCAGGTTCTGGTGTACCCATAACCAACCTTGGTGCATCTTTGATAATAAAAAGAGTA  
AGAAATTTGTAGGTTTCAAGTTCAAGAACTTGAAGAGACCATTTGACGACACTGCTCTCC  
AAATTTTAAATTTTGAAGGCGAGATAATAA

>YOL151W, 342 aa (SEQ ID NO 352)  
MSVFVSGANGFLAQHIVGLLIKEDYKVGSGARSQFKAENTJTFAGNNPKFSMEVVPDISK  
LDAEDHVFQKHGKQIKIVLHTASPCPDITDSEKULLIPAVNGVKGILHSIKKYAADSV

29/251

RVVLTS SYAAVFDMAKENLKS LTFNEESYNPATWESCQSDPVNAYCGSKKFAEKAWEFL  
 EENRDSVKFBLTAVNPFVYVFGPQMFDDKDVKKHLNNTSCELVNLSLMHLSTEDKITELFGGYI  
 DVADVAKAHLVAFQKREFIGQRLIVSEARFTMQDVLIDLNEDEPVLKGNIPVGKPGSGAT  
 HNTLGATLDNKKSKLLGFKFRNLKETIDDTASQILKFEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACCGGAGCTGCAGTTTCCTCACTACCTACACGCTCCTCTGACATACAAGATGAT  
 CCATCTGTGTTTGTTCGAGCAGGTTTCAGAACTCTTCCTCCTGGGGCTCAGCAAATGGATTG  
 TTATCCAGATCATCATATGGATCATTAAGGTACAGCCGAAAGTCATTGTTTCAGAGGATAGAT  
 GGATTGACTAAGGGTACAGTACGGCAAAAAAAATTAGATCAGCTTTTCAAAAACAACTA  
 TTTTGGCGTTTACCAAACCAAACAGTATATTCAACTAGTTCAATCACTCTTGAAAACG  
 TCCCCTTTCTACAAATTAGGCTTTGAACGGGTGCTATGCAAAAAAGTGTAAAGAAAACG  
 AAAAAACCAGAAAACTCATATATATCTTATAACGAAATATCAGGGTGTTCGACTCAATCG  
 CCAGGTGCCGCTAACACAATCATPAGGATAGTCCGGCAATATATACGGTTCAATAGTCAC  
 TGAAGTGTATTCACAGAATAATGACAAAGCTACAAGGACTACAGGGATTAAAACACATCA  
 AAGCGGTGTATTTGATATGGATGGCACATTATGCTTACCCAGCCCTGGATGTTTCCAG  
 CAATGAGAAAACGCCATAGCATTGGAGGACAAATCGATTGATATCCCTCATTTTCATTGATA  
 CATTTGCCCAACAGAAAAAGAAAAAAGAAGCGCATGATAGAATAGAATTAGTTGAGGCAA  
 AAGCCATGAAGSAGATGCAACCCGAGCCTGCTCTGTTGACATAATGAGGTATTTGACGA  
 AAAAAAGTATTTAGCAAGAACATACTGACAGAAATGTCGGAGCCCCGGTAGAGACTTTTG  
 TTAAAAGATTTATCCATCCGAGCTTTTCGAGCTTTGACTATATTGTGCACAGGGAGTTTA  
 GGCTACAAAAACCGCAACAGACCCATTATACACATCGCCTCGAAGCTAAATATAAGGC  
 CTTTGGAAATGATCATGCTAGGAGATTTCATTTGACGACATGAAATCCGGTAGATCTGCTG  
 GATGTTTCACGGTATTACTCAAGAATCATGTGAATGGACATTTACTGCTCGAACATAAAG  
 AACTAGTAGACGTTTCAGTAGAGGATCTTTCCGAAATAATTGAATTGATTCAAAATATGA  
 ATAAAGAAAGTTTCTAA

>YOR131C, 218 aa (SEQ ID NO 360)

NFKLQGLQGLKHIKAVVFDMMIXTLCLPQPMWPPAMRNATIGLEDKSIDILHPIDTLPTKHK  
 KKEAHDRIELVEAKANKEMQFQPLVDIMRYLTKNGTSKNICTRNVGAPVETFYKRFIPS  
 ELSRFDYIVTREFRPTKPDPLHLHASKLNIRPLEMIMVGDSEFDDMKSGRSAGCFTVLL  
 KNHVNGHLLLEHKELVDVSVEDLSZIEELIQNMNKESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTTCATATTCCTGCTTCCATCAATGTGCCATATAGATCGCAACC  
 CTGACGCATTTGCCTTAGATCCCTTAGAATTTGAGAAACAGATTGGCATCCCCAAACCTG  
 ACAGTGCCAAAGGAGCTAATATTTTATTGTGCTTCTGGCAAAACGGGGGGAGAGCTCAAA  
 AAGTTCGCTTCTTCATGGATATTCAAACACCTCACATATATCTTGGCTCTATGAATGATT  
 GGGTTTTCATGGGGGTGATAAACCTGACTTATAGCCTTGTATACCTCAGGTATGTACCC  
 TGCTGATTTTTCGTAAGCTAGTAACCTATTATGCCATTTATGTCACACCGTTTCATAATATT  
 TGCTTATTGCAATTCGCTCTCATAGCCGCGCCGCAAAATAATTAGGAAGTATAAAAAAAA  
 AATACAAAACCTTAATCTGAATGGAAATAAGATAGCGATAACTCTCAACAAATGGAAGCGAG  
 ACAGAAGAAAAAGACCAACGATGTTCAAGCATAGTACAGGTATTCTCTCGAGGACAGPTT  
 CTGCAAGATCGCCATCATTTGGTCCTGAGAACATTTACAACGAAGGCTCCAAAGATCTATA  
 CTTTTGACCAGGTGAGGAACCTAGTCCGAACACCCCAATGATAAAAAACTATTGGTAGATG  
 TAAGGGAACCCAAAGGAAGTAAAGGATTACAAGATGCCAACTACAATAAATATTCCGGTGA  
 ATAGTGCCCCCTGGCCTCTTTGGATTGCCCGAAAAGGAGTTTCACAAASTTTTCCATTTG  
 CTAAACCACCTCACCATTAACAAATTGATTTTCTTTTGTGCCAAAGCAGTAAGAGCCAAA  
 CTGCCGAAGAGTTGGCTCGATCTTATGGGTACGAAAACACTGGTATCTATCTGCTGTTCTA  
 TTACTGAGTGGTTAGCTAAAGGTGGTGTGACGTTAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MFKHSTGILSRVTSARSPTLVLRFTTTPKAPKIYTFDQVRNLVEHPNDKKLLVDVREPKEV  
 KDYKMPCTTINIPVNSAFGALGLFEKBFHXVFQFAKPPHDXELIFLCAKGVRAKTAEELAR  
 SYGYENCSTYPGSITEWLAAGGADVKKPKK

30/251

&gt;YOR382W, 962 bp, CDS: 501-962 (SEQ ID NO 375)

AGTAAAGCTCCCTACAGTGAATATCTGGGTCCTACTGACGCCAAGCCCTACAGCGATCGGA  
 ATGCGGGAACCGGAAGTTAACGGGGCTTCCAGAACGGCGGAAGCGAATTGAACGAGGACGG  
 CAAACAAAACACCCCAAAATTTCAATTACTTAGAATGACUCCACAGAGCAGGGGTGCAATTT  
 ATCAAGCGATCATTGAACTAACTAAGTTTCATTCCTGTATAGGATTTAAAACAATGCACC  
 CTAAGTTCAATATGCACCCCCCTCGCCCCGCAGCGGACCCCTGAACAGAGAAGCTGTTTCG  
 AGGTTACCCCAATTTGGATCACTTGTATAATTTGTAAATCGAGTTTCGGATAAGATGTATACG  
 AATCTAACTGGGTGCAGTATAATTAGCATTTTATATTTACCTAGCAATATATGTATAAAAC  
 AGGAATGCTGTGGCTGCCTTCAGGCAGAAATTTTACCGTCCCTGTAAAAAAGTCTATCATAAA  
 GCCATCACAAAACAAATTAATATGAAATTCCTCAACATTTTCGGAGCTACTACAGTTATGA  
 CTGCCGTCTCGCCAGCAGCTGTGTGAGTGTAAATGACCACTAAGACTATTACTGTCTACTA  
 ACCCTAATAACCTTTTACACTAAGCTCGTTACCGACACCCCTGACCCCTATCATTAGTTACA  
 GTACCACCTAGAAGCTGTCGTTGTGTCAGTAATAGTGATGCTACTTACACAAAGGTTGTACCCG  
 AAGGACCAAGATACCACTCTCGAAAAGAGTACAAACAAAGACACTTACTTTGACAAAACCGTT  
 CAGGTTTCATCAACCAACCTTTTACACCAAGACCGTCACTCAAGCCGTCGAATCATCTACAT  
 CCTCCTCATCTCTCTCATCT  
 CTGCAATCCAAGGAGCAAGTGTGGGTGCATTGGCCCTTGGTTTGATTTCTTACCTATTAA  
 AA

&gt;YOR382W, 153 aa (SEQ ID NO 376)

MKFSTLFGATTVMITAVSAAVSSVMITKTITATNGNNVYTKVVTDTADPIISYSTTRTVV  
 VSKSDATYTKVVTGPDFTTSEKSTTKTLTLTNGSCSSFNLYTATVTQAVESSTSSSSSSSS  
 SSSSSASSSGAAPAAFQASVGAALGLISYLL

&gt;YPL078C, 1235 bp, CDS: 501-1235 (SEQ ID NO 379)

TAAACTGTGTTGTGACGCCAACTGCAACTCCCAGATGAAATACGGTCCGGTAAAGATAGGA  
 ATATCTTACTCTTACAAGCATGAATATTTTAAACCGCGCGCAGTACTATACAGCATAACA  
 GGTCTTCCACGCGATGAGAACTGTCCATGGCTAAATTAGTTCTCTCACACAGAATTAGAAA  
 TGTGCTGTGACAANTGGCACATACGTAGATMAAAGATAAATATAATTCAGAAATGGCTGTGG  
 CGACAACCTATTATCATAGAGGTGTCCCATCGAGCGAGCCTCATTGCCCCGGGTAATCGACA  
 TCAATAATTGAACCAATCACGACGCTTTTCTCTTTTACCCGCTCATTTCCGACCTTCACCACA  
 GGTTTGGGTAATTAAATAGCAAGGGATTATAATTGCAGTTAGCAGTTTATGTTGACAAG  
 TTTTACTGTCTTAGGAAGGGTTATATTTTATTTAAAGACTGACGAGAATTACGTACCTC  
 CTAAGTGCGCCAAGAGATAAAATGAGCATGAGTATGGGTGTCCGTGGCCTACCGTTAAGGT  
 CCGTTTTCTAAAACATTTATTTAGCCAAAGGTGTTCCGTGTGTCCTTUGATGGTGATTGGAGCCC  
 GTTATATGTCTTCCACTCCAGAAAACAGACAGATCCAAAAGCAAAGGCTAACTCTATCA  
 TCAATGCCATTCACAGGTAATATATTTTGACAAAGACGGGGGTPTTGGCGACTTCTGCTG  
 CCGCTGTCTATTCATGCCACTTCCAATGAATTGTACGTTATCAACGATGAAGTATTTTAT  
 TGCTCACTTTCTTGCTTCTCACTGGTTTAGTGGCAAGTATTTGGCCCCAGCATATAAAG  
 ATTTTNGCCGATGCAAGAAACGAAGAAAGTCTCCGACGTTTTTAAATGCTCGAGAAACAAAGC  
 ATGTCGAAGCTGTTAAAGATAGAATCGACTCTGTCTCTCAACTACAAAATGTGTGCTGAAA  
 CTACAAAGGCTTTGTTTGATGTTTCCAAGGAAACIGTTGAACTTGAAAGCGAAGCCTTTG  
 ANTTGAAACAAAAGGTAGAATTAGCTCACGAAGCAAAGGCAGTCTTAGATTCCGTGGGTTA  
 GATATGAAGCTTCTTGGCTCAATTGGAACAAAGGCAACTAGCAAAATCTGTCACTCTCCA  
 GAGTTCAGTUAGAATTGGGTAATCCAAAATTCGAAGAGAAAGTTTIGCAACAGTCTATAT  
 CTGAATTTGAACAATTGCTTTCTAAATTTGAAGTAA

&gt;YPL078C, 244 aa (SEQ ID NO 380)

MSMSMGVRLALRSVSKTLFSQGVRCPSMVIGARYMSSTFEKQTDPKAKANSIINAIPGN  
 NTLTKTGVLGTSAAAVIYAIISNELYVINDESILLTFLGFTGLVAKYLAPAYKDFADARM  
 K<VSDVLNASRNKHVEAVKLRIDSVSQLQNVAEFTTKVLPDVSKETVELESEAFELKQKVE  
 LAHEAKAVLDSWVRYEASLRQLEQRQLAKSVISRVQSELGNPKFQEKVLQQSISETEQILL  
 SK..K

&gt;YPL085W, 7088 bp, CDS: 501-7088 (SEQ ID NO 383)

TTTTTCATGAGGAAGAGCCAGTCGACACTAAATAATAAAAGGTGAAATGATTAAACAATGA

31/251

AAGCGGCAGAAAAATAAAATCAACACAGTGGCAGTATTGACTTTTGAAAATCAGAAGTTCA  
TCCTAAGTTAAGACTTTCTCTTTTAAAGTGCTTTCTCTCTCTCTCACTCTCTTTATCGCTG  
TATATCTCATTGTTGAATATATATAACACAACGTTATPAAGTGATCATCACTTTCTGATCCA  
TAATTTCAAACCTCAAGCCACCGTACATGTGGUATTTTUUACTATAAACCTTACGAGCAAG  
AGAAAGATATACGGAAAACCTTAATTOCCAGGTTACACAAAGATTTTGGTCATTGAATBT  
TGCAGCCCTCTCTGCTTGAGAACTGGACAACAACCTGTTATCAATATTCCCTTTTCAAAAT  
AGTGGTATTTAACTGGCCATAACCAACGAAACCGTTGTACCTATTATTTTGTATAGTCTT  
CATTTAATAACGTGTTAAGPATGACACCTGAAGCCAAGAAAAGGAAAAACCAAAAGAAAG  
AGTTGAAGCAAAAGCAAAAAAAGCTGCTGAGAAAGCTGCTAGCCACAGTGAAGAACCAC  
TTGAATTACCAGAAAATACGATTAAACAGCAGCTTCAACGACGACTCGGTGAACCGTACAG  
AATCTGACATAGCTTCAAAATCTGATGTTCTCTCCGCTCTCATCATCTACCAATATCTCTC  
CGGCTAATGAAACACAATAGAAATACCTGATACTCAAGAATTGCATCATAAACTGCTCA  
ACGACTCTGATCAACATGATATTACCGCGGACTCAAATGATTTGCCAGACAACCTCAATCG  
TTGAACATGACTCTGTTATTACCCAAACAAAACCCAGCCATGTCTCAAGAATACGAACAGA  
CTGCCGCTCACTTATCTTTGAGAAATCCATCGCTCGATGTAGTCGCGGAGAACTTCACA  
ATAATAATGAACATACCCAGAAAATTGCCGTATCCGCTGTGGAAGAGGATTCTTTCAATG  
AAGAAGAGGGTGAAAATCACGACAGCATAATAATTTTCATCATTAAACCATCTTACCCCTT  
CTCAATATAATCATTTTCTCCCATCCGATGGCAATCTTCTTTCTCCAGAATTATCTTCTG  
GTGATACGCCAACTCACAAATGTTCTCTAGGCACAAAAGACAATGAAATAAATGACGATG  
AGTATTGTAATGATTAAGGAAAATAGTTTGAACCCAAATATGTCTTCTCTCATGAATTT  
CAAGGAAGAAGATGAAAGATTAAPACTAGAAACGCATGTATCAACCGAAGAAAAGAAAC  
AGGATATCGCTGATCAGGAACTGCAGAAAACCTTATTTACGTCTAGTACAGAACCATCTG  
AGAATAAAATAAGAAAATTCTGGTGATGATACCTCCATGTTGTTTCAAGATGACGAAAGTG  
ATCAGAAGGTTTCCATGGGAGCAAGATGCGAAGAAAGATTTTCATAATGAGAAACAAATA  
ATACTCAAGAATCGGCACCGAACACAGATGATCGTGATAAGGGTTATGAAGGAAACGAAG  
CTTTGAAAAAGTCCGAAAGTTGTACAGCCGCGGACGAGAGGTCGTACTCTGAAGAAACTT  
CAGAAGATATCTTTACGGACACGACAAACAGGTAGTTCAAGCCCAAAATGATTTCACTC  
GGAAAAATATTGAGAATGAAGCCAGAAATTAATCGGGGAAGCGAATCATAACTTACCGT  
TGCTTCGCGAAGCTGACATTTATAGAACCTGCTAAGCATATTCAAGATCAAGCCGAGGATT  
TGTTTACGCAGAGCAGCGGAGACTTGGGAGAAGTTTTGCCATGGGAATCTACTGATAAAA  
ACCTCTGATCTAACCAACCAATCCCAAGAGAAACATGAAGATTTATTTGCTGCTTCTGGAA  
ACCATCACAAACTTCTTTGGGAGTTTCTGACGGTGAAGTATCATCGGGAAAGACGGAAA  
ACAGCATGCAGACTATCTAGGAAAATAGCTGAGUAAAAGTTTTCGTTTTTCGAAAACG  
ACGACGACCTTTTGGACGACGACGACAGCTTTTGGCTTCTTCTGAGGAAGAAGACACAG  
TACCTAATACCGATAATACAACGAATTTAACCTCAAAACCGATTGAAGAAAAAAGGCTT  
CAAGATATAAACCTATTATCGAGGAGGAAGCAGGAATCGCTCAAGAGCAAGTTTCATTTTA  
CCAATACTACTGGCATTGTAACACCGCAGCAGTTCCACCGTTTGACTAAAACCTGGACTAG  
GCACCTCCCAACCAACAAGTCAGTGTAACAAATATAGTTAGTCTTAAGCTCTCTCTGCTAA  
AAGACAATCGTTTCAAAATTTAAGATAAATGAGGAGAAAAAGAAGTCTGATGCTTACGATT  
TTCCACTGGAAATTAATTCAGAAAGTTCCAAGAAAGGTCACGCAAGCCGTTTGGCGTTT  
CTACTCAAAGCTTTCGCTTACGCAATTTCTTTTAGTTCTTTCCACAAACCAATTCACAGA  
GCAGGAAAGGCTCTAATAACTCAAATAGGCCACCCCTGATCCCATTTGCCGACCCACCAAC  
CTCGATCTTCGAGAACTAATCAGCGATCTCGCAATCTCCCGTTAATTAATGCTTTTCCCTA  
ACCCATACAAAATTCACCAACTACAACAGGCTCCTATCCAATCAGGTATGCCTTTTACCAA  
ATACCAACATACCTCCCCAGCATTAAGAGTGGAACCAACCGTTTCTGCTCCTCCAATTC  
GGGCAAGAGGGGTCAGCAATGCTCCGTGGGAAAGTTCAAGCTCTTTTGGTGCTAGACATG  
CAACACAGTACGGCTCAATAACGGGGTACCTCCGTTTTCGCCATATGTCAGCTACCA  
TAAATTTCCCAACTCGGAATAACTATCCCCCGTCTCTCTCTACAGTTTACGCAAGCAAT  
ATCCATCAGTTGTGCAAAACCTTGGCGCTTTCGGCCGTAAATACCCCCAATTTTGTAAAGA  
CCCATAGAGGCCATACAAGCTCTATTAGTTCTGATACACCAACCCAGAATGAACAGGCT  
CTAGATACGCACCCAACTATCAACAATCTTATCAGGTGCCATATACCTCACAACCTGTGTG  
GTCTGTAGCTGGGAATTCAGCTATCAAGGCCAAACCCGAGTTCCTATGCAGTCTCTA  
TGATGCCCCAGGCTCAAACTTCAGCAAGTATTCAGGCTCACGCGAACAATTCACCCGCTA  
CTGGCATTTTACCTTTAGCCCTTACGACCTCTAGACCCCTTACAAGCCGCTACGAACT  
TGCAACCCCGTGCAAGCAACATAACGGCTGCAAAATTCATACCTCTTTGCAAAATTTGCCAC  
TTGCTGAAAACTACTGCUAGAAATTATCAGGCATCGAGCTACAAGTAGTGTGCAACAC



32/251

CACGACAGGAAAATAATCCAAATTAAAATAGACAACGAGGCTTTATTACGCCGTCAATTTTC  
UATTTTTCATTTGGAGTGCTGCAAAZAAAGGTCTGTGTACGCAGTCCUUUCTATUCCTGACC  
AATGCCAGTACATGATTTTCATCAACCATTGTACACGAAATAAAAGTGACACCAATTGACC  
AGATAATTAACCGAACGATATGCTCAAAAGCTTTCCAGGTCTTTGGGTAGTGCCAAAT  
TAAAAAAGGATTTAACCAATGGATGGAAACCACTATTAAATCCATATCTGAAAATG  
AATCATCCACTGATATGACTATATGGCAACTATTGGAAATGAAACTAAACGATAAAGTTA  
ACTGGAAAAATATTTCAAAACTACTATACAAATCTGACGAACTTTTAATGTACCTATCTC  
AGCCCTTTTCAAACGGTGACATGATTTCCAAATGCATATAGACTGGATATAAATTTGTCAGA  
TGAGAGTCTTGCGCTTCTTACAAACGGGAAATCACGATGAGGCACTTCGCTTAGCTTTAA  
GCAAGAGGGATTATGCCATTGCACTATTGGTTGGCAGITTAATGGGTAAAGACAGATGGT  
CTGACTCATTCAGAAATATTTATATGAAGGGTTTACTGCGGGGCCAAACGACCAAAAG  
AAATGGGCACACTTTCTGCTCTTATCTTTCAAGTATTTGTTGGTAACCTCCAAAATGGCCA  
TAAAAAGTTTCTACACTAATPAATGAGAUCACTCAATGGGCAATCCGAAAACCTGGAAGAGTA  
TCGTTGCGAGCTCTTCTGATTAATATCCCAGAAAATAATGAAGATCCACTACTTTATACCAC  
CTGTTGTCTCTGATTTTGTGATAGAGTTGGTATATTTCTCACCAAAAAGGGCTTGACAG  
CCGCAGCTACTACATTTACTTATTATTGGTAACGTACCCTTTCTAATCAGCCAGTAATGC  
CAGATTCAGACCTTATATTTGAAAAGTATTTGGAAACATCAATACTTTTGAAACCATTTCTAT  
GGGATGAAATCTACGAGTATATATTCTCTATGACUCTAAATTCAAAGGATTTTTCATCTA  
TTTTGCCCCAGAGATATACCATGCATCTCTTTTACAAGAACGAGGTTTGAACAGCCTGG  
GGACAAAGTATACTGATTAACCTCAGTTTCTCAGTTTGGAAAATGCTTAAGAAAGATATTT  
TAACAATAAACTTCACTCTGTGAATTTGAGTGAGGTGGCTAGTAGGCTTTCCGAGTCTAATA  
CAGGATGGCTTTGCAAAAACCAAACTAAGCAGCTTATGCGGTCAATAGATAAATCTCTCA  
ATPAAATATATTTGGTGGCGAGTATTTGATGCAATGAATPAAAAAAATGATAAAAAAG  
TTTTTGATGGGTTCACACCGGATCTTCTGCCAATTCGTCAACTGTGGATCTCACCCAAA  
CATTCACACCTTTCCACCTCACTTACTTCGCAACCTATGTCGATACCTACACCTCTTT  
TGCAATAATGCCATAATGTACCAAGCCATAGTGTGCTGCATTCAAAGCCTTCCAATGTGT  
CAAGGGGTTTAAATTGAAGCAAACTTACCGTATACGCATAGGATCGGTGATAGTTTGCAGG  
GATCTCTCAGCGCATTCATAATACACAGTTTCTGCTGCTGCTGAGCCTCAAATGGCTTCTT  
TGAGAAGAGTTTGAACACAGACCAGCATACAAAAGGAAAGGCTTTGAAGAGTCAGCAGATTT  
TAGAGAAAAGTCTTACGGCTTACACTTCCACAAATTTGGACAGAACCATAGCGTCCAATGG  
AAAAGCTTAATTGGAATGTGCGCATCTTTATTTGCCGACTTCCCTGCTCCACCCAAACTTG  
GATCAGTGGCGTCTAATTATGTCTTACTCTCTGACTTAGTAACAAGGCAGTCTATCATA  
CTACCGGATCAGAAATTTCTTCTCTCTCCAAAATTTGGGTAOCTACTAAAGCTAATTCC  
CGCAGGGATCGCTTATGTACTCACCAGTGTGGAAGCTTTGCCATATCGACCTGTCTGCTC  
CGCAAGTTCTAGAGACGGGATACAAATGATTTTGGTAACAAACATTCTCAAAAAGTATGC  
CTGATGATGAATCTCACACATCACATGATAATAGCAATGCTGATCAAAATACATTAAAAG  
ACTCTGCAGATGTTACAGATGAACAAATGGATATTGAAGGACCTGGCTTCAACGATGTGA  
AGAATCTTCTTCTATGGAGCCCCACCACUAGCCTACGTCTACAGTAAATCCTATACAAA  
CTATTAGTGACGATATCCAAACGATTTCTTCAAACTAACGTGGAGGTCCGGGCTACTGATG  
CATCGAAAATGGAAAATTTCACTTCCCTCCATTTGAAAATGAAGAAGTAGCGGAGGAGGC  
CAGAAAACATTTCAAATCAGCACTCATCAGCATATCTTACCATCAACTGCTGGATTTGTCAC  
TCGAAAACAGACCGCTAACTCAGGATGAAAACASTATCTCAGAGACAGTTCAATCCACAT  
ACTTGCCAGCGGAAGTATTTCAATGGAAGCTTAAACCAATTTCTCAAGTGCAAGATGTTT  
CAAGAANTGTTAATAATAAAGCATCCAACTTGTGGAGCAACATATGGCACCACCAAGC  
CAAAAAGTACTGACGCAACCAAAATGAACCTACTCACCATACGTGCTCAATCAACTGCCG  
CTAGTCCAGATGGCGATGAATCAACGATTTCTGAAAACATGCCCTGCTATATATGCAAGAA  
CTCACCAGCAGCATTCGATCCAAATCCATCACAATACTTTCTCTTTTGGTCAACCAAGCAATG  
AAACTGCTTCAATTCGAATTTATCTGAATCAACATCCCAGGCACAAAGTAATGGAAATGTTG  
CTTCAGAAAATAGATTTCAAGCCCAATAAAGAAAGCCCAAGTCTTCCGAGAAAGACACTTTTC  
AACCTACTATTTAGGAAGGCTTCAACTAACCAATACAGGGCTTTTAAACCGTTGGAATCAG  
ATGUGGATAAATAAATGACGTTATTGAAGATGAATCCGATGACGACAATATGTCTACTG  
ATGAGGCAAGAACAGAAAGGAACAAAAAAGAAATGTGAATATCAAAAACGAAACAAAAC  
CAAGTAAACAAGGACATAGATGACAAGTCTAATGGTTGGTTTGGTTGGTTGAAGAAAGAA  
CTGCGGACAAAAAGTGTATAGGCCAAGCTAGGTGATATAAAAACACACTATCTATGATG  
AAATTTCAAAACCTTCCGCTCAATAAGGACGCAACCGAAGAGCAAAAAACAAAATATTTG  
AAAGTTCCGGCACCACCCTCTCTCAATCGTCAACCTTAAAGATGGCGGCCCAAGACAA

33/251

AGCCACGTTTCACGCCCCCATCAATAATTCCTTACCTCCAGTACATGCCACATCAGTTATTTC  
CGAACAAATCCAAATCACTGGTGAGCCCTTTGCCGATCAAAACATCCCCCTTCTCCTACAGGAC  
CCAATCCAAACCAATTCTCCATCACCATCCTCTCCCATATCAAGGATTTCTGGCGTAAACT  
TGACTAGCATAAAGGCAAACGGTTTGGATGATTTATTGAGTTTGGCAGGAGGACCCAAAC  
CAGCAAGTACGAGAAGGAAGAAGAAAAACAGCGAGAGGCTATGTTAATGTAATGCATAACA  
TACAATAA

>YPL085W, 2195 aa (SEQ ID NO 384)

MTPEAKKRKQKQKQKKAABKAASHSEEPLELPSTINSSFNDDSVNRTESDIASK  
SDVPPVSSSTKISFANETQLEIPDTQELHHKLLNDSQHDITADSNLDPNLSIVEHDSVT  
TQTKPAMSQYEETAAHLLSSRNPSLDVVAGELINNNENITQKIAVSAVEEDSFNEEDQENH  
DSIIISLNDATPSQYNHFLPSDGNLLSPELSSGDTPTHNVPLGTDKNEINDDEYCNDE  
TSLNANNVTPDELKSKFEDERLKLETHVSTEEKQDIADQETAENLFTSSTEPSENKIRNS  
GDDTSMLFQDDESQKVPWEEDVKKDFHNENTNNTQESAPNTDDRDKGVEGNEZALKKSES  
CTAADERSYSEETSEDI FHGHDKQVVEGQNDFTGKNIEVESQKLMGEGNHKLPLSAEADT  
IEPGKDIQDQAEIDLFTQSSGDLGEVLPWESTDKNADVTSSKQEKHEDLFAASGNDEKLPW  
EVSDEGVSSGKTENSMQTSTEKIAEQKFSFLENDLDDDDSLASSEEEDTVPTNNT  
TNLTSKPVEEKKASRYKPIIEEEAACMRQEQVHFTNTTGI VTPQQFHCLTKTGLGTPNQV  
SVPNIVSPKPPVVKDNRSNFKINEEKKKSDAYDFPLEII SESSKKGHAKPVAVPTQRFGS  
GNSFSSLDKPIFQSRKGSNNNSNRPPVPLGTQEPSSRTNSAISQSPVNYATPNPYKIQQ  
LQQAPIQSGMPLPNTINIPPPALKVETTVSAPP IRARGVSNASVGSSASFGARHATQYGLN  
NGVPPVSPYQQTINLPTANKYAPVSPVQKQYPSVVQNLGASAVNTPNFVKTHRGHTS  
SLSSYTPNQNEHASRYAPNVQQSYQVPYTSQPVGPVAGNSSYQSQTSSSYAVPMPQAQT  
SASIQPHANIQPPTGILPLAPLRPLDPLQAATNLQPRASNTAANSPLANLPLAENILP  
EII THRATSSVAPPKQENNP I KIDNEALLKRPPIFHWSAANKVVYAVPPIPDQSUYMIS  
SSIVQELKVTPIDQIIKPNMMLKSFPGLCSAKLKKKDLTKWMETTIKSI SENESSTDMT  
IWQIM EMKLNDRKVNWNKISKLLYNSDELLMYLSQFPNGDMI PNAYRLDINCQMRVLAFL  
QTGNHDEALRLALSRRDYAIALLVGSLMGKDRWSEVIQKYLEGFTAGPNDQKELARHLL  
LIPQVVGNSKMYAKSFYTNNETSQWASENWKSTVAAVLINI PENNEDPLLI PPVLEFL  
IEFGIFLTKKGLTAAASTLFIIGNVPLSNEPVMADSDVIFESIGMMNTFESILWDEIIEY  
IPSYCPKFKGPSSTLPQKTYHASILQRCGNSLGTKYTDYLSSSVRKLPKKDILTINLTR  
ELSEVASRLSEENTQWLAKPKLSSVWGQLDKSFNKYIGDDIDALNKKNDKKKVFQGFTE  
GSSANSSTVDLTQTFTFFQAQVTSQS YVDTTALLHNAHNVPSHSLVLSKPSNVSKGLVEA  
NLPHYTHRIGDSLQGSPQRIHNTQFAAAEFQMASLRVRVTDQHTNEKALKSQQIIEKKSTA  
YTPQFGQNHSEVPMKSNENVP SLFADFPAPPKLGTVP SNYVSSPDLVRRESII STGSEFL  
PPPKIGVPTKANSSQGSIMYSPSVEALPIDPVVPQVHETGYNDFCNKHSQKSMPEDESHT  
SHDN SNADQNTLKDSAEVTDETMDIECPGFNDVKNLLPMEPNHQPTSTVMP IQTI SDNIQ  
PTLQTNVFEVRGTDASKYENS LPSIENERSSEEQPENISKSASSAYLPSTGGLSLENRPLT  
QDENSISEFTVQSTYLPAGSISMEAKPI SOVQDVPRNVNWKASKLVEQHRAPPKPKSTDAT  
KMNYSPYVPQSTAASADGDESTILKTSPAIYARTHQAHASNPSQYFPLVNQANETASPEL  
SESTSQAQNGNVASENRESPIKKAEVVEKDTFQPTIRKASTNQYRAFKPLESDADKYND  
VIEDESDDKNYSTDEAKNRKEBKRVNMKKETKPSNKDIDDKSNGWFCWLKKTQCKRVY  
KAKIGHKWPIIYDEKLKRWVNKDATEBEKQKITESAPPPPIVKKRDCGPKTKPRSGPI  
NNSLPPVHATSVIPNNPTTGEPLPIKTSHPSPGPNPNNSPSPSPISIRISGVNLTSEKKAN  
GLDOLLSLACGPKPASTRKKKCTARGYVNVMDNIQ

>YPL190C, 2909 bp, CDS: 501-2909 (SEQ ID NO 387)

TAATCTTCCCTACTTCAAGTTTCATAATCAATCGACTTCTGTACGGSTAAGCATCTCGT  
GAGATGCAGTTTCATTAATGACACCCACAAATACAAAAGAGACTATTTAATATGTATATAG  
ATCACATTCCAAAAAGAAAACCATTAACTAATATCACTCTTTAATATTCCAAACTGAAAC  
GAAAAAGCGCTATTCTTATTCGCTTCCTAACTACCCCCCTAGTTCTGTGCTTGCAATTTTTT  
TGTAGAACGATAAATTATGGTATCCCACTGATTGAGTGTAACCCCGAATTGTGGAAGAG  
AAAAATGAAGCGGAAGCAAGCAAGGACAAAAACAATTTCATTTGACTTTGCCACTCTCTAAA  
TGAAGGTCTAATAAAGCTATCTTGAGCATCTTTATTACATTCAGCACAGCAACAGCGA  
TPTTCTTTGGTCAAAATATAATAATTGACTTACCTTTTCCCGGACTGTCTTTCTATAAT  
ATAATAACCATCTTGCAAGCCATGTCAGATGAAAAACATAACAGTGATGTTCAAGATATTC

CTTCACCTGAACTATCCGTCGATAGTAACCTCTAACGAGAATGAATTGATGAATAACTCAAC  
GCGCAGACGATGGAATCGAATTTTGACGCCCCAGACCAAGAAACACAAGCCGAAACCGGACG  
AGGAAAATGPAAGAACCAACACGAACCTGGAAGATGTGAACGATGAAGAGGAGGAAGATAAGG  
AGGAAAACCGAGAGGAAAACCGGGGAAGTAATAAACACAGAGAAGAAGAAGAAGAAGAAC  
ATCAACAAAACCGCCGCAATTCATCATGACGATGATGATAATGAAGAGGAAGAAGGGAAG  
AAGAGGATGATGACGATGATGATGATGACGACGATGATGATGAAGAAGAAGAAGAGAGAAG  
AAGAAGAGAAGCGCAACGACAACAGTTCCGTTAGGCTCAGATAGTGCCGCTGAAGACGGTG  
ACGATGAGGAAGACAAAACGATAAAACCAAGATAAASAGCTCCAACTTCCCCCTGAAA  
CATTCGAAAAAGAACAAAACGACGTAGATGAAGCTATAAAAAAACTAACTCGTGAAGAAA  
ATGATAATACTCACCTTCCAACTAATATGCAAAATGTTAATTACGATCTTTTACAAAAGC  
AATCAAGTACATTATTCACAGTAACATGCTAATTTGCCTCAGTTTCAACATTTACCTC  
AAGAAGAAAAGATGTCTGCGATTTTTCGCAATGTTAAATTCAAATTTCTGACACAGCTCTTT  
CCGTACCTCTCTCATGATAGTACTACTATCTCAACAACAGCTAGCGCTCAGCCACAAGCGCGC  
CAAGAAGCATATCATCAAGAAAACCTCCATTTCTCAGATGCCCAAGACCTACACATTTTC  
CTAGGGCGGATTTATCTTAAGCCGATTTACCGAAGAAACACGACCGTTATGACGCTTATTT  
TGCACGGTGAAAAAATAATCACCGAGATGCACAAATATTTCTCCGAAGTCAAGATTATTC  
TTGCTAATTTCCCGCTTAABGAACGTTTCTAAGCAGCATTTATTTAGGATTTCTCTCCAT  
ACGGTCATATCATGCAAAATCAATATCAAAAATGCCCTTTGGATTTCATTCAGTTTGACAACC  
CTCAAAGCGTTAGAGATGCAATTGAATGCGAGTCTCAAGAAATGAATTTTGGCAAAAAGT  
TGATCCCGGAAGTTTCTAGCTCGAATGCTCGTCTCTCAATTTGATCATGGTGATCACGGTA  
CAAACAGTAGTTCTACTTTTATTTCTTCCGCAAAACGACCATTTCAAACTGAATCTGGTG  
ACATGTACAATGACGACAATGGTGCTGGCTACAAGAAATCCAGAAGACACACCGTTTCTT  
GCAACATTTTGGTTAAAGAAACCGCAGATCGTAAGTATGCCATTGAGGTTTTCAACAGGT  
TTAGGGACCGGACTGGTTTGGAAAACCTGATATGATTTTCTTGAACCAAGAATGGAACCTGG  
GAAAGCTTATCAATGATGCCGCATATAATGGGGTCTGGGGCGTTGTTTATGTTAATAAAA  
CACACAATGTAAGTGTTCAAACTTTCTACAAGAGCTCACAAAGTGAAACGAAATTTGATG  
AATATATTAACCATATCCCGCTGATGACCGCACTTGCCATTTTAAATACATCAAAAACAACA  
GAATATAATTTCTCTCTCTACTGATTAACCGTCTCTATGAGCCATCAGCAAAACATATATGGCG  
CTCTCTCTCTCTCTGTTTCAAACGGCCCCAGCTGTCTGGACCTCTCTCTCAAACAAACTATC  
ACCAGGGTTACAGTATGCCCTCTCCACAACAACAACAGCAACAGCCATATGGTAATTATG  
GGATGCCACCACCATCCCATGACCAAGGATATGGTTCTCAACCTCCAATTTCAATGAATC  
AGAGCTACGGTCTGCTACCAAGCTTTCTATTCCACCACCACCTCCACAACAACAATTCCTC  
AAGGGTATGGTGGTTATCAGGCTGGTCCGCCCTCTTCAACCACCTTCTCAAACCTCCAAATGG  
ACCAGCAAGCAACTATTATCTGCCATTCAAAACCTTCCACCTAACGTTGTATCGAATTTGC  
TTTCAAATGCCCCAACAAACAGCAACAACAACCTTCATGCTACGACGAATTTGGTTGGTTTAA  
TACAATCAATGCAAGGCCAGGCCTCTCAACAACAGCAACAACAAGTTGGGTGGATATTTCT  
CTATGAACTCATGCTCTCCCCCTCTATGAGTACCAATTACAATGGTCAAAAATATATCTG  
CAAAACCTCTCTGCCACCAATGTCAACACCAACCTCCGCCACCTCAACAACAACAACAAC  
AACAACAACAGCAACAGCAACAGCAACAGCAACCTGCTGGCAATAAGTTTCAAAGTCTAT  
TAGATAGTTTTCAGCAAACTCAAAAATAG

```
>YPLI90C, 802 aa (SEQ ID NO 388)
MSDENHNSDOVQDIPSPELSVCNSNENELMNNSSADDGIEFDAPEEEREAEEREENEEOH
ELEOVNDEEEBEDKKEKGEEKGVEINTEEEEEEEHQQKGGNOCDDDDNEEEEEEEEDDDDD
DDDDDDDEERKEEEEREGNDNSSVGSDSAAEDGEDDEEDKKKOKTKDKEVELRRRETLEKQK
DYDEAIKKITREENDNTHFTTNMERVXYDOLLQKQVKYIMDSNMLNLQFQHLTQEEKMSA
JLALMNSNSDTALSVPPHDSYISTTASASATSGARSNDQKKEPLSDAQRRMRFPADLSK
PITEBBHDAYAAYLHGENKITEMHNI PPKSRLEFIGNLPKKNVSKEDLFRIFSPYGHIMQI
NTKNAFGFIQFDNFPQSVRDAIECESQEMNFGKKLILEVSSSNARPQFDHGDHGTNSSSTF
ISSAKRPFQFESGDMYNDONGAGYKKSREHFTVSCNLPVKRTADRTYALEVFNPFREGTGL
ETDNIPLKPFMBELCKLINDAAYNGVGVVVLVNKTHNVDVQTFYKGSQGETKFDEYISISA
DDAVAIFNINIKNRKXNSRPTDYRAMSEHQNNIYCAPPLFVPNCPAVCPPPQTNYYQGYSM2
PFOQQQQQPYGNYGYMPPSHDOGYGSOPPIPMNQSYGRYQTSIPPPPPQCOIPQGYGRYQ
AGPPPPQPSQTPMDQQQLLSAIQNLNLPNVVSNLLSMAQQQQQQPHAQQQLVLGLIQSMQGO
AFQQQQQQQNGGYSSMNSSPPPMSTWYNGQNI SAKPSAEPMSHQPPPPQQQQQQQQQQQQ
CCQQPAGNYSGLLDSLAKLQK
```

35/251

&gt;YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)

ATTTTCATCACTTCATTAGTATATAAAAGGAGTTCCCATTCGACGAGAGAAAATAATCATTTGT  
 TTATTTGTCGCTAATTTTCTTTCCATAAACCATAACTGCAGTTTCCATTTCAGGGTCGCCA  
 ATTGGTTGGACAACGTTGATGTTACCTTCCCTTGTATGGAACCAATCCATCACTTTCTAGT  
 TCTTCTTCTGCAATATTGCCCTTTTGGGAAGAAAGGATCGAAAGTAGCCATTTCGAGACACCG  
 TTTTCTACTATATTTACTGTATCTTCGATTCCGCCGCTAAAGTTGCCATATTATTATTATA  
 TTGCAGCTCAACCCCGCATTTCCGGAGCTTTCTTTTATTTTGGGGTAATTTGGGAGG  
 TCGCCCGCTATTGGTCCGCCGGAAATGGTGACACACTTGTAATATATAAGGAGGAAATCC  
 TACATGTGTATAAGCGAATCACAAGGATAATTAATGTATTTGCTAAACACCCCTCAAGAAAG  
 AAAATAATCATAACGAATCATTGGGTATACCTATGCAATATATACCAGGATGGGAAGGGGG  
 TCCATTTTACCACACGAGATATCAGAACGTATTTGACGAACGGCGGAGCAAGTATGGCA  
 ACTACACGGTGAATAATGATTACCCACAGCTTCCAGATACCATTAAGGAACATATCCACC  
 AGCTTACCTTTAGCAATGTUGGAGAGGATGGTGGAGATGTTGGAACTATTCTGAAGAAG  
 ACGATGTATGGTGACGAAGAAAAGGAACCTTGAAGATGTTTTCGAAGTAACCGTGGGTTGG  
 AATTGTACGGATTAATAACTATTTTACTACCCACGATTTACAAAGTTTCAAAAGTTTTA  
 GAAATTTCAALAGCAAGTACTGGATTTTATTATCTAATCAAGCAGAGGACAAAAATTAC  
 TCTGTATGACTTTAACGGCCAACATTTGATTTTATTAAAGCAGCAATTTTACGGGCAGT  
 TGAATTTACTGCTATCGGACGCAATATATGTATGGACTGCAATTTTGGTTATAATTCAA  
 ACACCAITCAAATTTTAGTTTGAATTTACAGAAATGGAAGTTTGTAAAGCTAAACTGCGACT  
 TGAACGGAAACGTAACAATCACTTGCCTTTGAAGGATCCCTCAACCTCCCTCATCAAAA  
 GCCACCTATCTATATTAAATGTCTGGGCAGCTTTGTTCACCATTCGTTGTTCTTTTA  
 GTTTGAAAGATGGGCTGCTAATAACTTCTTTAGATCACCAACAAACCAATCCAACTTTTC  
 AAAGTTTCCATACCAACATTTGATTTGCCCTGTAGATCTACGCACGACCACAAAATGTCAAGT  
 CCGTTTTAAATTTCCCTCAGTTTACTTTATACAAAGGAAATGATATGATTTTCCUACTGCA  
 AGAATCTATTAGGATCGGATGCTTCCACGCTAAACAAGGAAATAAATCTCATGCTTAAAA  
 TAGACGAAGACGTTCAAAAGATCGACTATCTTCTTAAACGAATCACATTTACTCGAAA  
 CCAACATGAGATATCTGTCCATTCUACAAGAGACCCCATAGAGAAATCAAAATTCCTCTC  
 CACCCGTTCTCAGACAGGAGGTTTATCCAAATATTTTACAAGACACAAGAACTTCATGTC  
 ATGCTTTCAGGAACAGGAGGTCAGATAGCAAAACAATGGGAAGTATATTTTATTAACCGACC  
 AACATCTCTACGGAACAGCGTTATCGGTATACAAGTACTCTATATCTTTTCAAACGGTGGC  
 TGTTCGTGGGCTACTCAGACATTTAGCGCCAAATACGGTATAAGGAGTGTCAAAGATCTCT  
 TTGTTGGTAAGTGTCCCTCTCTAAATAGCCCACTGCTGACAATTTCTACTGATGACAATA  
 ACATTCAAACAATTTCTTCTTAAATAA

&gt;YPL201C, 461 aa (SEQ ID NO 390)

MGIEMQIYQDGKGVQFYHTRYQNVFDERASKYGVNYTVNNLYPQLPDTIKEHEDQITFSNV  
 QEDGGDVGNYSSEEDFDGDEEKELEDVFRSNRGLFPVRLNNYFTTHDLQSPKSPFNNSKY  
 WIFYSNQAEDEKLLLYDFNGQHLLFIKQQFYGQLNLLSDAIIICMDCNFGYNSNTIQILV  
 GFQNGKLLKLNCDLNGVNNHLLKDPSTSSHQSHLSILNVWACLLPHFVVSFLKDCLL  
 ITSLDHQQSNGSFQSFHTNIDLFPVDLRTTINVKSVLNFPQFTLYKGNDMIFICKNLLGSD  
 ASTLNKEINFMLKIDEDVQKIDYLLKCNHLLLETNMRVLSIPTRDPIENSNSPPVSDSE  
 VYPIFYKTQELHVHASGTGRQIANNGKYIFITEQHLYGTALSVYKYSISFKRWLFVGYSD  
 IRAKYGIRSVKDLFVGNCPVNSPVLITLTDNNIQTILLK

&gt;YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2: 685-1176 (SEQ ID NO 393)

ACAACCCCTGTCAATCTCCTGAAAAACAAAAATTAAAGTGCTTGAGAAGACCTTCAGAAGA  
 GTTCCATAGATAGGATGGGTGAGCGCAATTACTAGTTAUGCAAGTAAGTAGGTATATATGGC  
 TGTGAGACGGCCACTACTGATTTAATCACAATCCGGATTAAACTTCTCCTGAAAAAAA  
 AAAACTACATCAAGTCAAAAGATTTTCATTCACTCTTTGGAAGGCTGTGTGGCATTCTAA  
 CCTTTATTTTTTATCACCATTCTCGAATTTTGGTGGTTTCGCTTCTTAGCGCCGTTAT  
 CTCTCTTCTTGTCCACGTCAAAAGGGAGTATGCGTAACCCCTTTCAAGTTTGAACGAAAAA  
 AAAAAAATATGTCTTCAAAATTTTITTTGATTTTAAAACTAAAAACAATTTCCCTTTGAAG  
 CTCTTTATTCGAAAGAAAGAAATCTAAAAATGCAATTTGGTAGTGAAAAACAATAAACAAA  
 GACATAACCCCACTCCAATCATGTCCGAATATGCATCTAGTATTCACTCTCAAATGAAAC  
 AATTCGATATCGTATGTAAGATGGTTTTATTGGTTCCATCGTCATCATGTTTCAACAGC

36/251

CAAAATGACCCGACACACCGTAACCGAAGCAGTTATACTAACAAAGAAAGCTAATTTTCACCC  
 TCCTTGCTACATTTTCTTCTACAGAACTACTCTCGTAATAAGAAATTTACACCAATTAGAA  
 AATRAAACTAATTTGCCCTAAATCTTATTTAGTTGCTGGTTTAGGTTTCGCTTATCTCCTT  
 TTGATTTTTATTAACTCGGAGGTGTAGGTGAAA'TTCTT'CCAA'T'CTGCTGGGTTTG'G  
 TTGCCAGCATATTTATCGTTGGTTCCCTTTGAAGACACCAACGTCCACCGATGACACACAA  
 CTCTTGACCTACTGGATTGTCTTTTCATTTTGAAGTGTCAATTGAATTCTGGTCCAGGCA  
 ATTCTATATTTGATCCCATTTCTACTGGTTTGTGAAAACUGTTTCTTAATCTACATTGCC  
 TTGCCCTCAAACCTGGTGGCGCTAGAAIGATCTATCAAAAGATCGTACCCCCATTGACCGAC  
 AGATAATATCCTAAGAGATGTTAGCCAAGACAGAAAAGGATGAAATTAGAGCTTCCGTCAAT  
 GAGGCTTCTAAGGCTACAGGTGCTTCTGTTCATTAA

>YPR028W, 180 aa (SEQ ID NO 394)

MSEYASSIHSQMKQFDTKYSGNRILQCLENKTNLPKSYLVAGLGFPAYLLLIIFINVGGVGE  
 ILSNFAGFVLPAYLSLVALKTPFTSTDETQLLTYWIVFSFLSVIEFWSKAILVLTIFYWFI.  
 KTVFLIYIALPQITGGARMLYQKLVAFLTDRYILRDVSKTEKDEIRASVMEASKATGASVH

YDR145W, 2120 bp, CDS: 5C1-2120 (SEQ ID NO 99)

AAGTGATATCTGAATAATGAAAGATGGTAGGAAATAAGGTATTGAAACA  
 GGTTCAAAACCTTTAAAGAAAACCTGCCAAATAAACTTTCTCGATGCGTAG  
 CTGAAATTTCAACTTCAAAAAAAAAAAAAACGCGTGTAACCTTTCTACGTGC  
 AAAACGATGTGTATGAATCCCGTCTTAATTAGTAAATAGGCTCTAGTAAG  
 CGTAGCGAGGATGAATTAAATGCATTGTTGAATATGAAGAGCACCTTATG  
 GTATATAAATCTACAATCTTGATTCAATGACAGCTTTGCAAGTAAACGTAAT  
 CAAATGAATAACAGATTTTGGCTGTATTAACCCGGGCACTATACCGCGCG  
 AATTTTGTAAAAAATGTCTTAGACTTTAAGTCGGAGCAAAATGAATAATGG  
 GCATATATAGCGCATAGCTTCGCTAGTGTAAGACAGGAGACTGTCCAATA  
 GCATTCGAATCATACCGAATCTTTCCCGTCTCTGTATATAAATACGACA  
 ATCTCTTCCAAATCCACAAAATTTCTGCTGTTAATGCGAATAATAAATACGGG  
 CACTGGTAACGCTGATGCGATCACAGGAGCTCAGCAAAATATGCTACTGC  
 AACCGAGACAGTTGCAAGAAATGGCCGCTAAGTTCAAGGACATTACTGAAT  
 GAAGCAAGAAATGTAGGTGAACTACTTCTAGGGGCAAGGAATTGATGTT  
 CCAAGCCGCAAAAGATCAAAACAGGTATATGATGCCCTTACACTGAATAGGA  
 GAAGACAACAGGCTGCGCAAGCCTACAATAATACCTCAAATTCAAATTCA  
 AGCAATCCAGCTTCTATCTCTACTGAAAATGTCCCTAATTCATCACAGCA  
 ACAACAACAACAACAACAACAACAACAACAAGAAACAACAGTAACAAATTTAGCA  
 ATATGATAAAACAGGTTCTCACCCCGGAAGAGAACCAAGAAATATGAAAAG  
 CTATGGCAGAAATTTCCAAGTCCGTCTATACGAGTATAAAGGAGAAAGAGAC  
 CTACTTGAAACAAAATATCTGATAGGTTAGAACAAGAAATAAATAAACAGA  
 CCGACGAAGGGCCCAAGCAGCAGCTACAGAAAGAAAATTTGAATCTGCTT  
 AACGATTGGAAAGGTGCTAAAAATTGAGTATACCAAGCTGTTCATAAATTA  
 TCAAAACAGTAAAAAAACATTTCTATGTAGAGTGTGCAAGACACAATTCGG  
 CTTTACATAAAATTTCTTGCAAGAAAGCACTCAACAGCAACGAGTGCAGCAA  
 CAAAGGGTACAACAACAACAACAACAACAAGCAGCAGCAGCAGCAACAGCA  
 GCAACAGCAACAGCAACAGCAACAGCAACCGCCAGGGTCAAAACCAAAGAA  
 AGATTTCTAGTTCTAAATCTACTGAATACCCCTCTGTAACCGGCTCTGAT  
 GCACTGAAATCGCAGCAGCAGCAGCAGCAATACAAATACTGCCACCAATAA  
 TCCAGGGGCAATGTTAACACTTCACAGACTGAACAATCGAAAGCTAAGG  
 TAACCAATGTAAATGCAACGGCATCTATGTTGAATAATATAAGTTCGAGC  
 AAATCGGCAATATTCAAACAACAACAAGCCTCCCTATACCCNTATCCGAAA  
 TATATCTACCAAAACACCAGCACCGGTAGCTATAGATCCAACAGACCTA  
 CAATAACTCGAGCTTCTGCTATGAATGCCAGTGTTTGAATACACCAGCA  
 ACAACTAATTTACCCCTATGAATGCATACTCAGAGAGTTATGTCAAA  
 GCGTAAATTAAGAGAGTTAGTGAAGACTGTGGAATTGATGAGGGTGAAG  
 GTGAAACTGTCACTGACGGTGAATGTGAGGAATTACTAATGGATCTTGCC  
 GACGATTTTGTACCAATGTACAGCTTTTCTTGTAGATTCCCAAAACA  
 CNGAAATCCGACAATTTGGAGGCAAGAGACATTCAATTACATTTGGAGA

37/251

GAAATCGGAATATTAGGATTCCTGGTTATTCCGCAGACGAAATAAGAAGT  
 ACAAGAAAATCGGAATCCCTTCCTCAAAATATATAACAGAAATTCAGAGTAT  
 CACATCAGATTAAGGTAGCAGCTGC AAAAACAATCGAAACAATGTTTGCAG  
 GUTTGAAATACAAAAAATAA

YDR145W, 539 aa (SEQ ID NO 100)

MSSNPENSGVNANNNTCTGNADAITCAQQNMVLQPRQLQEMA AKFRLLLT  
 EARNVGETTPRGKELMFQAAKIKQVYDALTLNRRRQQAQAYMNTSMNS  
 SNPASIPTEENVNSSQQQQQQQQQTRNNNSNKFNNMIKQVLTPEENQ EYEK  
 LWQNFQVHITSIKKETYLKQNLDALEQLINKQDDEGPKQQLQEKKIELL  
 NDWKVLKIEYTKLFNNYQNSKKTFFVECARHNPALHKFLQESTQQQRVQQ  
 QRVSQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQRQQNQRKISSNSTEIPSVTQPD  
 ALKSQQQQQONTTATNNPRGNVNTSQTEOSKAKVTNNVATASMLNWISS  
 KSAIFKQTEPAIPISENISTKTPAPVAYRSNRPTITGGSAMNASALATPA  
 TTKLPVYEMDTQRVMSKRKILRELAKTVGTBEGDGRTVFDGDVRELIILDLA  
 DDFVTVNTAFSCR LAKHRKSDNLEARDIQLHLERNWNI RIFGYSADETR  
 TRKWNPSQNYNQKLSITSDKVAAAKNNGNNVASLNTKK

YDR216W, 4472bp, CDS: 501-4472 (SEQ ID NO 109)

CAAAGAACAACGCCTTAAAAATAGGAAAACGTTTTCTGCFACAGGTGTTGT  
 TATTATTGTTGTTGTTGCTGTTGTTTATTGTTGCTATACTTGTTGTTATTTAT  
 TCTGGACTTCGGATCGGAATTTTCTTCCCTTGAAAGACCTTTTGAAAGACA  
 ACAGTTATATATCATTTGATCTGAATTTCTCAGGCTATTTTCAAATTTCCA  
 TACUUCUUTATTUUAACATTTGCTUGACTACTATAGAAAAGUUTTATTCT  
 TTTATCTTTGAAAGAAAGAAAGGTGTCATAGCAAAAGTTTATCTGTTACT  
 CTGTTTGTGATATACTCCCTCTTATTCGTTGGAAGTATAAGATTGATTTGC  
 ATAAATTAACCAATCATTTTGCTACTTTTCCCGGTTCTCCCTTTATATATA  
 ACACCTTCAGAAAAATATTCTGCTACTATTTCCTTACTTTACTATAAGAAAT  
 TTGTTTTCCAAAAAATAATATATMAAAATAAATCATACTCTATTACT  
 ATGGCTAACGTAGAAAAACCAACGATTGTTTCAGGCTTTCCCGTTGTTGA  
 CTTGAAATTCGTGCTTTTCTAACGGCTTCAATAATGAGAAACAGAAATAG  
 AAATGGAACCGGATGATTACCGGATTTTATTAATGTCATCATCAGCTTCC  
 ACACAAAACCTCAAACACTTTCTCTGTGATACAGAGGACGCCAGATGGAAA  
 GATCATTACCACAAATAATAATATGAAC TCCAAGATTAAACAGCAACTGS  
 ACAAGTTGCCCGAAAAATTTAAGGCTTAAATGGTAGAACCCCGAGTGGGAAA  
 CTAACCTCATTTCTTTCCCGAGCTTTGTACCGAGAGCGTTCCCAACACAAAG  
 GCCTTTGAAAAGACATTACAGATCGCATACAAATGAAAAACCTTATCCCT  
 GTGGUUTUTGUAACAGATGCTTTACTAGGAGGGACTTACTGATCAGGCAT  
 GCTCAAAAAATCCATAGTGGTAATTTAGGGGAAACGATTTCCCATACCAA  
 GAAAGTGTGAGAACTACAACATAAGCTCGGAAAAATTTCTGCA TCTTCAG  
 TCAAGTTTCAAACCTCCAACCTATGGTACTCCAGATAATGGTAAATTTTGT  
 AATCGCACTTACTGCCAATACAAGAAGAAAAGCAAGCCCTGAAGCTAATGT  
 TAAACGTAAGTACTTTGAAAAAACTGACGGGAGGGCTTTCATTTAGCGCAC  
 AATCAGCATCCAGCTATGCTTTTGCCTGACCAATCTTCGCTAGAACACAT  
 CCAAGGATCGTGTTAAATTTTCTACGCCCTGAATTAGTTCCACTTGACTT  
 GAAGAATCCTGAACCTGACTCTTCTGTTTGACCTGAATATGAATCTAGATT  
 TAAACCTAAATCTAGATTCCAATTTCAATATAGCATTAACCCGTTCTGAT  
 TCTTCTGGATCAACAATGAATTTGGATTATAAATTTGCUUGAATCAGCAAA  
 TAACTACACATAITCTTCCGGCTCACCACCCGCGCATATGTGGGCTTA  
 ACACCAATTTCTAAGAAGCTTTCATTTAATGACGAGACTTATTGTCTGCG  
 TCGTACTGGATAAAAGCCTATAATGATCATTTGPTTTTCAGTATCTGAAAG  
 TGATGAAACTTCTCCAATGAACCTCTGAATTAACGACACTAAATTAATCG  
 TCCCAGACTTTAAATCGACTATACATCATTTCAAGCATTAACGTCCTCC  
 TCTTGGACTGTTTGCTATAGATAATAATAGCAATAACAATAAGCTATCAGA  
 CAACCAACCTGATTTCTGTCATTTTCAAGAACTGCTGGATAATGATACTT  
 TAGGTAAATGATTTCTTACACACCACTGCGGTTTTTAAAGAAATTTGAACTT

38/251

TTACATGATGATAGCGTAAGTGCTACCGCCACCTCAAAATGAGATTGACCT  
 TTCCCATTGTAACCTATCAAACTCTCCAAATTTCTCCACATAAGTTAATTT  
 ATAAGATAAAGAGGGGAUCCAATGACGATATGTTGATTTCTTTGGGACTC  
 GATCATCTCTCCAATCCCAAGATGATCTGGATAAGCTATGTAATATGAC  
 CAGAGATGTTCAAGCCATATTCAGTCAATATTTGAAAGGAGAACAGTCTA  
 AACGATCCCTGGGAAGACTTTTTATCAACGTCAAAACAGGAAAAGAAAAGCCA  
 GATAGCGGCAACTATACCTTTTTATGGGTTAGATTGTTAACCTTATCGAA  
 AATATCAAGAGCTCTGCGCGCCCTCCACTGTGAACAACAATCAGCCATCGC  
 ATTCCATAGAAATCAAAGCTATTTAATGAACCAATGAGAAATATGTGCATT  
 AAAGTACTTATGATACTATGAAAAGTTTCACTCATGATAGTAGTGAGAGTGT  
 CATGGACTCTTAATCCAAACTTTGCTGTCCAAAGAAATGTTAATGCCAGCTG  
 TGAGTGAATGGAACGAATATTTAGATCTTTTCAAGAATAAATTCCTTCCC  
 CATTTCCCTATTTATTCACCCAAAGCTTCCTTCATTTCGATTTGGATAGCTT  
 GCACCGATATACCTAATGAGGATGGGTATGATGACGCTGAAAACGGCCAGT  
 TGTTCGATCGATTAAGTCAAGGGACAGATAAAGAATATGATACGAGCAC  
 TATCAAAATCTTGTCCATTTGAAAAATCGTTTGTPTACCTTATTTATCCC  
 CACATTTGGTTCTTTTGATAAGTTTGGGTACAAATCTCAAACAATAGAAT  
 TGTATGAGATGAGTAGAAGATTTCTACATTTCTTTTTTGAGAGCTAAAAGA  
 AGGTGTCGCAGTACAACAGTAAATGACACTTATCAGAACATTTGGTTGAT  
 GCAATCCCTAATATTGAGCTTCATGTTCTGCTCTAGTTGCTGATTATTTGG  
 AGAAAAITGACTCCCTCTTGATGAAAAGGCAATTTGTCCGCATTATGTTCA  
 ACGATCAGATCAAACCTGTTTACCGACAATTTCTGCAAATTCGAGAGAG  
 TATCAATANTAACANTCAACCTTTAACAATTTGGTTCTCTCTTCAATACA  
 TCATTTTGTAGTCAAAAATTAGATGCACCTTAATGGCTTATGATTTTGT  
 CAGTTCTTGAAATGTTTCTTUCATATTAATTTGATTTTGTCTATAAAGGA  
 AAAAGATGTTGAAACCATTTATATTTCCCGACAAAGAGTCAAAATGCCCCA  
 GTGAATCGATAACATGTAATGGGCATGTTGTGCAAAAGCAAAATTTTAT  
 GATTTTAGAAACTTTTATTACAGTTTCAAGTATGGACACTTACACTCAAT  
 ACCAGAATTTTACGGTCTCTATGATTTTATTATGAATACGATTTAAGAA  
 AAGGAACCAAAATCACATGTGTTTTTGGATCGAATCGATACGAAAAGGCTA  
 GAGAGGAGTCTTGACACTTCTTCTATGGCAATGATAATATGCCAGCAAC  
 CAATAAAAATATTGCGATCTTAATTTGATGACACCAAAATTTTGAABAATA  
 ATTTAATGTCAATGAGATTCATCAAAACAGATTGATCGCTCGTTTACTGAG  
 AAGGTTAGAAAAGGACAAATAGCAAAGATATATCATTCCTTTTTTGAACCTC  
 TGTGAGGTTGAATTTTTTGAAGAATTATTCAGTTGAAGTATTGTGTGAAT  
 TTTTAGTAGCGTTGAACTTTTCAATCCGTAATATTTCTGTCTTTATACGTA  
 GAAGAAGAAAGTGATTGCTCCCAACAAATCAATTTCTCCAGACCTGCCAAC  
 GATCCACCTGAATAATCAAGCGCTTCTGTCTTCAATTTACAAGGCTATT  
 ACTATTGCTTCATCCTAATATCAAAATTTTATTTGAAATTTTGAAGUAAC  
 CCAAAATTTAAGTTACTGAGAATTTTATTEAGTTGAGAAGCCTTGCGAA  
 TTCTATTTTACTTCCCACACTTCAAGATTGTATCCGCAAGAGTTTCTG  
 GATTTCTGTGATCTTGTATTTACGCAACAATTTATRAATAAAGATAATGGT  
 ATGCTTGTCTTCTGGTTTTATCCGCAAAATGAACACCATATTTGGTGCAGTGC  
 AGCTGTTAAGACTAAGTTAGCUAAAAAGATCAATGTTGAAGGGCTTTGCAA  
 TGTTTTATTAATGAAATCCTAGTTAACTCTTTTAAAGGATACCTCTTTTTTG  
 AATATGGAGGATCCTATTGCAAAATGAATTTTCTTTGATAATGGGGACAG  
 CCCAGTGACAGACTTGCTCTGTTTCAAGCACATTTCTATCGGATACCGGCC  
 TAGAAGGTATTAACCTTACGGGCTTAAATGATTCGCATCAAACTGTTTCT  
 ACTTTGAATCTTTTACGTTACGGGAAAAATCATTCATCAAAACATAAAAA  
 TGGTGGAAAGGGGCAAGGATTTGCCGAAAAGTACCAATTATCTCTGAAT  
 ATGTTACTATTCCCAAGTTATTTTTTACCATACTTAAAGAAAACACTACATT  
 CATTTGTACATGTTAGATAAGATGGCAAGTGATTTCCACACTTTGGAAAA  
 TCTATCTAAAGGGAACAGTTGA

39/251

YDR216W, 1323 aa (SEQ ID NO 110)  
 MANYEKPNDCSGFVVDLNSCFNNGFNNEKQEIEMETEDSPILLMSSSSAS  
 RENSNTFSVIQRTPDCKIITTNMNMNSKINKQIDKLPENLRINGRTPSGK  
 LRSEVCEVCTRAFARQEILKRIYRSHNTNEKPYTCGLCNRCFTTRDLLIRH  
 AQKIHSQNLGRTISHTKKVSRITTKARKNSASSVKFQIPTYGTPDNGNFL  
 KRRTANTRRKASPEANVERKYLKKLTRRASFSQAQSASSYALPDQSSLEQH  
 PKDRVKFSTPELVPLDLKNEPDLSSPDLMNMLDLNLNLDNPNIALNRS  
 SSGSTMNLDYKLPESANNYTYSSGSPTRAYVGANTNSKNASFNADLLSS  
 SYWTKAYNDHTFSVSFSQFTSPMNSRNNDTKLIVPDFKSTIMHLEDSRSS  
 SWTVADIMNSNNKVSQNPDFVDFQELLDNDTLGNDLLLTAVLKEFEL  
 LHDDSVSATATSNEIDISHLNLNSPISPHKLIYKNKEGTNDMLISFGL  
 DHPKSNREDDLDKLCNMTREVCQALPSQYLKCEESKRSEDFLSTSNRKEKP  
 DSGNYTFYGLDCLTLQKSRALPASTVNNNQPSHSISEKLFNEPMRNMCI  
 KVLRYVYKFKFSHDSSESVMCSNPMLLSKELLMPAVSELNEYLDLFLKNFLP  
 HFFIIHPSLLDLDLDSLQRYTNEDGYDDAENAQLFDRI.SQGTDKKEYDYRH  
 YQLSISKIVCLPLFKATFGSLHKFGYKSOTIELYEMSRRILHSFLETKR  
 RCRSTTVNDSYQNIWLMQSLILSFMFALVADYLEXIDSSLMKRQLSALCS  
 TIRSNCLPTISANSEKSINNNNFPITFGSPLOYIIFESKTRCTLMAYDFC  
 QFICKQFW[KKFL]SIKKKCVETPIYTPDNESKWASESIIICNGINVOQKQNFY  
 DFRNFYYSFTYGHLSIFEFLGSSMIYYEYDLRKGTKSHVFLDRIDTKRL  
 ERSIDTSSYGNDNMAATNKNIAILLDDTIILKNLMSMRFIKQIDRSFTE  
 KVRXGQIAKIYDSFLNSVRLNPLKNYSVEVLCEFLVALNFAIRNITSSLYV  
 EEESDCSQRMNSPELPRHILNNQALSVPNLQGYCYCFILIIIFLLDFEAT  
 PNFKLLRFIELRSLANSILLPTLSRLYPQEFSGFPDVVFTQJFINKDMG  
 MLVPGLSANEHHNGASAAVKTKLAKKINVEGIAMFINETLVNSFNQTSFL  
 NMEDPIRNEFSFDNGDRAVTDLPRSAHFLSDTGLEGINFSGLNDSHQTVS  
 TLNLLRYGENHSSKHKNCGKGQGFAEKYQLSLXYVTIAKLEFTNVKENYI  
 HCHMTDKMASDFHTLENHLKGN

YBR122C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)  
 GGGTGCGGTATCGGCTCTAATTATTTTATCTCTCTATTTTCTTTCTTTTC  
 TCTGCGCTACTCCCTTTCTCGATCGTTGCTACTCCCGTCGCTAGCCACTGG  
 TCTCCCGCGGTACTGTACTCCATCTTTTGGCGTFFFTCCCTATCCAA  
 CTGGAACAAGGTTTGTTTAAATTTAATTTTATTTTCTTTCTTTCTTCGGTCCG  
 TCGTTCTTTTCCCTTCCGATTATCAAAGCAAAAGCCCATTTTCTTTCTTTG  
 TCTTTTGTTTTGTCTTCTCTGTTCTCTGTTTTTTACAAAACCACGTCCAG  
 GAGTTCAATTTGAGAGAACTAGAATCAACAAAGCCAAATACGACAAACGTCA  
 CTAGTCTTTGAACCAGAGGCGTATTCCCGTTACCTCTTTTCCCATATTTTC  
 TGCTTTTCTTTTCACTCCTATAAGCCTTTAGACTAGTACTACAACTACA  
 ACAGCAACAACAACAACAACAACGAGCTGGAAAAAAAATTAGGAAAA  
 AATGAATCCGGCCGGTGAACAACAACAAATATCGGAACAAACCGCTCAACAGCA  
 ACAACAACAGCAACAACAACAGCAGCAACAGCAACAGCAGCCAGCAGTTC  
 CTTAGCAGCCACTCGACCCATTAAACAAATCAACTGCGGAAACTTCCCTC  
 TCCATTGCTTCTTTGSCAGAAACCCCTTGGTGATGGCGACAGGGCCGCAAT  
 GGCATATGACGGCCACTTTACAGTTCAATCCCTCATCTGCAAAGGCTTTAA  
 CATCTTTTGGCTCACTTGTACCGTTCCAGAGACATGTTCCAAAGAGCTGCA  
 GAATTATATGAACAGGACTTTTGGTAAATCCCGAACTATCAGATGTGTG  
 GGCTACTTTAGGTCAATTGTATCTGATGCTGGATGATCTGAAAGAGCTT  
 ACAATGCCTATCAACAGGCTCTCTACCACCTCAGTAATCCCAACGTACCG  
 AAATTATGGCATGGAATCGGCATTCTTTATGACAGATATGGTTCCGTCGA  
 CTATGCGCGAAGAAGCTTTTGCCAAAGTTTGGAAATGGACCCCTCAATTTG  
 AAAAGGCAAAAGCAATTTACTTTCAGACTAGGTATATTTATAACATACAG  
 GGTAAATGGTCTCAAGCTTTTGGAAATGCTTCAGATACATTTCCCTCAACCC  
 TCCCTGCTCCCTTGCAGGAGTGGGACATATGGTTTCAAGTTGGGTAGTGTTF  
 TGGAGAGTATGGGAGAGTGGCAAGGTGCGAAGGAAGCCTACGAGCATGTC  
 TTGGCTCAAAATCAACATCATGCCAAAGTATTACAACAATTAGGTTGTCT



40/251

TTACGGTATGAGTAAAGTACAAATTTTATGACCCCTCAAAAGGCATTGGATT  
 ATCTTCTAAAGTCGTTAGAAAGCAGATCCCTCCGATGCCACTACATGGTAC  
 CATCTCGGTAGAGTGCATATGATTAGAACAGATTATACTGCCGCATATCA  
 TGCTTTTCCAAAGCTGTTAATAGAGATTCAAGAAACCCATATCTTTTGGT  
 CCTCAATCGGTGTATTATATTACCAATTTCTCAATACAGAGACGCCCTTA  
 GACGCGTACACAAGAGCCATAAGATTAAATCCTTATATTAGTGAAGTTTG  
 CTACGATCTAGGTACTCTTTACGAACTTGTAAACAACCAATTATCTGACC  
 CCCTTGATGCGTATAAGCAAGCTGCAAGACTGGACGTAAATAATGTTCAC  
 AATAAGAGAAAGATTAGAAGCTTTAACAAAGCAGTTAGAAAACCCAGGCAA  
 TATAAACAAATCGAACGGTGGCGCAACGAATGCCCTCTCTGCCCCACCTC  
 CTGTGATTTTACAACTTACCTTACAACCTTATGATCAAGGAAATCCTTTG  
 AACACTAGAATTTACGCCCAATCTGCCAATGCTACTGCTTCAATGGTACA  
 ACAACAGCATCCTGCTCAACAAACGCTTATTAATCTTCTGCAACAATGT  
 ACAGTAATGGAGCTTCCCTCAATTACAAGCTCAAGCTCAAGCTCAAGCT  
 CAAGCAAGCTCAAGCAAGCAAGCAAGCAAGCTCAAGCAAGCAAGCAAGCA  
 AGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCTCAAGCAAGCAAGCAAG  
 CACAAGCACATGCACAAGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA  
 CAAGCACAGGCGCAGGCAACAACAACAACAACAACAACAACAACAACAACA  
 ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA  
 AGCAGCAGCAATTAACCCCCCTACCAAGCAACAGCTGCAGCAAAAGGGA  
 GTTTCTGTGCAATGTAAATCCTCAACAGGSCAACCATATATCACACA  
 GCCAACAGTCAACAAGCTCACCAACTGCAACCATTTTCTACACAAGCTA  
 TGGAAACATCCGCAAGCTCTCAACTGCCAGCTCAACAGCAACAACTAACA  
 TCTGTTCACAACCCACAACAACCTTCAAGGCCAGCTCAAGCTTCAAGCTCC  
 CCAACCTTTAATCCAGCATAACGTGGACAGAACGTTTTTACCTCAAAAGA  
 GATACATGGGAAGGTGCAATCCACACTTTAGTAGATGCCGCCGTATCCAGT  
 AGCAGCCACACAGAGAATAACACAAACTCTCCTCGTCAACCAACCAATGC  
 CATTTCCAAAGCAAGCTCCCGCAACAGCAATTAACGAAGCTGAACCAAGG  
 TAAAGCAAGCAAAAGCTGAACTCTCCAAATTCAACATCAACAAATTAAGTA  
 AATACTGCTACTTCCATTGAAGAAATGCAAAATCTGAGGTGAGCAACCA  
 ATCCCCAGCAGTAGTGGAGTCTAATACCAATAATACTTCACAAGAAAGAA  
 AACCTGTAAAGCAAACTCAATACCTTCAGTAATTGGCGCACAGGAACCT  
 CCACAGGAAGCTAGTCTGTGCTGAAGAAGCTACCAAGCAGCTTCTGTGTTT  
 TCCTTCTAUAAAACUGCTTAATACGGAACAGAGTCATCTAGTGTCCAAC  
 CAACTGTATCATCAGAAAGTTCAACAACAAACCAATCACCAAAAGCACT  
 GCTGAGACCATAGAATTTCTACTGCTACTGTTCTCTGCAGAAAGCAAGCCC  
 TGTAGAAGACGAAGTAAGACAGCATTCTAAGAGSAAAACGGCACAACTG  
 AAGCATCTGCACCTTCTACTGAAGAGGCGGAGCCAGCAGCTTCCAGAGAT  
 GUTGAAAACAACAAGATGAACCCGCTGCTACAACGATAACTGTATCAA  
 ACCTACTTTGGAACAATGGAAACAGTGAAGAGGAGGCCAAAATGCGGTG  
 AGGAAGAGCAACATCTCAAGAAAAATCCCAACAGGAGAACACACTTCCA  
 AGAGAAAATGTAGTAAGCCAACTCCAAGAAGATGAAAACACGACGACTA  
 A

YBR112C, 966 aa (SEQ ID NO 52)

MNPGGEQTIMEQPAQQQQQQQQQQQQQQAAPVQQPLDPLTQSTAEQWL  
 SIASLAETLGDGDFAMAYDATLQFNPSSAKALTSLAHLVRSRDMFORAA  
 ELYERALLVNPFLSDVWATLGHCYLMMLDDLQRAYNAYQQALYHLSNPNVP  
 KLWHGIGILYDRYGLDYAERAFKVIELDPHFSEKANEIYFRLGIIYKHQ  
 GKWSQALECFRYILPQFPAPLQEWDIWFQLGSLVLESMGEMQGAKEAYEHV  
 LAQNQHAKVLQQQLGCLYGMSNVQFYDFQKALDYLLKSLEADPSEATTWY  
 HLGRVHMIRIDYTAAYDAFQQAVNRDSRNPIFWCSIGVIVYQTSQYRDAI  
 DAYTKAIRLNPY1SEVWYDLQTLVETCNNQLSDALDAYKQAAARLEVNINVH  
 IRERLEALTKQLENFGNINKSKGAPTNASPAFPFVILOPTLOFNDQGNFL  
 NTRISAQSANATASMVQQQHFAQQTFINSSATMYSNGASPOLQAQAQAQA  
 QQA

QAUAGAGQQQZQQQQQQQQQQQQQQQQQQQQQQQQQQQLQLPLPRQQLQQKG  
VSVQMLNPQQGQFYITOPTVIGAILQLQFPSTQAMEHPQSSQLPFPQQQQLC  
SVQHFPQLQCCQPQAQAPZPLIGHNVEQNVLPOKRYMEGAHTLVDAAVSS  
STHTENNTKSPRQPTHAIPTQAPATGITNAPQVKKQKLNSPNSNINKLV  
NTATSTENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQLP  
PQPASPAEFATKAASVSPSTKPLNTEPESSSVQPTVSSSESSTTKANDQST  
AETIELSTACVPAEASPVDEVRQHSKEENGTTASAPSTFEAEPAASRD  
AEKQQDETAATTITVIKPTLETMETVKEEAKMREEEQTSQEKSFOENTLP  
RENVVROVEEDENYDD

YMR043W, 286 aa (SEQ ID NO 306)  
MSDIEEGTFTNNGGQQKERRKLEIKFLENKTRRHVTFSEKRIUGIMKKAFEL  
SVLTGTQVLLLVSEFGLVYTFSTPKFSPVYVQOEGRNLIQACLNAPDDE  
EEDDEEDGDDDDDDDDGNDMQRQQPQQQQPQQQQVNLNAHANSLGHLNQ  
DQVPAGALQKEVKSQLLGGANPNQNSMIIQQQCCHTQNSQPPCCCCQQPQQ  
QMSQQQMSQKHPRQQGIPQPQQSQPQQQQQQCCQLQQQQQQCCQPLTGI  
HQPQQAFAKAAAPYLNAEQNAAYQOYFGZPQQGOY

YPL089C, 2531 bp, CDS: 501-2531 (SEQ ID NO 385)  
TTCCACGTTTCGCAAAAAATACTTCCACGGTGACGAAGTCTGTCTCAGTCG  
TATATTAAATGCAGAAATCGTCTTATCATTATTGGGCTCTCTTAAACGGCG  
CAGCATCACCGGGTGATGAATGCCAAGCCGCGAAGAAAGAAAAAAATT  
TACTTCAGATCTCTGTATAAAATAAACCGAAGAGATGAAAGCTAATAAI  
AGAAACAGCTCGATCTTCTCTGAAACAATATATATTAAAGCAGCAGACAA  
AAGAAACGTAAGAAAGAAGCGAGCTGTCTTAAAGTGTTCACGACTGAT  
TCATTAGAAGTCCCTACTGCTGATAGCCAACTCAACTTTTGACTCGTAT

42/251

AAGTAATTGAAAGCTGGCAAGCAGAATTATTCTTTTTTTTTTCAAGGFT  
 TCTATCACCATTGTGAGCTTAATATCCCCCGGAGCAACAGGCTGAAGCGT  
 GAAAAAACTTAAATATTAAAGTGTCCCAAACTATACTATAGATACAC  
 ATGCGGTAGACCGAAGATTGAAATCCACAGAAATTCTGATGACAGAAATAG  
 GGCTGTACCGTTTATAAAAACCTAAAGCTGGCCTTTTTAAGAAGGCCCATG  
 AACTATCCGTTCTTTGTCAAGTAGACATAGCCGTCATTATACTGGGGTCC  
 AATAACACGTTTCTATGAGTTTCCCTCTGTGGATACGAATGATTTAATCTA  
 TCACTACCAAAATGACAAAAACTTGGCTTCACGAAGTGAAAGATCCTTCCG  
 ATTATGGAGACTTTTACAAAAAGTGCAATCCGTTAAACATAAAATCAAGACCTA  
 CTCAGGTGGTCTATGTCAAATAAGCCTTCGAAATCAATGTAAAGGAAT  
 GAACCACTCAGAAATGATGATGATGASAACTATGATGAGGACGACCATG  
 ATCATGGCAATTTTGAGAGGAATTCAAATATGCATTGGAATAAAAAACCC  
 TCTGATAAAAAATATACCGAGTGACACATGAAATGTATATCCCCGACCGC  
 ACTCATTTGCCAAAGATGGATGGTAGTGACAAATAAAACGTCATCCTGAGA  
 ACCGCTTGGCCCTTTTACAAACATTTGAAAAGGATTGAAACCGGATCCTTTG  
 CAAATTAAGTAGAACTCCGCAACAGCAACAGCAGCAAAATATATCGAGACC  
 ATACCATAGTAGCATGTACAATCTTAACCAAGCCTTCATCCAGTTTATCTT  
 CTCCCTCCACGATGGATTTTCCAAAATTACCAAGCCTTTCAAACTCTTCC  
 TTTAATGGTGGTCTTCCACCCATTTCCATTTTCAACCGAACAAGTTCAGTAA  
 GCCATTTACAAATGCATCCTCAAGGACCCCTAAACAGGAGCAAAAATTA  
 ACAATAGTGGCAGCAATAATAATGACAACAGCAACTACACTCAGTCCACCA  
 TCTAATTTCTTTGGAAGACTCTATTCAGCAGACTCTCAAAACCAACAAACCA  
 ATTGTCCGCGAGACCGGTACTTCCGTGTGAGAAATTCGGAACAACAATTCA  
 GCAGTAATTTCCCTATTCCCAAGTGAAACCTCTCTCTGCTCTTCCACATCG  
 GCCAACGGCAATAGTATGGGCTCTTCGCAGATAATGAAAGAAAACAAAAC  
 AAGTAGGTCTAGCAAAATTTCTCCACTATCCGCATCTGCCCTCAGGCCCTT  
 TAACTCTCCPAAAAAGGTAATAATGGCAGAAATGGTAATAAAATTCGCAAT  
 GCATAATGGCCCTAACCGTTCTAACAAATGGTAATGGCACTAACATAACAA  
 TCACCTTTATCCTTTTCGGAAGTGGGTCTTCACTCTTTTTTTCTTCCAACAC  
 AGCCATACATTGCCACTTCTTTGCAACCAATCGAATATTCTTGGCGGACCT  
 TTCCAACAATAACATCTTTTTTAGCTCAAAGACAAACCCAGCAATACCA  
 ACAATGTCTTTCAAAAACAGAGCCAAACAGTACCATTAACTACAACAT  
 TAACCGGACGCCCCCTTCAACTTTTTCCGGCCCTGAAACCAAGCAATGGC  
 CCTCCAACGTGTTCACTGCCATCGAAGTTGTTACATGATTTGATGAGTAA  
 TTCTCCAAATGTTTCTTCTATATCGATGTTTCCAGACTGGTCAATGGGAC  
 CCAACAGTGGCAAGCCGGGAACACAAACAATCCTGGTACTTTCCCTCCC  
 GTACAGACGGCCGTAAACAAAGGCAACTCCAGCAATATCAGCAGCACTAA  
 CAACACTAACAAACAACAACAATAACAACAACACAGCAGCAACACA  
 ACAGCAACACAGGCAACGACAATAACAGTAACAATAACCAATAACAGTTAC  
 TATAGTAATAATGAAGATGCACCCGTAAATGGAGCTGCTATTTTCAAGACA  
 TACTACCGAATGGTGACTCGAACAAATCAGTCCAACTCAAGTACATATGATC  
 CTGCTGCCACCGCATATAATGGAAATACCGGGCTGACTCCATACATAAAT  
 ACTGCTCAAACACCACTAGGCACTAAATTTCTTTAATTTTTCGACTCATAT  
 TTTCAAGGAGAAAAAATTCAAGCAAAATATAA

YPL089C, 676 aa (SEQ ID NO 386)

MERRKIEIQRISDDRNRVTFIKRKAGLFKKAHFISVLCQVDIAVILGS  
 NNFFYEFSSVDITNDLIYHYONDKNLLHEVKDPSCYGDPHKSASVNIQDL  
 LRSSMSNKPSSXSNVKGNNQSENDDDENDEDDDHGNNFERNSSNMHSNKA  
 GDKNTPSAIMKLLSTAISSKMDGSEQNKHHFENALPPLQHLKRIKPDPL  
 QISRTPQQQQQNI SRPYHSSMYNLNQPSSSSSSSFTMDFFKLPSPFQNSS  
 FNSRPPPEISISFNKFSKPFETNASSRTPKQEHKINSGSNNDNMSNYTQSP  
 SNSLEDSIQCTVKARRKLSARFVLKVHIFNNNPSNSAIPSEPPSSASSVS  
 ANGNISMGSSQIMKENKLSRSSKISPLSASASGPLTLQKGNNGRMVILPN  
 ANAPNGSNMNGSNNNNHFPYPGSGSSPLFSATQFYLATPLQPSNIPGGP  
 FQQNTSPLAQRQTQVQVQMSFKKQSOTVPLITTLTGHPSTFSGPETSNG

43/251

PPTGSLPSKFWHDLMSNSPNVSSISMFPDWSMGPNSAKTGNTNNGTFFP  
 VQTAVNNGNSSNISS'NNTNMMNNNNNNNNSSNNNSNNGNDNNNSMNSNSY  
 YSNNEADPVNGAAISEHTTEGESNMQENSSYDAAATAYNCNTGL'PYIN  
 TAQTPLGTFKFFNFSTDISGEKNSSKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)  
 AAAATCGTGGTTACTTTTCATATTCCTTAAACACTTTACCCTGTTACTGT  
 GCGCGTTTCGAGCGTAGCTTTTCGTGGTGAATTPA'TTGTAAAGATTCCTCCAGC  
 TGGCTCGATAGTTCTGCCTCCTGCGTATCCACATCCATTTCCGGTATGCTT  
 TTACTATTCAACCTAGTCGGCAATTTTTCACCTGAATATTGTTCAACAC  
 TTCTGGCATUCTAGATACTCATCTGTATTTATTTCAATTAATCTGTTGTGCA  
 CGTTAATAGCATTCACGTAAACAAGTTTAGGTCACCTACCCGCATAAGCCT  
 TTTGGCGTTTGGCGTAACCCCTCCTCGCGAAAAGAAACGGCACCCCAAAAA  
 AAAAAACAACAAAACAAGAACAAACAAAACAAATAGGACAGAGCCCTTAA  
 CGAGCTGCAAGGATCTTCTCAATATTTGGCATCGGCATTCGTGGTGGAAA  
 AAGTGTCCAAATTGGAATAAAATTGGTCAGAATAGAGCATTGAATCCAACT  
 ATGGACAGAGATATAAGCTACCAGCAAAATTAATACCTCAACTCGGGCAAC  
 TGCNACTTCCCTCAAGACAGCCCTCTACGGACAATAATGCAGATACAAATT  
 TTTTGAAGGTAATGTCAGAATTCAAATATAATTTTAACAGTCCGTTACCT  
 ACAACGAGTCAATTCGCCACGCCCTATCTTCTTAATCAGTATCAACAGAC  
 TCAAGATCAATTTGCCAATACAGACGCTCACAAACAGTTTCGAGCAACGAAT  
 CGTCTGTTGGTAGAGAACAGTATATTTACCGCATCATCAGCAGATACAAACAG  
 CAACAACAACAACAACAACAACAACAACAACAACAGCAAGCTCTAGCTTC  
 ACTTGTACCTCCTGCTGTCAACAAGGACAGATACAAGTGAGACTTTTGGACG  
 ATATCAACCTTCAACCTTCTTCTGTTTTTGCAGTTTGGCAACTCTTTACCC  
 AGCGAATTTTGGTTGCATCCCCAGAGCAATTCAAAGAATTTTGTGTTGA  
 CTCTCCGTCCACCAATTTCAATTTCTTTACAAAACCTCCGGCAAGACAC  
 CACTTTCGATTTGTAAACAGATTCTAACGGTGCCTCAGCAAGCACCCACAGAG  
 AATCCAGATTCAACAACAGAATGTTTTTTAGCAATCTCGATTGAAACAATCT  
 TTTTGAAGGTAATGGAATAAAACACCCCTCAATCTTCATGCCACCCGGCATTTT  
 CACGCACCTCTGTAGTAGATTTGACATGAATCTCATGTTCAATCAACCG  
 CTGCCGACATCTCCATCAAAAAGGTTCTCTCTCCCTGTGGTTGACACCAATA  
 TCGAAGAAAAATTTCTGAATGACGTCCGTACACCTTATGCAAAAGCATTGA  
 TATCGTCTAACACGCGCTTAGTGGATTTTTCAGAAGCCCAAGAAAGGATATT  
 ACCACTAATGCAACATCCATAGGGCTGGAAAAATGCCAACAACATCTTACA  
 GAGAAGCCCGCTAAGATCTAACAATAAAAAAT'TATTTATTAAACCCCCC  
 AGGATACCATCAATAGCACTAGCACACTAACTAAGGACAACGAAATATAA  
 CAGGACATATACGGCTCTTTCACCGACTACCATCCATTTAAATTCATCAAT  
 AACTAAATCTATCTCCAAATTTGATAAATCTAGAA'TCCCTTGTATGCTT  
 CGAGATCAGATAACAATTCCTGGATTTCCAATGTGGATGACCANTTGTTTGAT  
 TTGGGGTTGACAAGATTACCTTTATCACCACACCAANTTGTAAATCTTT  
 GCATAGTACAACCACAGGTACATCTGCCTTACAAATTCCTGAGCTACCCA  
 AGATCGGGTCTTTTAGAAGTCTATACGGGAATCAATCCAATTTCAAGTTCA  
 AACACAGATTTCTTTTAAAGACAAATCAGGCAATAATAA'TCAAAGGGTCG  
 AATCAAAAAAATGGGAAGAAACCTTCCAATTTTCAAATTATTGTGGCAA  
 ATATTGATCAATTTAACCGGATACATCATCGTCTATCTTTATCATCATCA  
 TCTGAATCCAAGTTCCAGTGCACCGAATTCMAATTCAAACGTAACAAAGAA  
 AAGAGCAAGTAAACTCAAAAGATCACAGTCTTTACTTTCTGATTCCGGAT  
 CGAAATCACAAAGCAAGGAAAAGCTGTAATTCATAATCTAATGGAAATTTA  
 TTCANTTCACACTAA

YOR372C, 554 aa (SEQ ID NO 372)  
 MDRDISYQQNYTSTGATATSSRQPSTDMNADTKFLKVMSEFKYNFNSPLP  
 TTI'QFPPTPYSSNQYQQTQDHFANTDAHNSSSNESLSLVENSILPHHQIQQ  
 QQQQQQQQQQQALGSLVFPFAVTRTDTSETLDDINVQFSSVLOFGNSLP  
 SEFLVASPEQFKEFLLDSPSTNFWNFHKTPAKTFLRFVTDNMGACQQTTE

44/251

NPGQQQNVPSNVBLNMLLKSNGKTPSSSCTGAFSRTPLSKIDMNLMFNQP  
 LPTSPSKRFESLSLTPYGRKILNDVGTIFYAKALISSNSALVDFQKARKDI  
 TTNATSTGLEMANNILQRTPLRSNMKKLFIKTPQDILNSTSTLTKDNENK  
 QDIYGSSPTTIQLNSSITKSISKLDNSRIPLLASRSDNILDENVDDQLFD  
 IGIWRLPISTPENCNSIHSTTTGTSALQIPELPKNGSFREDTGINPISSS  
 NTVSPKSKSGNNSKGRICKNGKKPSKFQIIVANIDQFNQDTSSSSLSSS  
 LNASSSAGNSNSNVTKKRASKLKRSQSLLSDSGSKSQARKSCNSKSGNL  
 FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)

TTTCTTCAACAACGACGAGTTAACTPATTTGTGCTCTTTTTTTTGAGCCACCA  
 AATACACTCCCATTCCAATAGCTTCGCACAGTGAGGCGAAAACTTTTGAAC  
 AGCGCTAATGAATTATTTGTGAGCTCCCGGAGTTCAAATTTCAAGAAAAC  
 GCGGTTGCGTCGTAACTATGGTATAGACGCTCAATGTGCCCCGAAAGSGA  
 AGGCTGTTCTCACTTTTTTCGCGCGTTGCAACCTTTCTTCCCGCAAAAAAT  
 GAGAACGATGGATTTAAATCAAGAGAAATGCCCCTTACTAGTGGCAATA  
 CTACCTTGGTTGGTTATCTTGTAAAGATTGGTAAGAAAGGGGCATCTCTG  
 TTTTCTTGATGTATATAAACAACATGATTTGATCATCTCAGATGOTCAGA  
 TTTATTAAAGACGCTTCTCTTTTCCGCATTTTCCATTATTGTTATATTTAA  
 TTTATTCCTATATATAGACAACTCAAACCACAAATAAAACCATACACACATACA  
 ATGTCTGCTAAAGUUGAAAAAGAAACCAAGCTTCAAAGCCCCAGCTGAAAA  
 GAAACCAGCCGCTAAAAAGACTTCCACTTCCACTGATCGTAAGAAGAGAA  
 GCAAGGCTAGAAAGGAACATACTCTTCTTACMTTACAAAGTTTGAAG  
 CAAACTCACCTTGACACTGGTATTTCCCAAAAGTCCATGTCTATCTTGAA  
 CTCTTTCTGTTAAGGATATCTTTGAAAGAAATCGCTACTGAAGCTTCTAAAT  
 TGGCTGCGTATACAAAGAAGTCTACTATCTCTCTCTAGAGAAATTCAAACC  
 GCTGTAGATTGATCTTACCAGGTGAATTGGCTAAGCATGCTGTCTCTGA  
 AGGTACTAGAGCTGTTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)

MSAKAEEKKPAKAPAEKKPAKKTTSTTDGKKRSKARKETYSSSYIKVLK  
 QTHPDGTGISQKMSILNSFVNDIFERIAEASKLAAYNKKSTISARELQT  
 AVRLILPGELAKHAVSEGTAVTKYSSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)

ACCAACCAACTTCTTCTTTGTCTCTCAATATCAAAGAAAAAAAAAAAAAAC  
 CCACTGCTCAGATGTTATAAGCAAGGGCTGTTAACTTATATACACCTTCA  
 TCTACCAGTCACCAGTCCATACAAACTTGAACCGTCTGCGTACCAGTCTT  
 AATCAAAATGTTCCCTATCGCTTCCAGAAGAATACTGCTTAATGCTTAAG  
 TTTCTCCCACTCAGACTGTGCAATAGAAATTTCACTACCCACAGAAATATCC  
 TACAACGTCAACAAGATTTGTATTTGAGGGAACTAAAAGACACCAAACT  
 GGCCTCAAAGTAUCTTCCAAGATGCTGAAGGTAATGTTAAGCCTTGGAAAC  
 CACCACAAAAACCAAACTCTACCAGAAATTGGAACTTCAAGGCCACAGAGGC  
 TTAAGAGGCTTACACCGAGCAAAATGTAGAAACCTGCTCATGTTCCCTAAAGA  
 GCTGGAAGAGGCTGAGTCAGAGCCAATTGAAGAGGATTTGGCTAGTTTTGG  
 ATGATGCTGAGGAAACCAAGAAAGTCATTGAACCTTTTCATAGCATCCCTC  
 CTTCTCGAAGAAAAACAAACAGAACCAAGCTGAACAAGATCATTTATTT  
 TTTGGCTTTCTTCCCTCTATCTTTTTATATTCGAATCCAGTACAATAAAG  
 AAAAAGCAAAATACACTAUGGACTCTTTTGTAAATCAGCCACACAAAAATCA  
 GAATTTATTTTTTAAACAAAAAATACAATTGTACATAGACACGTCCTTAT  
 CTTTCTTATTAATACTATCTTTTTATTTCAATAACTATTACTTTCTAAGT  
 ATGACCTACGCTTCTTTGGTAAATAAATAA

YLR294C, 169aa (SEQ ID NO 282)

MMLRKPKKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLPFESSSTLK  
 KKQNTLRTLGNQPHKMQNLFFKQKIQLYIDTSLSPLLLLFFYPNNVYPLS

45/251

MTYASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)  
CTTTTCAGTTATTTACCTTCCTTTCTCTCACGTGTAAATATTTGTGTGTC  
ATACACACCCGCTAAAAACCTTTGCAATCAACTTATACCCTACATTTCTATA  
GACGCTATTTCGAAACAAGATGTAACCCCTTTTTCCTTTTAGTTTTGAGA  
TTTCTACTCGTAAAGAGTACGTTTATTTATTTATTCAAAATTTTATCTTC  
ATACCATGTAAATATAAGCGCATATAATCACTACGATCTTAGTACAGCTA  
GAATTGCTGACGCTTACAAATTGCTTTATTTGTTTGATTATATGCACGTATA  
CATATAGTGTTCAGCAAAAAAAAAAAAAAGGCAGTACTTGATTGGCTACGCC  
GCCCATCGTCCGAGAAATCCGGCCTGGTAGGGGCAGGTTTGAAAAGGGCG  
ATAGAAATAAAGATGATATTATTTATTCATCCCATGAATAGTAGAACTC  
GATATAAGATTCTAAACCAACAAGTACAGAAAGCAAAACAATAATAAATA  
ATGGCTAATAAAGTTTATTCAACTACAGAAATCTTCCAATCTTCCACTAA  
ACCTCTATGGTGCAGACATCCAAGGTCAGCTTATACCTGTATCCATTTT  
ATCCATATTTTTCGCTAGCCGTCGTTACACCACTTCTATACATTCCAAAT  
GCATATTAGAGGTATCAAAGCCAAGAAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)  
MANKVIQLQKIFQSSTKFLWWRHPRSAIYLYPHYAIFAVAVVTPLLYIFN  
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)  
TTCTCATACGTAATGTTTCTTTTAGATTATGCACCTTCTTTGCCACAGTAAA  
TGTTCGCCGGLAAGATGTTTGAGCTAGCGCCGTGCACAGTGGAAAGAGACGGA  
CCCCATTCGTGGGGTTTCATCGGATTGTGCGGGAAGAAGGCTACACCGTC  
TTGAGCCACCCCCCCCCCAGGAGTAAATTTACACAAACAGTGGTGGTCCC  
TATGGTGGTATACGAGATAGTGATAGAAGCTGCTGGATTGGGTAGAAAT  
TTTGTAGGCGTTTATGGAATTCGGTATCGGATATGGTATGGCTGAGGTAGG  
TAATCCAGACACCCACTCGAAATATATATAAGGAGAGAGTTCTGGCAGGTA  
GATTTCTACTCCTCTCTACCACTTTCTTTCTACTCCTTTTATTATGTAATG  
TTTATTATATAAGCACACGCAAAACGTTAAATAAATCTAATAAGATTTCAAT  
ATAACATAACATTAAAGCACACAAATTTCTAACACAAACACAATTCAAAC  
ATGACCAAGAACTAGCAAAATGGACAGTCCACGAAGCAAAGTCTAACCCAAA  
GTATTTCACCCATAACGGCAACTTTGGGGAGTCTCCCAACCACGTCAGA  
GAGGAGGCTATGGGAAAGGCAATTGGGGCAAGGCTGGGATGAGATTAAAT  
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAGACCAGAAG  
GGGCTCTAACTCCCAAAACAATGAAAGAAGGCTTTCTTGATTTGCCAACAAT  
ACCAATCTAA

YLR327C, 86 aa (SEQ ID NO 288)  
MTRTSKWTIVHEAKSNPKYFTHNGNPGESPNIHVKRGGYKGNWGGKPCDEIN  
DLJDSGEIKIVFNKTRRGSNSQNNERRLSDLQQYHI

YLR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)  
GTTCATGCGCGCATAGGAAAGCGCACGAAACAAATGAGTAATTCGTAGGA  
AACAATGCAGCCCCCAGGGTCAGCAACTGACGTGACTCAGCCTGGCTTTT  
GTAGAAAAAGATGACGCCCTGGCAGACAGCTGGGGGAATTGACCGGTCCT  
CGCTACCCACCTTAAGTATGGAAGAATATGATGAAGAATATGATGATAAC  
TCTTGGAAGCGAGCGCGGGTTCCATCACTTTTACGGATTGGTAACACA  
GGGGCCTCAGTTGATACCTTGGTATTCAGGCTTCCAGCCTTGGTGAGTTT  
AGTTAGCGGTATGGTATGCACATGGTGTGATGCTTGGTGGTAATCATTC  
GTTAGGTGAATPGAGCAGTAGCGATAATTAGATAATATTTAGTATTTTATAG  
CGTCTTTTGGTGGGGGAGGAAGGACAAAACCTGTCTCGTAAATATAAAG  
GGACTGTTCGATATCGCAGATACTAGAGTATAAATTCGATTGAGGCGAG  
ATGACAAATATTTCAAGTTGGTAAAAGGTGCTACCAAGATCAAGTCAGC

46/251

CUCGCGCCAAACAGAAAGTATCTCGATCCGACTACTGTTGGGGACCAACAA7G  
 AAGAGGATTTCTATGAGATCGTGAAGGGTTTGGATTCCCGAATTAATGAC  
 ACGGCGTGGACTATTGTGTATAAAATCGCTGTTGGTGGTTTCATTTGATGAT  
 AAGGGAGGGTTCCAAAGATGTTTGCATATCGGGTACTACTCTAGGAACCTGG  
 AGTTTTTTTGACATTGAAAACATAACGTGGCTCCAATGGCAGTGGCTCTGGA  
 GACATGAGGGCACTTCATAGATAACGAATATTATCTGAAGGTGAGATGACG  
 GGAGTTTGGTAAATCAAAALGGACTATGTGACAGACCGCTATTCGAACAC  
 TGAAGCTCAACAGTGGCAATTACGGAAGCTCCAGAAACAAGCAACACTCT  
 ATCAATATAGCACTAGATCATGTGGAGTCCCTAGACGTACAAATACAAGC  
 CCTGATTAAAAACAAGTATACACAATATGATTTGAGTAACGAATTGATCA  
 TATTGGTTTCAAGCTGCTTATTCAAGACCTGCTAGCGCTATATAATGCT  
 CTCAACGAAGGTATCATAACTCTGCTGGAGTCTTTTTTCGAACATATCTCA  
 TCATAATCCAGAGAGAACTCTAGACCTCTACAAGACGTTTGTTCATTGGA  
 CCGAGCACGTTTGTTCAGGTACTTGAAGAGCGGGAAGACTGCGGGCTTGAAA  
 ATACCCGTCATCAAGCATATCACTACCAAACTGGTCAGATCGCTAGAAGA  
 ACNTCTGATAGAGGATGATAAGACGCACAACACTTTTGTGCCCGTTGACA  
 GTTCATCAAGGAAGTCTGCGGCGGTAGTAGCCAAATCTACTGCACAGGAA  
 AGGTTGGAGCAAAATCCGGGAACAAAAAAGGATACTAGAGGCACAATTGAA  
 AAACGAACAAGTAGCGATTTCCTCTGCTCTAACTACTCTCACGGCGGCTC  
 AATCTTACAACCCGTTTGGAAACAGACTCTTCTATGCATACTAAACATTCOA  
 ATGGCTGTGGCTAATCAAACGCAACAGATCGCAAAATAACCCATTTGTATC  
 TCAAACCTCAGCCACAGGTGATGAATACACCAACCCCTCATACAGAGCCCG  
 CAAATTTAAACGTTCCCTGAATATGCAGCGGTCCAACACACAGTGAACCTC  
 AACCTGTACAAAGATGCTGGCGTAAGTGCCCAACAAACGGGGTACTATTC  
 GATTAACAACCAATTTAAACACCCACATTTACAGGTGACAGGGTTTGGAGGAT  
 ACTCCGTTTTACAGGATACAACTGCGCGCTTCTAATCAACAAGTCTCTCAT  
 TCACAAACTCGTTCTAACAACCCGTTCCGATTGCACAAACGCGCGAGGAT  
 CGCAACAGGGGAATCTGCACACGAAATGCTTAAATAACCCATTTTAC  
 GACCAAACTTTGATGAACAAATACCAATATGCCCTACAACAACAGATA  
 ATAAGTAACCTTTTCAAAACCAACGTTACAATCAACAACAATTTCAACA  
 ACAAAAAATGCTTTGAGCTCGATCAATAGCGTTATGACAACCCCTACTA  
 GCAATGCGAGGGATCGATGAATATTCCTCAGCGTTTTGATAAAATGGAATTT  
 CAGGCTCACTACACTCAGAATCATCTCCAACAACAGCAACAACAGCAACA  
 GCAACAACAGCAACAGCAACAACAGCAACCAACAACACGGTTATTATGTGC  
 CTGCAACTGACAGGAGCCAAACCTGTTACAAATATAACTGGGACAGTTCAA  
 CCTCAAAATTTCTCTTTCTATTCACAACAGCAACCAACAGCAACAGTC  
 TCAAAACACAGCAACAGTTTATAGGAAACCAATATGCTAACCAACCTCAATT  
 TAATTGATATGTAA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKGATKIKSAPPKQKYLDPILLGTSNEDFPYELVKGLDSKIMD  
 TAWTIVYKSLLVVHLMIREGSKDVALRYYSKNLEFFDIENIRGSNGSASG  
 DMRALDRYDNYLKVRCREFGKIKKDYVRDCYRTLKLNSGNVCSSPNKQHS  
 INIALDHVESIFVQIQALTKNKYTQYQLSNELIIFGPKLLIQDLLALYNA  
 LNEGIIITLLESFFELSHHNAERTLDLYKTFVDLIEHVVRYLKSGKTAGLK  
 LPVIKILITTKLVRSLEBHLIEDDKTHNTFVPVDSQSAGAVVAKSTAQE  
 RLEQIREQKRILFAQLKKTQVATSPALTTVTAQSYNPFQTESSMHTNIP  
 MAVANQTQQIANNPFVSQTQPOVMNTPTAHTEPANLNVIEYAAVQIITVNP  
 NPVQDAGVSAQQYGYYSINHLTPFTGAGFGGYSVSQDTTAASNQQVSH  
 SGTGSKNPFALHNAATIATGNPAHENVLMNPFSPNFDQNENMPLQQQI  
 ISNPFQNTVYQQQFQQQKMPISSINSVMTPTSMQGSNNIFQREDKMEF  
 QAHYTQNTLQQQQQQQQQQQQQQQQQQQQQQGYVPAITAGANFVINITGTVQ  
 PQNFPPYPQQQPQPEQSQTQQPVLGNYANNLWITDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)

TACACCCCTGACTTTUCCCATCATACGAGATGCTCTAGTAAACTTCCAC

47/251

CGCACCTGTTAGATAAACAAAGTGCGCCCAAGATCACAATACCGAAGGGGC  
 GATATCACCACCTCAGTATCTTACAGTCGAGCATAGCCTAGTCTGCCAGTA  
 TCCCGCAGGATCCATTGCTATTGTTTGTCCAAACCGCATTTTATGTGTAA  
 GATTAAATCGTAATACAGGCCATACAGAAATTACCCATGGGCGAAGGGT  
 GAAAAAAAAGTAGTGGAAACTAAAGAAAGAAGAGTTTAGTTACGGACCC  
 TTTCAAGGATTGACACACTCCCAATATTTTGTCTACATTATTGACCTTTGT  
 TGAAGGAGGGCTTCGTTTATTTAATTATTTTGTTCCTTTTGGCTACAAC  
 TGGCAATACGGCTCACAATCTAGTTTCACCTTCACAAATTCTTATCATCTT  
 CTTTTGTTTATTTTGAACACACCCCTATTAAGTGTATTTGTTTTGTAAAGTA  
 ATGCTTAAGCAGTTTGTTCGTTCTGCAAGAACATGATGAAGGGCTACTC  
 ATCCACACAAGTGCCTTGTGAGAGATGCCACGGCGAAGGACTCGAGCACTC  
 CATCGATAGACACTCTCGACGATTTGGCACAGAGATCTTACGATTGGGTG  
 GACTTCTTCGAGATTATGGATATGTTAGACAAAGAGGCTGAACGATAAGGG  
 CAAATACTTCGAGACACGTTGCCAANTCCCTGACCGTTTTCGACTATCTTG  
 TTGTTTTCGGGAGTGAAGACCTGCTGCTGCTATGGTGGCAGAGAGAAATTTT  
 GTAAATAAGACATTAAGGGATTTGACACAGGAAATGAGTCCGGATTGGA  
 CGAGGGACAAATTTATCAGCTAAAGCCTAAAGAACTCTCTCTTTGTTGA  
 ATGATGAAGAAAGGCTACCGGAAGACAGGCTCTATGAATACAAGAAACAGA  
 AGGGGGAACAGAGCTTATAGGCCAAGGCCAAGAGACAAAGAACAGGAG  
 CAAACACACAGATTCTTCTCCCTCTTACCAGGACGATTGGAAGAGGCC  
 TAGAGGAGAGCAGAATTACTGCTCAAGAGATGAACAACTAGAGAGAA  
 CTGGCCACGATACGACGATGAAGATCCTGACTTCCAAGCTGCCCTTACAAC  
 AAGTAAAGAAGAAGAGGAGTTGAAGCAATTGACGGAACCTACAGAGATTAC  
 AGAAGCAACAACAGTCTCTGCTCTCAATTTCAAGCTGCTTTACAACAACA  
 CAACCACAACAACAACAGGCTACTACGACATTTTCGGTAATCCAATCTC  
 CCAAGATGAATACTTACAGTATCAGTACCAACAGGACCAGGAACAAGCAA  
 TGGCTCAGCAAAAGATCCCTGGACCAACAGCAACAACAACAGCAGCTTGT  
 GAACAACAATATTTTACCAAGCAACAACAAGCTGCGGCCGCGCTTCTGC  
 CTTGCAACAGCAACAACAACAGCCGCTAATATGCAACAACAACAACAACAGC  
 CCGCTGATTTTCAACAACCTTTGGCTACAGGTTCTAATAATCCGTTTTC  
 ATGGATAATCTTGAAGACAAAAGCAGGAGCAACAGCATGCTCAATTGCA  
 AAGACAACAAGAAGAAGCTAGACAACAACAAGAACAATTGAAGCTACAAC  
 AATTGCAAGACACAACAACAAGAGGAGCTCAATTACACCAAGAGGCA  
 GAAGAAGCCCAATTACAACAGCAGCAAGCCCAATTGCTACAACAGCAAGC  
 CCAGTTCCAGCAACAACAACGCTTGAAGCAACAAGGACTGGGAACCACT  
 CTATATCGGATAAATACAGCGACTTGAATACCTTGTATAGCAACTGGTACA  
 GGGATAGATACTTTTGGTAACACTGGAGAGGCACGTATTCCTGCACAACA  
 TACAAGACAGGCACATTTATAAATTTCTCAGGCTACAGGCTACAACAGG  
 TTACTAATGAACCCAGAACAACCTTTCTTAAGCAACCAATAACAATGGT  
 TTACCAAGCACAAATATCGTGCCCAAGCAACAGGGTACGGGTTTGGTAA  
 CCAACCTCAAAAGTCTCTCTACTAATTTCTCTCAGCAAAATCCTACTGGTA  
 TAAGCTACTCTCAGCCACAACAGCAACAACAGCCACAGCAACAACCCCAA  
 TACATGCAAAATTTCCAACAACAGCAACCTCAATACGCCCAAAACTCCA  
 ACAACAACCAACAATACACTCAAAATATCAACAACAACCAACAATACATT  
 AACCTCATCAACAACAACAGCAGCAGCAGCAGCAGCAACAGCAGCAACAG  
 CGATATACTCTGACCAAGGTCTAAGCTTAATTGATCTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVRSKNNMMKGVSSQVLVRDATANDSRTPSIYVTLCDLAQREYDSV  
 DFFEIMDMLDKRLNDKKGKYWRIVAKSLTVLDYLVRFSGSENCVLCWRENFY  
 VIKTLREFRHNESGFDEGQIIRVKAKELVSLINDEERLREPRSMNTRNR  
 RANRAARPRPRRQTRSNPHDSPPSYQDDLEKALEESRTIAQEDEQRREE  
 LACYDDIEDFDFOALQLSKEEELKQLQELQRLQKQQQSLSCFQAPLQQQ  
 QPCCQPAYYDIFGNPISQDEYLQYQYQQDQEQAMQQRWLEQQQBQQQLA  
 EQQYFQQQQQAAAAAALQQQQTAAAMQQQQQQPAPFQQQFIPTGSNNPFS  
 MDNLERQXQEQQLAQLQRQQEEARQQQEQQLKLQQQLQNCQQQBEAQLFQKRO



48/251

EEAQLQQQQAQLLQOCAQFQQQQPLKQFRTGNQSIISUKYSDLNFLLATGT  
 GIDTFGNTGEARIPACHFKTGTFINSQGTGYKQVTNEPKNNPFLSNQYTG  
 LPSTNIVFTQGTGYGFGNQPSPTNSPQQNFTGLISYSPQQQQQPQQQPQ  
 YMQNFPQQQPPUYAQNFQQQPOYTQNYUQXPOYIQPHQOOOCQQQQQQQQQ  
 GYTPDQGVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)

CACTTCTCAGAAATGCATGCACTGCCACCACGCTANTTCGAAAAAATTCT  
 CCAGAAAGGCAACGCAAAATTTTTTTTCCAGGGAATAAACTTTTATGAC  
 CCACTACTTCTCGTAGGAACAATTCGGGCCCTCGGTGTCTCTCTGAGG  
 TTCATCTTTTACATTTGCTTCTGCTCGATAATTTTCAGAGGCAACPAAGGA  
 AAAATTAGATGCCMAAANGTCCTCTTCAAGCAAAAATCCCCACCATCTT  
 TCGAGATCCCTGTAACTTATTGGCAACTGAAAGAATGAAAAGGAGGAAA  
 ATACAAAAATATACTAGAACTCAAAAAAAAAAAGTATAAATAGAGACGATA  
 TATGCCAATACTTCACAATGTTTGAATCTATTTCTTCATTTGCAGCTATTG  
 TAAATAATAAAACATCAAGAACAACAAGCTCAACTGTCTTTTCTAAG  
 AACAAAGAATAAACACAAAAACAAGTTTTTTTAATTTTAATCAAAAA  
 ATCTCACAAACACGCTCTTATTGCAGAGCAAACTCTGTGGAGCATCTCTC  
 TGCTGTTGACTCAGCCTCCCACTCGGTTTTATCTACACCATCAAAACAAGG  
 CTGAAAGAGATGAAATAAAAGCTTATGGTGAAGGTGAAGAGCAGCAACCT  
 GTCGTTGAAATTCCAAAGAGACCAGCTTCTGCTTATGTCACCTCTCTCTAT  
 TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTTCGGTTGGCATACTG  
 GTACCAATTCGTGGTTTCATCAATCAAACCGATTTTCATCAGAAGATTTGGT  
 ATGAAGCATAAAGATGGTAATAATTATTTGTCTAAGGTTAGAAGCTGGTTT  
 GATTCTCTCCATTTTCAACATTGGTTGTGOCATTGGTGGTATTATTCTTT  
 CCAAATTGGGTGATATGTACGGTCTTAAGGTGGGTTTGATTGTCGTTGTT  
 GTCATCTACATCATCGGTATTATTATTCAAATTGCATCTATCAACAAATG  
 GTACCAATATTTCATCGGTAGCAATTATTTCCGGTTTCGGTGTGTGGTGGTA  
 TTGCCGTTTTATCTCTATGTTGATTTCTGAAGTATCCCCAAAGCAATTA  
 AGGGGTACTTTAGTCTCTTGCTACCAATTGAATGATTACTGCCGGTATTTT  
 CTTCGGTTACTGTACCAACTTCGGTAUTAGAAGTACTUCAAATCTGTGC  
 AATGGAGAGTTCCATTAGGTTTGTGTTTTGCCCTGGGCTTTGTTTATGATT  
 CCTGCTATGACATTTGTTCCAGAGTCTCCACGTTAFTTGGCTGAAGTCGG  
 TAAGATCGAAGAAGCCAAACGTTCTATTCGCCCTTCTAACAAGGTTGCTG  
 TTGATGATCCATCTGTTTTGCTGAAGTGAAGCTGTCTTGGCTGGTGTGA  
 GAGGCAGAGAAATTAGCTGCTAATGCATCTCTGGGTCAATTGTTTAGTAG  
 CAAGACAAAGGTCTTTCAGCGTTTGATCATGGGTGCTATGAATCAATCTC  
 TACAACAAATTGACAGGTGATAACTAETTTCTCTACTATGGTACTACTATT  
 TTCAAGGCTGTTGGTTTGAATGACTCTTTTGAACCTCTATCTCTCTCGG  
 TATTGTTAACTTTGCTTCCACCTTTGTTGGTAATTAAGTTGTGTGAGAGAT  
 ATGGTGGTGGTACTTGTGTTGCTATGGGTGCTTCCATCCATGACTGCTTGT  
 ATGGTTGCTATGCTTCCGTGGGTGTCACCAAGATTATGGCCAAATGGTCA  
 AGACCAACCAATCTTCCAAGGGTGCTGGTAAGTATGATTGTCTTGGCT  
 GTTTCTATATTTCTGTGTTTGCTACTACATGGGCTCCAATTCCTTACGTC  
 GTTGTCTCTGAAACTTTCCCATTTGAGAGTCAAGTCTAAGGCTACGTCTAT  
 TGCTACAGCTGCTAATTTGGTTGTGGGGTTCTTGATTGGTTTCTTCACTC  
 CATTTATTACTGGTGCTATTAACCTTCTACCTACGGTTAAGTTTTCATGGGC  
 TGTTTTGCTCTTCATGTTCTCTATGTTTTGTTAGTTGTTCAGAAACTAA  
 CGGTTTGACTTTTGAAGAAGTCAACACCATGTGGAAGAAGGTGTTCTAC  
 CATCGAAGTCTCCCTCATGCCCTCCACCATCCAGAACAGGTGCCAACTAC  
 GACGCTGAAGAAATGACTCACGATGACAAGCCATTTGTACAAGAGAAATGTT  
 CAGCACCAAAATAA

YDR342C, 570 aa (SEQ ID NO 120)

MSQDAALAEQTPVEHLSAVDSASHSVLSTPSNKAERDEIKAYGEGEEHEP  
 VVEIPKRPAAYVTVSIMCIMIAFGGPFVFGWDTGTISGFINQTFJRRFG

49/251

MKHKDGNTNYSKVRTGLIVSIFNIGCAIGGLILSKLGDMYGRKVGLIVVV  
 VIYIIGILIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL  
 RGTLVSCYQLMITAGTFLGYCTNPGTKNYSNSVQWRVPLGLCSFAWALFMI  
 GGMTFVPHSPRYLAEVGKIBBAKRSLAVSNKVAVDPPSVLAEVEAVLAGV  
 EAEKLAGNASWGELEFSSSKTKVLQRLIMGAMIQSLQQLTGDNYFFYYGTTI  
 PKAVGLSDSFETSTVLGIVNFASTFVGIYVVERYGRRTCLLWGAASMTAC  
 MVVYASVGVTRLWPNQDQFSSXGAGNCMIVFACFYIFCPMTTWAPIPVV  
 VVSEFFPLRVKSKAMSLATAANWLWGFLIGFFTPFITGAINFYGYVFMG  
 CLVFMFFYVLLVVPETKGLTLEEVNFMWEEGVLPWKSASWVPPSRRCANY  
 DAEEMTHDEKPLYKRMEFTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAATGTTTTTTAGGCAACGGAGATTCTGTTTTATCCACGTTTACCCC  
 ACAAAAAGTGCAGGTACATTGTGGGGCCCCGGCATCGAAAATCACTTTT  
 TTCCCTTAACCGCTCGA/AAAAACGAGAAATTATTGGAACCTTGCCAGAGA  
 ATAGTCCGTAGGCAAAATTGAAANTGTTCCCTTAAAAAATTTCTGTTTCTTAC  
 TCATTGAGATTATTTCAGATCCCCCTCCGTGCCCTTCATTGAAAAAATCCAA  
 GAGATGCTCTGGATCTCTATGCCAGATTTTGGCTTGCCAGACAATGGAGAGC  
 AAA/CGGTATACAATATAGAAAGCACAGAAACATATAAAAAGAGCTCCAG  
 AAAAGACATATGGTTTGTAACTATCTTCTTCTTTTTCCAATTATTCTGT  
 TTTAAATAA/AAAAAACAAGAACAACAAGCTCAACTTGTCTTTTCTAAG  
 AACAAAGAATAAACACAAAAACA/AAAGTTT/TTAATTTTAATCMAAAA  
 ATCTCACAAAGACGCTGCTATTGCGAGAGCAAACTCCTGTGGAGCATCTCTC  
 TGCTGTTGACTCAGCCCTCCUACCTCGGTTTATA/TTACACCATCAAAACAGG  
 CTGAAGAGATCAATAAAAGCTTATGGTGGAAGGTGAAGAGACCGAACCT  
 GTCTGTTGAAATTCCAAAGAGACCAGCTTCTGCTTATGTCACTGTCTCTAT  
 TATGTGTATCATGATCGCCTTTGGTGCTTTTCGTTTTCGGTTGGGATACTG  
 GTACCACTTCTGTTTTCATCAATCAAAACGATTTTCATCAGAAGATTTCCT  
 ATGAAGCATAAAGATGGTACTA/TTATTTCTCTAAGCTTACAAC/CG/TT  
 CATGTCTCTCCATTTTCAACATTGGTTGTGCTTGGTGGTATTATTCTTT  
 CCAANTGGGTGATATGTACGGTCTGAAGGTGGGTTTGATTGTCTGTTGTT  
 GTUATCTACATCATCGGTATTATTATTCAAATTCGATCTATCAAC/AAATG  
 GTAUCAATATTTCAATCGGTACAATTATTTCCGTTTGGGTGTTGGTGGTA  
 TTGCCCTTTTATCTCCTATGTTGATTTC/CAAGTA/CCCCAAAGCATTTA  
 AGGGGTACTTTTAGTCTCTTGC/TAACCA/TTGA/AGATTACTGCCGGTATTT  
 CT/TTGGTTACTGTACCA/ACTTCCCTACTAAGAACTACTCCAACTCTGTGC  
 AATGGAGAGTTCCATTAGGTTTGTGTTTTGCTTGGGCTTTGT/TTAAGATT  
 GGTGGTATGAUA/TT/TTTCCAGAGTCTCCACGTTATTTGGCTGAAGTCCG  
 TAAGATCGAAGAAGCCAAACGTTCTATTGCCGTTTCTAACCAAGCTTGCCTG  
 TTGATCATTCATCTGT/TTTGGCTGAAGTCGAAGCTGTCTTGGCTGGTGT  
 GAGGCAGAGAAA/TTAGCTGGTAATGCATCCTGGGGTGAATGTTTACTAG  
 CAAGACAAAGGTCTTTCAGCG/TT/CGA/TCATGGGTGCTATGATTCAATCTC  
 TACAACAA/TTGACAGGTGATAAC/PA/TT/CTTCTACTATGGTACTACTATT  
 TTCAAGGCTGTTGGTTTGAGTGACTCTTTCGAAACCTCTATTGTCTTGGG  
 TATTGTAACTTTGCTTCCACC/TTTG/TTGGTA/TTTACGTTGTTGAGAGAT  
 ATGGTCTGCTACTTGT/TTGCTATGGGGTGCTGCATCCATGACTGCTTGT  
 ATGCTTGTCTATGCTTCCGTGGGTGTCACCAGATTATGGCCAAATGGTCA  
 AGACCAACCATCT/TTCAAGGTG/TC/TTGTAAC/TTATGATTGTCTTTGCCCT  
 GTTTCTATATTTCTGTTTGTCTACTACATGGGCTCCAATTCCTTATCTC  
 GTTGT/TTCTGAACCTTTCCCATTCAGAGCTCAAGTCTAAGGCTATGTCTAT  
 TGCTACAGCTGCTAATTTGGTTGTGGGGTTTCTTGATTGGT/TTCTTCACTC  
 CAT/TTA/TTA/CTGCTGCTATTAACTTCTACTACGGTTACGTTTTCATGGCC  
 TGT/TTGGTCTTCATGTTCTCTTATGTTCTTGT/TTAGTTGT/TTCAAGAACTAA  
 GGGTTTGACTTTTGAAGAAGTCAACACCATGTGGGAAGAAGG/TTTCTAC  
 CATCGAAG/TTTCCCTCATGCTTCCACCATCTAGAAGAGGTGCCAACTAC  
 GACGCTG/TAAGAATGCTTCAAGATGATAAGCCA/TTGTACAAGAGAAATGTT

50/251

CACCACCAAATAA

YDR343C, 570 aa (SEQ ID NO 122)

MSQDAATAEQTPVEHL SAVDSASHSVLSTPSNKAERDEIKAYGEGKKHEP  
 VVETPKRPASAYVTVSIMCIMIAFGGFVFGWDTGTISGFINQTDIFIRREG  
 MKHKUGTNYLSKVRTGLIVSEFWIGCAIGGIILSKLGD MYGRKVGITVWV  
 VIYIIIGITIIQIASINKWYQYFIGRIISGLGVGGIAVLSPMLISEVSPKHL  
 RGTPLVSCYQLMITAGIFLG YCTNFGTKNYSNSVQWRVPLGICFAMALFMI  
 GGMTFVPESP RYLAEVGKIEEAKRSI AVSNKVAVD DPSVLAEVEAVLAGV  
 EAEKLAGNASWGELFSSKTKV LQRLINGAMTQSLQCLTGDNYFFYYGTI  
 EKAVGLSDSPETSIVLGIYNFASFVGLIYVVERKGRRTCLLWG AASMTAC  
 KV VYASVGVTRLWPNQDQPS SKGAGNCMI VFACFYIFCFATTWAPIPYV  
 VVSETFPLRVKSKAMSTATAANW LMGFTJGFETPFYTGATNFYGYVFMG  
 CLVFMFFYVLLVVPETKGLLLEEVNTMWEEGVLPWKSASWVPSRRGANY  
 DAEEMAHDDKPLYKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCTCTGGCATCCACTAAATATATAATGGAGCCUGCTTTTTTAAGC  
 TGGCATCCAGAAAAAAAAGAATCCCAGCACCAAAATATTGTTTTCTTCA  
 CCAACCATCAGTTCCATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAG  
 GGGCACAACAGGCCAAAAACGGGCACAACCTCAATGGAGTGATGCAACC  
 TGCCTGGAGTAAATGATGACACAAGGCAATTCACCCACGCATGTATCTAT  
 CTCATTTCTTACACCTTCTATTACCTTCTGCTCTCTCTGATTTGAAAA  
 AGCTGAAAAAAAAGGTTGAAACCAGTTCCCTGAAATTATTCCTTACTTG  
 ACTAATAAGTATATAAAGACGGTAGGTATTGATTGTAAATTCTGTAAATCT  
 ATTTCTTAAACTTCTTAAATTCTACTTTTATAGTTAGTCTTTTTTTTAGT  
 TTTTAAAAACCAACAACACTTACTTTTGAATAAACAACATAAACAACAAA  
 ATGCTTAGAGTTGCTATTAAACGGTTTCGGTAGAAACGGTAGAATTGCTCAT  
 GAGAATTGCTTTGTCTAGACCAAACGTCGAAGTTGTGCTTTGAACGACC  
 CATTCATCACCAACGACTACGCTGCTTACATGTTCAAGTACGACTCCACT  
 CACGCTAGATACGCTGGTGAAGTTTCCACGATGACAAGCACATCATTTGT  
 CGATGGTAAGAAGATTGCTACTTACCAAGAAGAGACCCAGCTAACTTGC  
 CATGGGGTTCTTCCAACGTTGACATCGCCATTGACTCCACTGCTGTTTTC  
 AAGGAATTAGACACTGCTCAAAACACATTCAGGCTGGTGCCAGAAGGT  
 TGTATTCACTGCTCCATCTTCCACCGCCCCAATGTTGCTCATGGGTCTTA  
 ACGAAGAAAAATACACTTCTGACTTGAAGATTGTTTCCAACGCTTCTTGT  
 ACCAUCAACTGTTTGGCTCCATTGGCCAAAGGTTATCAACGATGCTTTCGG  
 TATTGAAGAAGGTTTGATGACCACTGTCCACTCTTTGACTGCTACTUAAA  
 AGACTGTTGACGGTCCATCCCACAAGGACTGGAGAGGTGGTAGAACCGCT  
 TCCGGTAACATCATCCCATCTCCACCGCTGCTCTTAAGGCTGTGGGTAA  
 GGTCTTGCCAGAATTGCAAGCTAAGTTGACCGGTATGGCTTTCAGAGTCC  
 CAACCGTCGATGTCTCGTTGTTGACTTGACTGTCAAGTTGAACAAGGAA  
 ACCACCTACGATGAATCAAGAAGGTTGTTAAGGCTGCCGCTGAAGGTAA  
 GTTGAAGGGTGTTTTCCGTTACACCGAAGACGCTGTTGTCTCTCTGACT  
 TCTTGGGTGACTCTCACTCTTCCATCTTCCATGCTTCCGCTGGTATCCAA  
 TTGTCTCCAAAGTTGCTCAAGTTGGTCTGCTGGTACGACAACGAATACGG  
 TTACTCTACCAGAGTTGTGACTTGGTTGACACCTTGCCAAAGGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVALNGFGRIGRLVMRIALSRPNVEVVALNDPFITNEYAAYMFKYDST  
 HGRVAGEVSHDDKHIIIVDCKKIATYQERDPANLPWGSSNVDLAIDSTGVF  
 KEUDIAQKHIDAGAKKVVTAPSSSTAPMFVMSVAAEKYTSULKIVENASC  
 TFWCLAPLAKVINDAFGIEGLMTTVHSLTATQKTVDGPPSHKDWRCGRTA  
 SGNITPSSSTGA AKVGVKLP ELQGKLTGM AFRVPTVTVSVVDLTVKLNKE  
 TTYDEIKKVVKAAAEGLKGV LGYTEDAVVSSDFLGDSHSSIFDASAGIQ  
 LSPKFVKLVSWYDNEYGYSTRVVDLVEHVAKA

51/251

YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)  
 CGACCCTCTGGTTAGATGACACTCCTGCCCCAACTGCCACGAATCTGTAA  
 CCCCATAACTATAACCCGTACGCAGTACTAAAAATGTATGTAATTAGTAAA  
 TGTATGTAAACAATTTACCCGTTTTGTGTAAACAATTCATTCAATTCATTCTT  
 TTGATCCTTTTAGTACCGTCCGCACATGATGTCATTTCCCCCTCATTTTTG  
 TTTTCTGTGTATGATTCCCCGCCCGGGGACGGTACGGCTGTTATCCAGCG  
 ATGCGGGACTTCCGTCCACAGGTATCTTTTCTCTCCAACTCCAACAGAGAT  
 GGAAAATGAGGGGGCGGGTGTAGGTAAGCAGAATGACGAGAAATTTGTAAT  
 GAAAATGGAAGTTUGGGCGGTTATATAAATGGGGGGGGTTTGTGGGTGACA  
 ATTGACTTCACTCTCTTTTCTCTCAAAATTTCTTGGCTCTTACGATTAGAA  
 GTATCTGGAAAACCAACCAAGAAAACACAAATAACAAAATAAATAAAGC  
 ATGTTCACTAGATCTACGCTCTGTTTAAAGACGCTCTGCATCCTCCATTGG  
 GAGACTTCAATTTGAGATATTTCTCACACCTTCTTATCACAGTCCCTATCA  
 AGCTGCCCCAATGGGTTGGAAATATGAGCAACCAACGGGGTGTTCATCAAC  
 AACAAGTTTGTCTTCTTAACAGAACAGACCTTCCGAAGTCATTAACCC  
 TTCCACCGAAGAAAGAAATATCTCATATTTATCAACCTAGAGACGACGATC  
 TGGAAAGAGCGCGTGCAGGCCGCCGACCGTGCCTTCTCTAAATGGGTCTTGG  
 AACGGTATCGACCCCTATTGACAGGGGTAAGGCTTTCTACAGCTTAGCCGA  
 ATTAATTGAACAGGACAAGGATGTCATTGCTTCCATCCAGACTTTGGATA  
 ACGGTAAAGCTATCTTTCTCGAGAGGAGATGTTGATTTAGTCATCAAC  
 TATTTGAAATCTTCTGCTGGCTTTGCTGATAAAATTGATGGTAGAATGAT  
 TGATACTGGTAGAACUCATTTTCTTACACTAAGAGACAGCCTTTGGGTG  
 TTTGTGGGCAGATTATTTCTTGGAAATTTCCCACTGTTGATCTGGGCCTGG  
 AAGATTGCCCTGCTTTGGTCCACCGGTAACACCGTCCGTGTTGAAGACTGC  
 CGAATCCACCCCATGTCGGCTTTGTATGTTCTAAATACATCCCACAGG  
 CGGGTATTCACCTCGGTGTCATCAACATTGTATCCGGCTTTGGTAACATT  
 GTGGGTGAGGGCCATTACAAACCATCCAAAATCAAAAAGGTTGCCTTCAC  
 AGGGTCCRCGGCTACGGGTAGACACATTTACCAGTCCGCAGCCGCAGGCT  
 TGAAAAAAGTGACTTTGGAGCTGGGTGGTAAATCACCAACATTGTCTTC  
 GCGGACGCCGAGTTGAAAAAAGCCGTGCAAAACATTATCCTTGGTATCTA  
 CTACAATTTCTCGTGAGCTCTCTTCTGCGGCTTCAAGCGTGTATGTTGAAG  
 AATCTATTTACGACAAATTCATTGAACAGTTCAAAAGCCGCTTCTGAATCC  
 ATCAAGGTGGGGCGACCCATTGATGAATCTACTTTCCAAGGTGCACAAAC  
 CTCTCAAATGCAACTAAACAAATCTTGAATACGTTGACATTGGTAACA  
 ATGAAGGTGCTACTTTGATTACCGGTGGTGAAAGATTAGGTAGCAAGCGT  
 TACTTCAFTAAGCCAACTCTCTTTGGTGACGTTAAGGAAGACATGAGAAT  
 TGTCAAAGAGGAAATCTTTGCCCTCTTCTCACTGTAACCAATTCAAAT  
 CTGCCGACGAAGTCATTAAACATGGCGAACGATTTCTGAATACGGGTGGCT  
 GCTGGTATTCACACCTCTAATATTAAATACUUGUUTTAAAAGTGGCTGATAG  
 AGTTAATGCGGGTACGGTCTGGATAAACACTTATAACGATTTCCACCACG  
 CAGTTCTCTTCCGTGGGTCAATGCACCTGGTTTGGGCAGGGAAATGTCT  
 GTTGATGCTTTACAAAACACTATTGCAAGTTAAAGCGGTCCGTGCCAATTT  
 GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MFSRSTLCLKT3ASSIGRLQLRYFSHLFMTVP1KLPNGLEYEQPTGLFIN  
 MKFVPSKQNKTFEVINPSTEEIICHIEGREDDVEEAVQAADFAFNGSW  
 NGIDPIDRGKALYRLAFILPQKXDVIASTETLDNGKATSSSGDVTILVYN  
 YLKSSAGFADKLDGRMLYGRIMFSYTKRQPLQVCGQ11FWNFPLLMWAW  
 KIAPALVTGNTVWLKTAESTPLSALYVSKYIPQAGIPPGVINIVSGFGKI  
 VGEAJTNHPKIKKVAFTGSTATGRHIIYQSAAGUKKVTLELCKSPNIVP  
 ADAELKKAVQNIILGIYNSGEVCCAGSRVYVEESIYDKFIEEFKAASES  
 IKVGLPFDESTFQGAQTSQMQLNKILKYVDIGKNEGATLITGGERLGSKG  
 YFIKPTVFGDVKEDMRIVKEEIFGPVVIVTKFKSADEVINMANDSEYGLA  
 AGIHTSNLNTALKVADRVNAGTVWINTYNDPHHAVPFGGFNASGLGRMS  
 VDALQNYLQVKAVRAKLDE

52/251

VER177W, 1304 bp, CDS: 501-1304 (SEQ ID NO 151)  
 AGATAGATAGATATAGATAGATAATGGACGTAGTATATAGAACAGAAAATC  
 GGTAGATCCAAAACACAGGGGAAAAGGGGGGGGGGGGGGGGAGACAGCG  
 CAGCCACGTGACGGGCTTCTCTTTGGAAAGTGGAGCGAAGTTTTCGGGA  
 AGCTACTTTTATTCGGCCTGGAGTCAAAAGAGGAAGCTUGGTGGUAAATA  
 CCTTCTCTTTTGTGGCCGGGGCCCGGGGGGACGAGGCAAAAAGCAAAGAA  
 AAGCAAAAATAAANAANAANCAAAAAACAGGGGTATGAGAAAAAG  
 ACACGCTTTTCCACGCGCAGCAAAAAGCAAAAAGCAAAAGCAAACTCTTT  
 ATTATTGGACCTTAAACCTGAAAACGAGACGAACCGTAACATAAAACCGT  
 GTAGTTTCGCAAAAATCAACTTAGTTTTTTCCTACTTTTCAAAATTCAGAG  
 UGCAAGCAAGTGAAGAAGAAAAGCAAGTTAAAGATAAATTAAGATAAABA  
 ATGTCAACCACTCGTGAAGATTCTCTGTACCTAGCCAAAGTTGGCTGAACA  
 GGCCGAACGTTATGAAGAATGGTCCAAACATGAAGACTGTTGCCCTCCT  
 CTGGCCAAAGAGTTGTCCGTGGAAGAGCGTAATTTGTGTGTCTGTTGCTTAT  
 AAGAAGCTTATTGGTGTCTGTGTGTCTCTGGAGAATTGTTTCTTCTAT  
 TGGCAAAAAGGAGGAGTCAAGGAGAAGTCCGAACACCAAGCTCCAGCTTGA  
 TTTGTTCGTACCGTTCGAAGATTGAGACCGAACTAATTAAGATCTCCGAC  
 GATATTTTGTCCGTGCTAGACTCCCACTTAATTTCCATCAGCCACCACTGG  
 CGAGTCCAAGGCTTTCTACTATAAGATGAACGGTGACTACCACCGTTATT  
 TGGCTGAATTTCTAGTGGCGATGCTAGAGAAAAGGCCACAAACGCCCTCT  
 TTAGAAGCATACAAGACCGCTTCTGAAATTGCCACCAACAGAGTTACCCCC  
 AACTCACCCAATCCGTCTAGGTTTGGCTCTTAACCTCTCTGTCTTCTATT  
 ATGAATTTCAAAACTCTCCAGACAAAGCCTGCCATTTGGCCAGCAAGCT  
 TTTGACGACGCTATTGCTGAGTTGGACACTCTGTCTGAAGAATCATACAA  
 AGATAGCACACTTATCATGCAACTGCTAAGGACAAATTTAACTTATGGA  
 CTTTCAGACATGTCCGAGTCCGGTCAAGCTGAAGACCAACAACAACACAA  
 CAACATCAGCAACAGCAGCCACCTGCTGCCGCCGAAGGTGAAGCACCAAA  
 GTAA

VER177W, 267 aa (SEQ ID NO 152)  
 MSTREDVSVYLAKLAEQAEERYEEMVENMKTVASSGOELSVEERNLLSVAY  
 KNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKLETELTKISE  
 DILSVLDSHLIPSAITGSKVFPYKMKGDYHRYLAEPSSGDAREKATNAS  
 LEAYKTASEIATTELPTTIPIRLGLALNFSVPYIEIQNSPDKACILAKQA  
 FDDAIAELDTLSEESYKDSLIMQLLRDNLTLWTSMDSESGQAEQQQQQ  
 QHQQQQPPAAAEGRAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 163)  
 TAGTTCTATTTCCCTATNTMTTCAGACTGACAAATCTTTAAGAGAGACA  
 AACTGAGAATTAGCATATAGAATCATTCTATCAACTGTTTACAAACAAGT  
 AAGCCCAAGACAGTTCCCAACCGCTTAAGAAGTTTTTCTAGAGGGAGC  
 AAGTTTCGTTTACATTTACACACACAGTTTTTTTTCACTTTTTTGGGCC  
 TCTTTCTTTTCCCGTTTTTTTCAAAAAGCTTAGAAATCTTCTTCACTTCC  
 TATTTTTTTCTAGAATCGTGAAGAATTTCCAGATTTAACAGTTTTTCCACTTT  
 TTCAATAAGGAAATAGTAGGAATAATAAAAAAGGATAGTAGTAACGATA  
 TACGTGCACTTTCCAGACTGGTCTCGAGCCGGAATTAATTAACAATAGCAG  
 CGTTTTCAGCTACCACATTTGTAGCTCCGCTAGAATTTGATCGAAAACAAAAAT  
 AATAACACTAATAATTTAATAATAACGGTAGAACTATTTCTTGTATAAAG  
 ATGCCATAATCTATTGTGAGCAACCCATTCCATGCTCATCATTAATGACCA  
 TCATCATGACCGTGAAAATTCGTCTAATAACCCGCCACAGTTGATCAGAA  
 GTTCTAAATCTTTCTTAAACTTCATTGGTAGAAAACAAAGTAATGACTCA  
 CTAAGAAGCGAGAAATCTACAGATTCCATGAATCTACCACAACCACTAC  
 AAAATTAACCTACAAACAAACCTTAATAACAACCCCATAGCCATCTTAATG  
 CAACCAAGTATCTCAACAAACAACCTACAATAATAACCTATGAAACAAACUAC  
 CACCATAATATTTCTCATGGGCTCCATGACTATACTTCTCCCGCCTCTCC

53/251

AAAACAAACCCACTCCATGGCAGAAATTGAAAAGGTTTTTCAGACCTTCCTG  
 TAAATAAAAACTATCTATGTCTCAACTTCGTTCCAAGAAACATAGCACC  
 CATTCCCCCCCCACCTTCAAAATCAACTTCTACAGTTAACTTAAATAACCA  
 CTATCGTGCUCUAGCATUUTCATGGUTTTAAGAGACCACTATGCTCATACCC  
 AGTCTGCTATACCGCCAGTACCGATTCTATGCTATCTTTGTUCAATAAT  
 ATTAATATATATACAGATGATTGTATTCTGGCTCAAAAATACCGGAAAT  
 GCGTAAGTATATTGGGTTCCGGTGCCGGTGGGTCCGTTAAAGTTCTTGTGA  
 GACCAACTCATGGTCCTACTTTTGCCCGTCAAAGAATTCAGACCAAGGAAA  
 CCGAATGAGAGTGTGAAAGAATATGCCAAGAAGTGCACCCGAGAAATTTTG  
 TATTGGTTCGACTTTACATCACCCAAATGTTATCGAAACTGTTGACGTTT  
 TCTCTGATTCTAAACAAATAAATACTATGAAGTTATGGAGTACTGTCCG  
 ATTGATTTTTTTTCTCTCTGTTATCACAGCCACATCTCTCTGCCCCAGAT  
 CAAGTGTTCCTTGAAGCAATGACTGAAGGTGTTAAATATTTACATTCTA  
 TGGGATTGGCAGATAGAGATTTGAAATTGGATAATTGTGTCTATGACTTCC  
 CAGGGTATTTTTGAAATTAATTGATTTTGGTAGTCTGTTGTGTTACATA  
 TCCTTTTGAAGATGGUGTACGATGGCTCATGGAATCGTGGGTAGTGACC  
 CTTACTTAGCGCCGGAAGTGATTACCTCCACCAAATCTTATGATCCTCAG  
 TGCGTCGATATATGGTCTATTGGGATCATATATTGTTGATGGTGCCTTAA  
 AAGGTTTCCATGGAAAGCCCCTAGAGATTCTGACGATAACTTTAGATTAT  
 ATTGTATGCCGGATGATATAGAACACGACTATGTTGAATCTGCCAGGCAT  
 CACGAAGAGTTACTGAAGGAAAGAAAAGAAAAGCGTCAAAGGTTTTTGAA  
 TCACAGTGAAGTGTTCGCCATCAATCAGCAACAACCCAGCTCATGAATCAA  
 ACTTGAAACAGTTCAAAATCAAGTTCCAAATACTCCAGCATCTATACAG  
 GGTAAAGCGGATAACAAACCCAGCATTTGTGGAAGAGAAAACUGAAGAAAA  
 TAAAGAAGATGATAGCAATAATGATAAAGAAAGCACGCCAGATATGACA  
 AGGAAAGTACCATCCATATTAAAATAAGCAAAAATGAGAATAAAAGCACG  
 GTAGTTTCAGCTAACCACAAAGAAAGTAGATGCCGATGCCGACGCTGATTG  
 CCATGCTAATCTGACTCTAACCCAGACTGCTTCCAAGCCTAACAGTG  
 ACTGCAATGACAAAACGGATTGTAATGCTAACCAATGACTGCAGCAATGAA  
 TCGGATTGTAACGCTAAAGTTGATACTAACGTCACACTGCTGCCAACGC  
 TAACCCCTGATATGTTTCCCCAAAACAAATCCACAACAACAACAACAACA  
 AACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA  
 CACCACCATCAAAATCAAGACAAGGCCCATAGTATCGCTTCCGATAATAA  
 ATCGAGTCAACAGUACAGAGGACCTCACCATAAAAAAATTATTCATGGCC  
 CATACCGTCTATTACGCTCTACTACCACATGCTTCAAGACCTATCATGTCC  
 CGTATACCTGCAAGTAGATCCAAAGAAAAGAGCAACCTTAGATGATATTTT  
 TAATGATGAATGGTTTGGCCCATATGCTGCTGTACCATGGATTCAAAAA  
 ATAAAGTTATTAGAGCGCCTGGCCATCACCATACATTGGTTAGGGAGGAA  
 AATGCTCACTTAGAGACCTACAACGTTTTA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPFHGHNDHHHDRENSSNNPPQLRSSKSPFNFGRKQSNDS  
 LRSEKSTDSMKSTTTTNTYTTMLNNNTHSHSNATSISTNNYNNNYETNH  
 HENISHGLHDYTSFASPKQTHSMAELKRFPRPSVNKKLSMSQLRSKKHST  
 HSPPPSKSTSTVNLNMHYRAQHFGFTDEYAHQSAIFPSTDSL LSLSN  
 INIYHDDCTIAQKYGKLGKLLGSGAGGSVKVLVRPTDGATFAVKEFRPRK  
 PMSVKKEYAKKQTAAPCIQSTLRHPNVIKTVDFVSUSKQNKYYEYMEYCP  
 LDFFAVVVTGKMSRGEINCCCKQLTEGVKYLHSMGLAHRDLKLDNCVNTS  
 QGTLKLLIDFGSAVVFRYPFEDQVTMAHGTVGSDPYLAPEVITSTKSYDPQ  
 CVDIWSIGIYYCCMVLKRFPWKAFRDSDDNFRLYCMPDDIEHDYVESARH  
 HEELLKERKEKRORFLNHSDCSAINQOOPAHESNLKTVONQVPNTPASIQ  
 CKSDNKPDIVEEETEEKEDDSMMDKESTPENDKESTIDIKISKNEKSC  
 VVSANPKKVDAADADCDANGDSNGRVDCKANSDCNOKTDCNANNDCSNE  
 SDCNAKVDNTNVNTAANANPDMVPQNNPQQQQCQQQQQQQQQQQQQHHH  
 HQHQHQDKAHSIASDNKSSQQHRGPHHKKIIGHGYPYRLRLRLPHASRPIMS  
 RILQVDPKKRATLDDIFNDEWFAAIAACTMDSXNKVIRAPGHHHTLVREE

54/251

NAHLEYTKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)

TATTCGGCGTCTGATTTCCGTTTTTGGGAATCCCTTTGCCGGCGCGCCCTCTC  
 AAAACTCCGCACAAAGTCCCAGAAAGCGGAAAGAAATAAAACGCCAUCAA  
 AAAAAAAAAATAAAACCCAAATCCTCCAGCGTGGCTGGTACCCCTTGA  
 TTATCCCGGTACAAGTATTTCTCAGGAGTAAAAAACCGTTTGTTTTGGAA  
 TTCCCCATTTTCGGGGCCACCTACGCCGCTATCTTTGCAACAACATCTGC  
 GATAACTCAGCAAATTTTGCATATTCTGTTTGCAGTATTGCGATAAATGGG  
 AGTCTTACCTTCCAACATAACGGCAGAAAGAAATGTCAGAAAACTTTGCAT  
 CCTTTGCCCTCCGTTCAAGTATATAAAGTCGGCATGCTTGATAATCTTTCT  
 TTCCATCCTACATTGTTCTAATTATTCTTATTCTCCTTTATTTCTTCCCTA  
 ACATACCAAGAAATTAATCTTCTGTCAATTCGCTTAAACACTATATCAATA  
 ATGCAATTTTCTACTGTCCCTTCTATCGCCGCTGTCGCCGCTGTCCCTTC  
 TGGCGCTGCTAAAGTTACCACTGCTACTGTACGCCAAGAACTTACCACTT  
 TGGTCACCATCACTTCTTGTGAAGACCACTCTGTCTTGAAACCTGTCTCC  
 CCAGCTTTTGGTTTCCACCGCTACCGTCACCGTCGATGACGTTATCACTCA  
 ATACACCACCTGGTGCCCATTTGACCACTGAAGCCCCAAAGAACGGTACTT  
 CTACTGCTGCTCCAGTTACCTCTACTGAAGCTCCAAAGAACACCACCTCT  
 GCTGCTTCAACTCACTCTGTCACTCTTACACTGGTGGCTGCTGCTAAGGC  
 TTTGCCAGCTGCAGGTGCTTTGTTCGGCTGGTGCCGCTGCTTTGTTGTGT  
 AA

YLR110C, 133 aa (SEQ ID NO 276)

MQFSTVASIAA VAAVASAA NVTTATVSQESTTLVTITSCEDHVCSETVS  
 PALVSTATVTVDVITQYTIWCPLTTEAPKNGTSTAAPVTS TEAPKNITS  
 AAPTHSVTSYTGAAAKALFAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGTCTATTACTAATCAAGAAAAGAACCCATAATCATCGGCGTCCCTCTG  
 GGGCTCTCGGAAAAACCGGTCTCTGACGTCACTGAAAAGATTTCCGGCACAT  
 GGTCAATGGGACCAGAGAAAAATTAATCCGACATGTGGAAATATTTCCCTCC  
 GTTAAGGTAGTGAGCGCGGATTTTTTCTGATTTGTAATTATACGGGGAGC  
 TCTGGCCAAAAGGTCAGTATTTGGTGATGAAGTTGAATATCATCTTTTG  
 ATTTTCTTCTGTATCATTCTTTTTCTTTTTCCACACCCCTTCCGGACGGT  
 ATTCACATATTGTTGAGAGCTTAAATGAAAAATAAAGGGGTGGAAATTA  
 AGCACGACATCTAAGGGAAAAGCATAAACGAAACATTATATAAAGGAGCA  
 CAATTTCTCTCTCCCTTGCCAATTGTGCATATACCGTTTCTTATAACGAA  
 ATTTCAACAAACCAGAACACACAAGTACTACCAATAACCACAAACAAAC  
 ATGTCTGACTTACTTAACAAGAAATTCACAGCTGGCCACTACAAATTCOA  
 ATACATTGCTATCAGCCAAAGTGATGCTGACAGTGAATCTTCTAAGAGGC  
 CACAAACAGTTCAATGGTCCAAATTAATTTCTGAAAACAAGAAGGTTATC  
 ATTACCGCTCCTCCAGCTGCTTTCTCCCCAACCTGTACTGTCAAGCATAT  
 TCCAGGTTACATCAACTACTTTGGATGAATTAGTTAAGGAAAAGGAAGTTG  
 ACCAAGTGACCGTTGTTACTGTTGACAACCGTTTCGCTAACCAAGCGTGG  
 GCTAAGAGCTTAGGTGTTAAGGACACCACACACATCAAGTTTGCTCCGA  
 CCCAGGCTGTGCTTTCAACCAATCCATTGGTTTCGAATTAGCCGTCGGTG  
 ACGGTGTTTACTGGAGTGGTAGATGGGUCATGCTTGTGAAAACGGTATC  
 GTTACTTACGCTGCCAAGGAAACCAACCCAGGTACCGATGTGACCGTTTC  
 CTCACTCGAAAGTGTCTTGGCTCATTGTGTAG

YLR109W, 175 aa (SEQ ID NO 274)

MSDLVNKKKFPAGDYKFQYTAISQSDADSFCKMPQTVEWSKLTSENKKVT  
 LTGAPAA/SPCTIVSHIPGYINYLDLVKKEVIXVIVVTVDN/PFANQAW  
 AKSLGVKDTTHIKFASDPGCAFTKSIGFELAVGDGVYWSGRWAMVVENGI  
 VTYAAKETNPGTDVTVSSVESVLAHL

55/251

YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)  
 TTGTTCCAACAATTTTGGGAGCTTCTCCGTCCTACGACCTGTATTTAC  
 CTTCTCTAGCTCATCGCTTCCAGGGTCCACGTTAATTTTTCAATTTTTT  
 CTTGCGTGTGGAAGATTTCAGGTCTCGAGAAATTTGTCAAAAATTTTTTAC  
 TAGATATTAAAGAACTATATACATCGAATAAGATGCCAGCACAGAAGAGAT  
 AGGCAATCAGTTTAGATACTACAGACACTATCCAATAGTCGAAAGCAAAA  
 GCAGCATAGAAAAAGAGAAATCCCGTTTCAGCTTTTCTCTTTTCCCA  
 TTGTTTTTTCCCGATCTTTTTTCTGCAATCGTGGCACCTAGAACAAGAGG  
 TACCATTCCAATCCATTGCGTTAATATTTGATACGACTTTTTTGATTTCCTCAAT  
 ATTATTATTTGTTACTATTATATTTTATCATTTGGGTTTGGGTTTTTTGT  
 AATBAATTTTCTTTTTTTTTTTTGGGCTCTATTTCACTAAGACATCGTATAT  
 ATGCCAGGCCAGATAATCAGCAATTCGGTTTTTGTGCGCAGACGAGGACAT  
 GGATAAATACTTGTGTGGAGTACCGCAGTTTGAAGCTCTTCATCAGTCCA  
 GTAAATTCCTCCAGTCTCACAAATGCGCCCTCCCAACAGTCGAACATACCAC  
 CCCCATTACAAATCACATGAATAACAACAACACTGGTAGCTATTACTATTAA  
 CAACAACAACAATAACAGCAGTGTAACCCACATAACCAAGCTGGTCTAC  
 AATCCATTAAACAGATCTATTCCATCGCCCCCGTACGGGGCTTACAACCAG  
 AACAGAGCTAATGACGTACCATATATGAATACCCAAAAGAAACACCACAG  
 ATTTAGCGCTAACAAATAATTTGAACCAAGCAAAATACAAGCAATATCCCC  
 AGTATACGTCCAATCCAATGGTTACTGCACATCTGAAGCAAACGTACCCCT  
 CAACTCTACTACAATAGCAACCTCAATGCTCACAAACAACAACAACACAG  
 CAACAACAACAACAACAACAACAACAACCAACAACAACAACAACAATCTTT  
 ACAACCAGACGCAGTTCTCCACGAGGTACTTCAACTCGAACTCCTCTCCC  
 TCGTTCACTTCTTCCACTTCTAACTCATCCTCTCCATACAACCAAGCAC  
 CTTCCGAATACATTTTGGCGTCAACTTCGGCAGCTTCCACAAATTTATCGT  
 CGTCATCATCAACAACCTCTATGCACACCAACCCAAACCACTGCAACATCG  
 ACATCCGCGGATTTAATCAATGATTTACCCGTGGGCCCCAAGTCCAGTTT  
 GCTTATCTCGGATCTACATTTCTCCACCAACTGTATCTTTCTTACCAGCAA  
 GCCAAACCCCTGCTCATGTCTCCACCAACAATCTAGCTCTATTTGGCACCAC  
 ATAAACCCACCGCAACAATCACCAATCCCATCGCAAAGGGACGATTTTTTC  
 GACGGCACCAAGTGAACATGTCTTCGTCCGCATCACTCTTGATCAATGATT  
 CTTCTTTTAGGATGGGGCTTAACCAATGAACGTATCTTCATCTCTCAA  
 CCAGCATCATCAAGACCCCTTTGGCATTGTGAATACTGACATGACCGTTTG  
 GAGTTGA

YBL081W, 368 aa (SFQ ID NO 33)  
 MPGQLISIFPLSQNEDEMKYLLFYRSLKLLHQSSMSFQSHNAPSHQSNYH  
 PHYNHMKYNNNTGSYYYNNNNNSSVNPHNQAGLQSIINRSIPSAPYGAYNQ  
 NRANDVPYMNITQKKHHRFSANNNLNQQKYQYPOYTSNPMPTAHLKQTYF  
 QLYYNSNVNNAIUNNNNNNNNNNNNNNGNNNNNLNQTQFSTRYPNNSSE  
 SLTSSTSNSSSPYNQSTFEYILPSTSAASTNLSSSSNNNSMHTNPTTATS  
 TSADLINDLPVGPTSSSLISDLHSPPTVSFLPASQTLLMSSTTSSSIGTN  
 INFPQHSPSPSQREDFETAPVNMSSASLLMNDSSLGWGSENMNVSSSSQ  
 PASSRFFGIWNTDMSVWS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)  
 CTGTGATATTTGGGTTACTTTGTAGTGTATTATTTCCATCAATATTAGCA  
 CTGTCTTCCAAGGTGAACCAATTGAGTGTAAACCATAGAGTAAAAACA  
 AGTGGAAATGGTATCGATTGTATAAAGTACGCAGATTTGCGAAAATACCA  
 GCAACTTTGGCTTATGAATCAAAATACAGCCCTTGTGAGAATACGATTAAAT  
 GTAAATACCGACCAAAGATATGCTATCCATTCGATAAAAACCAACGGATG  
 ACCCGTGAACAATGCTAAATATACCATAAGCAACCACTGCATTTGTTTTAGAA  
 TGGAATATCCTAAGACATCTCAACTGCAAGGTATAGCGGCATAAACCUC  
 AAAAAAGACTATGAAAAAAAATATGTTTGAGAACAGCTTAGTAAATTG  
 TGCTTTGCTTCGAATCCTTACAAGTTAACAAAAATTTATAGCGTTTGCCG  
 GAACATACTTTTGGGAAGGTTAGAACAGATGATCTCATAACTAAGGTTA



56/251

ATGGTTACAACITGGTAGTTCCCTCCCTGGTATTATTTCTTTTCTTCGTAGT  
 TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTTGTGT  
 GCACITTTTTTTTUGAAGATTATTGAAGAGGGATGCGTTTGGTACAATAAA  
 AAACATAGGTTCCCAAACCTATATAAATATATATATGTATATGTATATAT  
 ACTACATATATGCTTTGAGAAATATGTGAATGTTGAGATAATTGTTGGGA  
 TTCCATTGTTGATAAAGGCTATAATATTAGGTATACAGAATATACTAGAA  
 GTTCTCTCTCAAGGATTTACGAATCCATAAAAGGCAATCTCCAAITCTACA  
 CAATTCTATAAATATTATTATCATCATTTTATATGTTTATATTCATTGA

YDR366C, 132 aa (SEQ ID NO 126)

MVTIGSSSLVLFVFPVVFVQITYTALHRFSRLCTFFSKIIEEGCVWYNK  
 KHRFPNLKYIYVYVYILHICFEKYVNVETIVGIPLLIKAILLGIONLLE  
 VLLKELGIHKRESAILHNSINIIIIILYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)

TAGACGGGGCTTCCACGGCTTCCACTCATTTCGTCTCTGGTAATGGCCG  
 TCGCCCTTCTCACTTTGGTTGGGCTTACGCTGACAAGTGTCTGTTGGATT  
 CCGCTGATAAAATATAAAGCTATTCCTCTTGAGCCCTCTATCCCTTTTGGCAC  
 TGTCTGTCATCATTGTTCCTCCTTTTTCGCTAGATAGGTTATATTAAGAT  
 TTGTCTTGAATTTAATATCTCAACTCAAATCCAACTCAACCGCTAATACCT  
 ACCATGTCCCAAGTCTATTTTGATGTGGAAGCTGATGGCCAACCAATTCG  
 CCGTGTCTGTTTTCAAGTTGTACAACGACATAGTCCCAAAGACTGCAGAAA  
 ACTTCAGAGCTCTATGTACCGGTGAAAAGGGATTCCGCTACGCTGGCTCT  
 CCATTTCCACAGAGTTATTCCAGACTTCATGTTGCAAGGTGGTGACTTCAC  
 TGCTGGTAACGGTACCGGCGGTAAGTCTATCTACCGTGGCAAATTCACAG  
 ATGAAAACCTTCAAGAAGCACCACGACAGAACAGGTTTGTGTGTCCATGGCC  
 AACCCCGCTCCAAACACCAACGGCTTCTCAATTCCTTCATCACCAACCTTCC  
 ATGCCCATGGTTGGACGGTAAGCATGTTGTCTTTGGGTGAAGTTGTTGACC  
 GTTAAGACATCGTTAAGAAGGTTGAGTCTTTGGGTCTCTCTCCGCTGCC  
 ACCAAGGCTAGAAATTGTTGTTGCCAACTCCGGTGAATTATAACCGCTCTG  
 CCTGGAACAATAACAGCAAAAATTGAACGAACTATTCTCTCTTAAATTAT  
 ATGTATATGTATAAGGTATGTGTATGTATGACAATCAATTCCTATAACTA  
 A

YDR154C, 116 aa (SEQ ID NO 102)

MKTSRSTTTDQVCCPWPTPVQTFVVLNSSSPFIIAIGWTVSKLSLVKLLT  
 VTTSLRRLSPWVLLFPVPRLELLLPSPVNYNRSANNNNTAKIETNYSLIN  
 MYMYKVCVCMTINSYN

YHR102W, 890 bp, CDS: 501-890 (SEQ ID NO 213)

CGCTCGCTTCCAGAGTTATCATCATATCTTCATCATATTTCTTCCATAC  
 TTAAGGTGGGTAGCGAGGACCCCTCAATTCGCCACCTCTCTGCCAGGGC  
 GTCATCTTTCTCTACAAAAGCCAGGCTGAGTCACTGATTTGCTGACCCCT  
 GGGGGCTGCAATTGTTTCCCTAUGAATTACTTCACTTGTCTCGTGCGCTTTCC  
 TATTGCGCGCATCACTAGGATGGAAAAAAGAAAGAAAAAGAAAGCGT  
 TCAGTATATATAAGAAAGAAAGAAAAAGTCCGAGAGAAAAAGAACACAAA  
 GGTTTTTCTCTGAGGAAACAGTAAAGTTTGATACGGCACATCGTTGACAT  
 CGCTCACTCCANTAGGAAACTGAAATAGACGGCAAAACCAATTAGTTCATT  
 GAAAGAACGTATTGTGAGAAATTATCACTCACCATATCAGAAATTTGACA  
 CACGAATTATATAAACGAAGTTATACAGAAAAAGATTAAAGAAAAAGAAA  
 ATCTCTACATCTMTCCGTACGTTTTCCATTTAGCCCGGTTCTGCCAAAGTGA  
 GACAGGGCCCCAAGACGGTGCATTTCTGGGCTCCTACTTGGAAATGGGGTC  
 TGGTTTTCTGCTGGATTACGCGATATGAAGAGACCGGTGGAAAAAATTTCT  
 GGTGCTCAAAATTTGTCTGCTGCTATCTACTGCGCTGATTTCCGACTCGTTC  
 GTCTTTTGTCACTCAAGCCAGAAACATCTTGTGGCTTCTGTCACTCGT  
 TTCTTTCTCTGACCGCTGGCTATCAATTCGCTAGAATTGCCAACCTACAGG

57/251

ATACGGAATGGCGAUTCCTATATCGCAALGTTGTAGCTATATTTCTCAGCGG  
CGCCGACGAAAGCAAAAAGGAAATTACTACGGGCAGATAA

YHR162W, 129 aa (SEQ ID NO 214)  
MSTSSVRFAFRRFWQSETCPKTVHFWAPTLKNGLVFAGFSDMKRPVEKIS  
GAQNLSLLSTALIWTWSEFVIKPRNILLASVNSFLCLTAGYQLGHIANYR  
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)  
CCTCCACCAAAGCAAAATGAAAACAAAGCCATACTGGGAAAAATCTGAAA  
AAAAAATCTTAGGACTAAAAGAAAAGAAAAATAAAGGTTACCCCTGCAG  
TTTGGATAGTCGGGTAACATTTGGCCCTTTTCCTCCTTGATTGGATATTA  
TTACCCCGATTACCCCTCATCTTGGGAGTGGCCCGCTTTTATTTCTCCCG  
CCAATCCGCTATTAAACCCCTTTAGCTCATTCGGTGGCGGGTCAAGCCAG  
CCGCTCCCTGGTTTGGTCACGCAAAACCGAAAGGCTCAACAAAACCTAAG  
GCCATCATATATATATATCGCGCTGCGTGGCTGTATTCTCCCGGATAATA  
TGGTGGCTTGC AATTGGAGTATTGGAGAAAAATTTCTTTTCCCTTTCATT  
ACGCCCGAATACTTTCATATAAAAAAAGAATACAAATCAGTCTTTAAGA  
CTATACGCATAAGCATTC AAGACACATAGA AACACAAACCTATACTTTTA  
ATGTCAGCATCAGCTTTTAATTTTGCTTTTAGAAGATTTTGGAACTAGTGA  
AACAGGCCCTAAAACAGTACACTTC TGGGCCCAACTTTGAAGTGGGGGC  
TGGTCTTCGCAGGGCTAAATGATATT AAGAGGCCCTGTTGAGAAGGTATCA  
GGAGCACAAAATTTATCTTTATTAGCGAUGGCACTGATTTGGACGGCTTG  
GTCTGTTTGTTCATCAAGCCCAAGAACTATCTGTTAGCTTCCGTCAATTTT  
TCTTGGGTTGCACTGCAGGCTACCATCTAACAAGAAATGCTA ACTTTAGG  
ATACCGAAGCGTGATTCCTTTAAACAGGTTATTCACATACA AATAAAAGG  
GGAGACTCCTGCAGCCGTGCGAGCAAAAGCAAACTGCATCCACATCGATGA  
ACAAAGCTCTCATCCGTACTAATCCCCCAATAACGCACPGA

YGR243W, 146 aa (SEQ ID NO 190)  
MSASAFNFAPRRFWQSETGPKTVHFWAPTLKNGLVFAGLENDIKRPVEKVS  
CAQNLSLLATALIWTWSEFVIKPKNYLLASVNPFLCCTAGYHLTRIANFR  
IRNGDSFKQVIHYIIKGETPAAVAAKQTASTSMNKGVIQTNPPITII

YER056C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)  
AAGTACCNTATCTTATAACTCTAACATTGAAGCACTGAAGCACTCAAGCA  
CTGAAGGACTATAGTCAAGGGCCAATGGGGAAGGTCCCTTCCAGGCCATT  
TGCCCGGATAGTTTGTCTTCTCTTGCTTTTCCGACGGCCCGATTGCATGT  
CGCGGGGCGAGCACTGGATAAAAAACGTGGGGGGAGTGATTAAATTTATA  
CGCTTACTGTGTCAACACGGAAACCTTATAGTTATCAATTACTAACATCGC  
AACAAGCTGCTTTTTTACTGCTTTT TAGCCACACCAATACCCCTTTAATT  
AACTAACTAATGCATAAAATAGTTATTGCTTCTTGAGTTGCAGCTTCTTCC  
TGGACGTACTGTTATATATATGGCATGTCTTCCGATGTCCGTCAAATTTAGC  
GTGTCTTCGAAACTTAGGCTGTCTGTCTTGTCTTCTGTCTTCTGATAAAA  
TAATATAATTGGAATAAGAAAAAATAAGGAACAAGAAAGTGTGTGAGA  
ATGACTTTGAGTAATTTGCGACTCTTTTGATAACTTATTCCAGGACCCCTCC  
AGAGGAACAGAGAAAGTAGTAATTTGTTGAGGCGGTGAGAACCTTGATGA  
ATAGAAACGATATGGGATATCCTCCCGCCGCTGCAATGGTACGTATTGC  
TTAAAAAAAATCAAGTCTTTCAATGCCAAACAGTGC AAAATAAACAAGAA  
AAGATCTGTCATGTTGCCAGCAGTAAAGAAGAAAAATTTGACTTTACCG  
AGCAAGAAGTTTAATCTTGAATTTAATTTATGGAAATTCATCAAGTTT  
ATCAATTGTAGTAGTAAAAACAATTAACATAAAAAATAAAGCATCTGAC  
AAGCTTCAACCAACACTGTAAAAAATGAAAATGTTTTACCGTTACAAAAAC  
ACAGAGAAAGTGGACAATGATCAAAGATTGGAGAACCTTTTTTGCACAAGC  
TGGTTTAAAGCCACGCAAAAGGAGAGATATAATGGGCAAGCCACGAGAGAG  
GCATATCAAAATTTAACGATAACCTTGAACAGTGTATTATAACTGATGAGC

58/251

ATTTCATACAAAGGCTTCCTTCTACACGGTTGAATTCGACTGATCAACAG  
CGCCCTTGTTCAAAGTCTGAACTAGATCCCTGTATTGGCAAACGACGCAAG  
TAACCGAACTTTCTATCATTATAACAGCGTTTACCTCGCCACTGACGCAA  
TTATTACGACTGCCGCTGCCACTGCCATTATCAGTAGTAATAGTCCAGAC  
TATCAGCGTGGGCAAGATGTTCCGCGATGTTCCAAGAAATGTTTCTTACA  
GCCAGGAGAAACAGATTTTCAGTAGTGTGCTTCCCTTGACTCCSATCTCA  
AGTTATCCACATAGTCATCATTCCCCCGTAAACCTTCGTCAACTTCA  
AGTCATTGACCTTUATTTTTCGAGTCGGAAACTGACACTGATACTGATAC  
TGACGCTGAAACAGAAAATGACATTGACGCTTACATAGACACCAGTATAC  
CCAACCTGCTCTTATAA

YBR050C, 338 aa (SEQ ID NO 14)

MTLSNCDSLINLFDQDPPEEESSKPFVEAVRTLMMRNDMGYPAAANGTYC  
\_KKIKSLNAKQWKINKKRMCLPAVKKKNFDFHEQRLILNLNLWKFIKF  
INCSKKNYKKNKHVRSSNNTVKNENVLPLOKHKKVNDQRLFNLFWR  
WFKARKRRDIMGKPRERHIFNDNVEQCIITDEHFIQRLPSTRINSTDH  
RPSKSELDPICIGNAASERSFYDYSVYVASDAIITTAATAIISNSGD  
YQRGHVDRDVPFNVLLQAGETDFSSVLRVDSDLKLSNISHHSFVKPSST  
SHSTFIPESETDTDTCDAETENDIDAYIDTSIPNLLL

YEL071w, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TACCTTGACCTGCTCACATTAATCAGCTTCCAACGTTACTTCCCTTTTCGC  
AACAATCTACCCAAAATCTCTCCAGCATCTTCATAATTACACTATCGTT  
GTCCCGACTTGGCATTGTGTTAAATTTCTAAGATGCTTCCCTATAGGAACA  
TAATTTGTCAAGAAAGUACAACAAATTTGTCTGCAATGTCACACAGGAGTGGC  
GCATTTTATGTTTTTTTCATTTTTTTTTTTTTTGTGCGTGATCATTAAGCGG  
GATATTGTCCACAGTCATCTAAAAGAATGACCATTTCGACGACTTAGTTTC  
GGAAAATATTTCCAGCGGATGACACCACTTGGCCACAGTTGCTGACCGCCA  
AATCTAAGTCAACGCGCGGAACTGAAAGGTTGTGAGTATATAAGTGATCA  
CTCGCTTATATAAAGTACGAGGACAGGACAGGCTGCCAAAATGCTCCTCAA  
TATTTTATTTCATTTGAGATTCAAGGCTTAAAGACAGCATATATAAGAATT  
ATGACGGCCGCACATCCTGTTGCTCAGTTAACTGCCGAGGACATACCCATA  
AGTCAAGAGAAAACCCAAATTTCAAAGTTCTCGACTCGGAGGATTTGGCGT  
ACTTTTCGTTCCATTTTCTCAAATGATGAAATCTTAACTCTCAAGCTCCA  
GAAGAGCTTGTCTCGTTTAACCCAGGACTGGATGAAAAAATATAGAGGCCA  
GTCCAATTTAATTCCTTTGCCAACTCCACTGATAAAGTGTCCAAGATTA  
TGAAATACTGTAAAGATAAAAGTTGGCAGTAGTACCACAAGGTGGTAAC  
ACCGACTTGGTCCGAGCCTCTGTTCCCGTATTTGATGAGATTGTTCTTTC  
TCTAAGAAATATGAACAAAGTCAGAGATTTTGATCCAGTTAGCGGGACTT  
TCAAGTGTGACCCGGGTCTCGTTATGCTCATGCGCATCAATTTTACAC  
GACCATGACCATATCTTCCCATTTGGATCTGCCTTCTAGAAACAACGTCA  
AGTGGCGGGTGACTTTCACCAAATGCAGGTGGTTTGAATTTTTAAGAT  
ATGGGTCTCTACACCGTAATGTTTTGGGTTTGGAAAGTGGTGCTACCCAAC  
GGTGAGATTTATCAGCAATATCAATGCCCTAAGGAAGGACAATACTGGTTA  
TGACTTGAAACAATTAATCATCGGTGCAGAGGGTACTATCGGTGTCGTTA  
CTGGTGTATUCATAGTTGCAGCAGCAAAGCCAAAAGCCTTGAATGCCGTA  
TTTTTTGGTATTGAGAAATTCGATACCGTTTCAGAAATTATTTGTCAAGGC  
TAAAGTGAATTATCTGAGATTTTATCTGCTTTTGAATTCATGGACCGTG  
GCTTCUATTGAATGTACGATAGAATACTTGAAGGAUTTGUUTTTCCCTCTG  
GAGAACCAACACAACCTTTATGTTCTTATTGAAACGTCAGGGTCCATPA  
GAGACACGACGATGAGAACTGACTGCTTTTCTCAAAGATACCAAGATT  
CTAAATTAATTTCCGAGGGGTATGATGGCTAAGGACAAAGCCGATTTTGAT  
AGACTTTCGGACCTGGAGAAAATCTGTTTCCAACAGCTTGAATTCCTACGG  
TGCTATCTACAAGTATGACATGTCACCTCAATTGAAAGACTTATATTTCCG  
TATCTTGGGCTGTGACGGAGAGATTAACCGCAGCCGGTTTGATTGGTGAT  
GCACCAAAACACAGTTGTAAATCATGTGGTTATGGTCATGTCGGTGACGG

59/251

AAACATCCATTTAAATPATCCCGCTAAGAGAATTTACAAAACAGATTGAGG  
 ACTTACTAGAACCATTTGTATGAAATATATTGCATCAAAGAAAGGTTCC  
 ATCAGTGCCTGAGCATGGGATCGGTTCCATAAGAAAGCTAAGTTACACTA  
 CACCAGAAGTGATATTGAAATTAGATTATGAAGGATATCAAAAATCACT  
 ACGATCCAAATGGATCTTAAACCCATACAAGTACATTGGA

YEL071W, 496 aa (SEQ ID NO 144)

NTAAIIFVAQLTAEAYPKVKRNPFPKVLDSSEDLAYFRSILSNDEILNSQAP  
 EELASFNQDWYKKYRCQSNLILLPNSTDVSKIMKYCNDEKILAVVPQGGN  
 TDLVGASVVFDEIVLSLRNMNKVRDFDFVSGTFKCDAGVWVRDAHQFTLH  
 EHDHIFPLDLPSRMNCQVGGVVSTNAAGLNFRLRYGSLHGNVVLGLEVVLPN  
 GEIISNINLALRKDNTGYDLKQLFIGAEGTIGVVVTGVSIVAAAKPKALNAV  
 PFGIENFDIVQKLFVKAKSELSEILSAFEFMDRGSIECTIEYLKDLPPFL  
 ENQHNFPVLIETSCSNKRHDDEKLTAFLEKDTTDESKLISEGMMAKUKADFD  
 RLWYWRKSVPTACNSYGGMYKYDMSLQLKDLYSVSAAVTERLNAAGLICD  
 APKPVVKSCGYGHVGDGNIHLNIAVREPTKQIEDLLEPPVYVEYIASKKGS  
 ISAEHGIGFPHKKGLHYTRSDIEIRFMKDIKNHYDPNGILNPYKYI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGTGAAATCAACGGCCCCCTCAGAGAAACCGGCAGGAATTTT  
 TCTGGTGTGTTTATTTTTTTTCTTGTACTTATCTCACTTTTCTTTT  
 CTAAGTATTTTTTTTGCATTTTTTTTGTGTACACTTTCCACAACATATAG  
 GATGGTTTAGTCATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTT  
 GTTCTTCATCGACTTCTCTCTGCTAGACTCTCTTTTTTAAATTTTTTCA  
 TAGAATAAAAAACCAAGCATAACAAACATCTTCTTTTCGTTTCGCTTCAAAA  
 TAACTACAAATTAATAATGCAATCTCTACCGTCGCTTCTATCGCTGCTA  
 TTGCCGCTGTGTGCTCCGCGCTTCTAACATTACCACTGCTACTGTACA  
 GATGAATCTACCACTTTTCTCACTATUACTTCTTGTGAGGACCAAGTTTG  
 TTCTGAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCACCGTAA  
 ATGACGTTATUACTTAATACACCACCTGGTGTCCATTTGCCAACCACCTGAA  
 GCACCAAGGAATAACCACTTCTCCAGCTCCAACTGAAAAGCCCAACCGAAAA  
 GCCAACTCAAAAAGCCAAACCAACCAAGGTTCTAGCACTCAAACTGTTACCT  
 CCTAGACTGCTGCCGCTTTAAGGCTTTGCCAGCTGCCGCTGCTTTTSTTG  
 GCTGGTGCCTGCCGCTTTATTGTTGTAAATTTACTCAACCTTTCTTTAATA  
 TATTTTTTAAAAAATGGTTAAGTACTTTTCCGTCAATACAGCTTCCACAA  
 AATCGTTTTATTTCAAATTAATACATATCTCGGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPPGVHCQPLKHQRIPLIQLQIKSQPKSOLKSQPNKVLALKLLP  
 PTLVPLIRLCQLPVLCLWLPLVCCNTLNIFFNIPLEKMLSTPFSIQLEQ  
 NRFISINKLPW

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAGAAATGATCAGGGAGCGTTTCTTGCAACAGCAGCAACACTACA  
 GGCAGCAACAGCAGGAAGGATGGCAATTACCTAAAGCCCTCTCAGGACAAC  
 GTGGATAGCAAGGACTAACCCAGACAGATTGAGGTCTTTTCATCCATTACC  
 ACCAGTAATATATTTATACCGAATAATATAGTTTATATAATATCCATAAT  
 CATAATCATAATCATAATCATAATCATAATCGTGATATTGTACCAGCCCC  
 GCTTCTCCCCCTTTTGAAGTACCATTATTATCGGACCCCTTTTACCTTTGA  
 ATGGCTCAGTAAGGACCTTTGCGCAGCCGTAAGGGGGTCGGGAATACATT  
 TCCGGGGTTGATCCTCGAGGAAAAGTGCTATCTATATAAGGAGAGCCCT  
 TCTAGATCCAAATATCAGGGGTAACTCTTCACAACTGGCCAGGAACATAAT  
 TCCAACTTAAAAAGAAAAAATAATTTATTAGAAACCAATTACCAACACCAAG  
 ATGCTAAGATCAAATTTATGCAGAGGAATCTCGAATUCCTTCGAAGACTGAU  
 CACTACACCAAGGACATACACATCTGCGGCGACAGCTGCGGCTCCGAATC  
 GGGGACATATCATCAAAACATACCTTCATAGACATTCTACGACAATTACC

60/251

TTCTCCATGGAGGAGTCCAGCAAGCCGGTTTCCGTTTGCTTTAACAAACGT  
 TTTTCTTAGAGATGCCTCCCATAGTGCCAAGCTGGTGACCACGGGAGAAC  
 TGTATCATAAACAGAAATTGACCGCTCCTUAGGACATTCAAAATTTCTGAG  
 GACGGAAAATCTCTAGTGGTGAAATGGAAAGATCCCGGTCTTCACCACTT  
 CCGTTTACAATTCCTTATCGACTATAAAGGTTCCAGTTTGTGTTCCGCCAG  
 CAACAAGAAAACAAGAATCCAGATATAGACCCCACTTATCGAATAAGCGC  
 ATCCTGAAAGATAACGTCARGGACTTACTTTCTGTGAGCTACAACGAGTT  
 TATTGATCCTAAGGATGACTCCAAGCTTTTCCAAACGCCTGGTCAACCTAC  
 AAAAGTTTGGTATCGCTTTTCATTTCCGGTACTCCTTCATCCCTCCTCTGAA  
 GGCCTTACCATACAAAAGATCTGTGAAAGGATCGGACCCATAAGATCGAC  
 TGTACATGGTGAAGGTACATTGACGTGAATGCAATCCCAAGCGACAAGTG  
 TTAATGCCCATTTATGCCAATAAAGACTTGCCGCTACATACGGATTTACCA  
 TTTTATAGAAAATGTGCCAGGTTTCCAGATTCTACAATCTCTACCTCCTAC  
 AGAAGGGGAAGATCCCAATACTAGACCCATGAATTACTTCGTGGACGCAT  
 TTTTACTCTACCCCTAATGTGTAGAGAAATCGGATTTTGAAGGCTTATGAGGCT  
 TTACAAATTTGTTCTGTAAATATATATATGAAAACGGCGATTAAGAGGTA  
 CTACCAATCCAAACCTTTAATCGAATCATCAGACATTATCGAGGACAATA  
 CTCTTCTGGGTAATTATGAGGCCTTGATTAAATGCATTAATACTACTCTCCA  
 CCATACCAAGCAACCTTTCACTTTCCGGAATTTATGATAAGCCCTCAGATCT  
 AAATAATAATCTGGACCTTGAAATTAATTAACACCCCAAGCAAACTAACAG  
 AGAGATTTTTGTTTAAAGTCTTTTCAATTAGUGGGTTTGAATTTGTTCCGAGGT  
 CATATCAATGACTTCAACAATCAATTTACATTGCAGTTGCCCGAAAACCTG  
 TTGTGTTATCTTTAACAACAGGAGAATTTCCATCCTAACTCTTTAACAA  
 GCTCAAAACCAGCAATGGTTAAAGGGTTGCTATTTGATTCTGATACTTTC  
 AAGACTAAATTAAGTTCTTGAAGAGAAAGTTTCCTCATGACAAATAA

YHL021C, 465 aa (SEQ ID NO 194)

MLRSNLCRGRILARLTTPRTYTSAAATAAANRGHIIKTYFNRDSTTIT  
 FSMRFSKPVSVCFNNVFLRDASHSAKLVTTGELYHNEKLTAPQDIQISE  
 DGKSLVVKWKDGGHQQFPLQKFLIDYKGSFVSPATRKQESRYRPQLWNKR  
 ILKDNVKKLLLSVSYNEFLIDPKDDSKLFQTLVNLQKFGIAFISGTPSSSE  
 GLTIQKICERIGPIRSTVHGEGTFDVNASQATSVNAHYANKDLPLHTDLF  
 FLENVPGFQILQSLPATEGEDPNTRPMNYFVDAFYATRNVRRESDFEAYEA  
 LQJVTVNYTYRNQOKRVYQSKPLTFHHDTNEDNTLIGNYEALIKCINYSF  
 PYQAPFTFGIYDKPSDLNNNLDLNLITTFAKLTERFLPKSFIRGLNLFES  
 HINDFMNQFRLQLPENCCVIFNNRRILHANSLTSSNQQLKGCYFDSDTF  
 KSKLKLFLSEKFPMDK

YK1054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

CCTGCTCTAGACGAAGCTACCGAAGGCGCCGTTTCAAAATCGCGGCAG  
 ACTAAAAGAAAGTTGACAAATGAAGTATATATTTTAGCACAGAATGTGCAT  
 TATTCACACATGTAAATACTAATACTGCANTATCCACTTATAATATGTAT  
 AGTCATCCGTATATTAATAGATCTGTTTCAATTCTTTACCTTTTATAGGAT  
 ATCCGTCACCCGTCATTCCGTCGGAGGTGAGCACTCGCCCAAAATAAATAA  
 CGGGAAATGGTGGCAAAAAGTAGTGGCGGGAAAAGGAAAAATTTTCGTTT  
 TCTCCCATATAAACGTTTCATTCCCTTTCCCTAAGTCITTTACAGTAATTT  
 CAGAACATTCGTATTTTATATTTGATCTTTTGAAGCTACAAAGAAAACCT  
 CTTACCAATTACCCCAAAAATCACCATCATAAAGTACTTACATATTTA  
 TTTTGTGTTGGTGGTCTCTCAATATAATCTACATCATCATATATATATA  
 ATGTCTACACAATTTAGGAAGTCTAATCATAATAGTCATAGTAGTAAAAA  
 ACTAAATCCTGCGCTAAAGTCCAAAATAGATACGCTTACAGAATTGTTCC  
 CTGACTGACGAGTGATGATTTAATTGAATATAGTTCAAGAATATGATGAT  
 TTGGAAACTATAAATTCATAAAATTACTTCCGCGCGCAGTGACAAGATGGGA  
 TGAAGTAAAGAAAACCTGCTAACGAAGGAAAATATCAAAAAAAGGAGCAAC  
 AACACTCATATGTCCCTCAACAACAATTTGCCAAAATCCAGAAGATGATATT  
 ACATATAAGAGTTCTAATAATAGCAATCTTTTACTTCTACAAAGCATAA

61/251

CAGTAAGTAACCAATTATACCTCAAGCCAGAAATAAGAAAGGTACAAACAC  
 CACGAGCTCCTACAAACCGGAACCATGTTAATCTCGACAAAGGCAACAC  
 GTACCCTCCAAAGCCTGTTTCAACACCTACATCGTGGGCAGCAGCTGTTTC  
 TGTAGATACTAAACATGACGTTCTCAAGATTCAAAATGATAACAATAATG  
 AAGAAATTAGAAGCACAAGGGCAACAAGCGCAGGAGAAAAATCAAGAAAAA  
 GAGCAAGAAGAGCAACAACAGCAGGAAGGGCATAATACAAAGAAGAACA  
 CAAACAAATAGAGCAACCTTCTTTATCTTCAAAGAAAACAACTTCTAGGA  
 CATCTGCTTCCACAACCAAGAAAATGTCTGTTGGGCTGCAATTGCTACACCA  
 AAGCCAAAGGCTGTTAAAAAGACCGAGTCTCTCTTTGAAAAAGTTGCTGA  
 ATTGAAGAAAGAAATRAAGCATATTAAGAAGGATGACCAAAAGTCTGAAG  
 CTAGTGAACAAAAAATTAATGAACAAGAAACATCTGCACAAAGAACAGAG  
 GAGGAGACTGCTGAACCTTCTGAAGAAAATGAAGACAGAGTCCCTGAAGT  
 GGACGGAGAGAATCCAAAGAAGAAGCTGAAAAAAGGAACAACTAAAAG  
 AAGACAACACACACACCGCAACAGCTCGAACAAAGAACAAATATGTTGCT  
 GCTCCAGAAGAAGAAGTTACAGTTGTTGAAGAAAAGGTTGAAATTAAGTGC  
 TGTATTATTCAGAGCTCCAGAAGATCAAGCTAATACTGTACCTCAACCCAC  
 AACAAANTCCCAACAACCCACAGCAACCCACAGCAACCCACAGCAACCCACAG  
 CAACCCACAGCAACCCACAGCAACAACAACCAACCCACAGCAACCCACAAACCC  
 ACAACAACAACCTACAACAGCAACAGCAACAGCAACAACAACCAAGTACAAG  
 CTCAAGCTCAAGCCCAAGAAGAACAATTATCTCAAAACTACTATACTCAA  
 CAACAGCAGCAACAATACGCTCAACAACAGCATCAGTTACAGCAACAGTA  
 TTTGTCCCAACAACAACAATATGCTCAGCAACAGCAACAGCATCCACAAC  
 CTCAATCACAACAACCTCAATCAGCAAAAGTCCACAAGTCAAAAACAA  
 GGGAAACAAGTGGGCTGCCCAACAGTACTACATGTATCAAAACCAATTTCC  
 TGGATATTTCTTATCCAGGTACGTTTGATTACAAAGGATACGCTTACGGTC  
 AACAAATATCAGCAACTTGCTCAAAACAACGCTCAAACTAGTGCTAATGCT  
 AACCAATATATTTTCCAACAAGCTTATGGTCAGCAGGCGCAACACTGC  
 TGCTGCTAATTTGACTAGTGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTA  
 CAGCTCAGGCCCAACCTCAACAACAACAGCCATACGGTGGCTCATTTATG  
 CCATACTACGCCCACTTTTACCAACAGTCATTCCCATATGGTCAACCTCA  
 ATACGGTGTAGCTGGTCAATATCCATACCACTTACCAAGAACAAATTACA  
 ACTATTACCAAACTCAAAACGGTCAGGAACAGCAAACTCCAAATCAAGGT  
 GTTCCCCAGCATTCTGAAGACTCTCAACAGAAGCAATCACAACAGCAACA  
 GCAACAGCAACCTCAAGGTCAACCCCAACCTGAAGTTCAAATGCAAAATG  
 GCCAACCTGTTAACCCACAACAACAATCCAGTTCCAACAATACTATCAA  
 TTCCAAACAACAACAGCAACAAGCTGCTGCCGCTGCCGCTGCTGCTGCCCA  
 ACAAGGTGTACCATATGGCTACAACGGTTATGATTACAATTCTAAAAATT  
 CAAGAGGTTTCTACTAA

YKL054C, 738 aa (SEQ ID NO 238)

MSTQPRKSNHNSHSSKKLNPAKSKLDTL/TELEPPIWTSDDLIDIVQEYDD  
 LETIIDKITS GAVTRWDEVKKPAKKEKYEKKEQQHSYVPQQHLPNPEDDI  
 TYKSSNNNSNFTSTKHSNNYTQARNKKKVQTPRAHTTGKRVNLDKGRH  
 VPSKPVSNITSRAAAVSVDTKHQVPQDSNDNMNEELEAQGGCAQEKNOEK  
 EQBEEQQQZGCHNNKEEHKQIEQPSLSKKTTSTRTSASQPKKMSWAAIATP  
 KPKAVKKTESPLENVAELEKKEISDIKKDDQKSEASEEKVNEQETS AQEQE  
 EETAEPSEBENEORVPEVDGEEVQEEAEKKEQVKEEEQTAELEEQEQDNVA  
 APREEVTVVEEKVEISAVISEPFEDQANTVPQPQQQSQQPQQPQQPQQ  
 QPQQPQQQQQPQQPQQPQQQLQQQQQQQQQPQVQAQAQAQEEQLSQNYTQ  
 QQQQQYAQQCHQLQQQYLSQQQQYAQQQQQHPQFQSQSQSQSQSQSQKQ  
 GNNVAAQQYYMYQNQFPQSYSGMFDSGGYAYGQQYQQLAQNNAQTSQNA  
 NQYKFGQQCYGQACANTAAANITSAAAAAAASPATAHAQPCQQQPYGCSFM  
 PYYAHFYQCSFPYGQFPQYGVAGQYFYOLFKNYNYQYQYNGQEQQSPNCG  
 VAQHSSEDSQQKQSQQQQQQQPQQQPOPEVQMQNQGPVNPQQQMVFQCYQC  
 FQQQQQAAAAAAAQQGVFYGYNGYDYKSKNSRCFY

62/251

YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)  
ACAAAACAGACTTAGTTACTTTATCGGTATACAAACAAAGCTCGAATGAAA  
GACGGTTGGCACAAGAGAATTAAACAAAATAAACGGAGGAAGAATAAAGTT  
ACACCTTATTTCTCAAGAACTCTTTTAAATCCGCTCAAGAAAGTTTAAGGG  
TATTGCATARAAGAACAGAAACGCCGCTGGAAAAGGCTCTTTGTGCTACTT  
CATATAAATACAGGCAACTTTCTCCACATATTAAAAGGTATTTCCATCA  
TTCTTGCCAAAAGCAAAACAATGTTGGTCCGGATCCAGATTGCACTTGC  
GCAACCTTCGTTTCAAGTCAATGAAACCATTCGGAGTTTTTCAGTTTAAG  
GTTTCGCAAAGATACCAACTGGTTTGTAAAGCAGCTGAAACGGTTCCGATT  
GAAATTACAGCATTCCAGGATGTATAAAGCGATGTGAGAATGCAAGGAAAA  
AAATTTATTTTAAGTGCAAACACTAGATCATCCAAAACCCAGCATGAAGA  
ATGAAATTAACAAAAGAAAAAAAACGACTGCTIAGTAGGAGTGTCTTA  
TATCCCTCCTTTAAATTTTTTTACACTTACTTTCTTTTTTTTATTTGAGAA  
TAGAAAAGCTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTAAGG  
TTTTATTAAGTTTTCATAACGTATGCTATCCATCTCTTTTCCCTTTTTTTTG  
TTTTGTTATTCCTTTTTTTTACTCAGTTAGATTTCATACTACTATATTTAC  
ATATTCTTCGAAGCTTTTATGAGTTAAATATTTTCTTGCTTTATGGGGCA  
GAAAATAGTCGACGTCAGTCACCTCCAGGTTAFTATGTAATTCGGCTAA

YLR311C, 115 aa (SEQ ID NO 284)  
MKLTKEKKNDCLVGVSYIPLNFFTHTELEFIJRIEKVHLSLSLSLSLSIR  
FYYFHNVCYPSLFLFFCFVIFPFYSVRFILLYLHILRSFYELNILLLYGA  
ENSRRRQSPPGYYVLR

YMR107W, 848 bp, CDS: 501-848 (SEQ ID NO 309)  
AGAGCAGAAATGATGAAGGGTGTTAGCGCCGTCCACTGATGTGCCTGGTA  
GFCATGATTTAGGTATACTAACACATCATGAGGACGGCGGCTCACCCC  
AAGCGCAAAAGAGTGACTTCCTGCGCTTTGCCAAAACCCCATACATCGCC  
ATCTGGCTTCTGGCAGGGCGGTTGATGGACATCAGCGGCCCTCCCTTAAAT  
GCTAAAGCCTCCACAAGGCACAATTAAGCAATAATTCGGGAAAGTACACC  
AGTCAGTTTGCGCTTTTATGACTGGGTCTTAAGGTACTAGATGTGAAGTA  
GTGGTGACAGAATCAGCGAGATAACAGCGACCCAGGGTGGGGTAATGATGT  
GCCATAACAATCTTGCTTGGCTAATCACCCCCATATCTTGTAGTGAGTAT  
ATAAATAGGAGCCTCCCTTCCTATTGCAACTCTATAAAATTTTTTTTGT  
AGCCACTTCTGTAAACAGATAAATAAAACCAACTAATCGAGATATCAAAT  
ATGGGTAGTTTTTTGGGACGCATTTCGCAGTATACGACAAGAAAAAGCACGC  
AGATCCAAGTGTATATGGAGGAACCCATAACAACACAGGAGACAGTAAAA  
CGCAGGTTATGTTTTCGAAAGAGTACCGTCAACCTAGGACACATCAGCAA  
GAGAAGTTGCAGAGCATGGAAGATCTTCCATAGGATCACAGGACACTTC  
CGATCTTGAGGACGTTAAGGAAGGGAGATTACCCCGCAGAAGTAGAAATAC  
CAAAGAATGTTGACATTTCTAACATGTCCGAAGGTGAGTTTTTAAGACTTT  
TACGAAAGTTTGAGGAGGGGGGAACCCGACAATAAAGTAAATAGATAA

YMR107W, 115 aa (SEQ ID NO 310)  
MGSFWDFAFVYDKKKHADPSVYGGNHNNNTGDSKTQVMFSKEYRQPRTHQQ  
ENLQSMRRSSICQDSSDVEDVKECRLEAEVEIPKNVDISNMSQGEPLRL  
YESLRRGEPDNKVMNR

YKL066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)  
GAAAAACATCTCATAAATCATCCCTGGAAAAATGCTAGTCAAPCAGAAA  
GAACTTTTATTGCGGTAAAACAGATGGTGTCCAGAGGGGCTTACTATCT  
CAAAATTCATCTCGTTTTTGAAAAAAAGGTACAAACTAGTTTCTATTAA  
ATTAAGTTAAGCGGATGATAAATTAATAAGCAACATTACGCAGAGCATG  
TTGGTAAGACCATTTTTTCCCAAAGATGGTATCCCTTATGAAGTCTGGTCCC  
ATTTTGGCCACGGTCTGGGAGGGAAAAGATGTGGTTAGACAAGGAAGAAC  
TATCTCTGGTGCTACTAATCCTTTGGGCAGTGCACCAGGTACCATTAGAG

63/251

GTCATTTCGGTATTGACCTAGGCAGAAACGTCCTGTCACGGCAGTGATTCT  
 GTTGATAGCGCTGAACCTGAAATCAATTTGGTGGTTTAAGAACGAAGACTT  
 AGTTGATTGGGAATCTAATCAAGCTAAGTCGATTTATGAATGAATAACTT  
 ATGGCATGGGAGGGTACATATGAGCGCCCTTTTTTTCTTCGCTTTGGCCAG  
 CTCATATCATGTTCCCTCACTAGCTAATAATATAATGAATTTTTTAGAAG  
 GAGCACGATTATATAAAAAAATACCACTTATGTTGCTACCCCTTATATAC  
 GAATTTATAATACCTAATGACGCTTCAATGACGCCCTGATGTCAAAATGCTT  
 TTGGCTCCGAGTGAAATGCCACACTCCCTTCTCTTTCCGAACTTTTATA  
 GTATCATCGAAAAATACAAGTTGGCAAGGTCATTTACAATCCGGGAACG  
 TACGATGTTTCATACGGTTTCAGCGAATAGTCCTGTAATATCCGGGAAGCAT  
 GCCTACCGGCATTATTTACAGGTAGTTCATCGCCCTTGGACTATGTAGGGG  
 TACAAGTAATAGGCAACTTGAATGGATCTCCCTATTGAATGA

YKL056W, 147 aa (SEQ ID NO 244)

MAWEGTYERLFFLAIGSSYHVPISLANNIMNFLEGARLYKKNITTYVATLIY  
 EFIIILNDASMTDPVKCFWLPVKLPHFLLLSELYSIIERYKLAQVYVNRGT  
 YDVHTVSANSLVISGSMPTGIIIGSSSPLDYGVQVNRQLEMDLPIE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)

GAGGCGACACCTGCTAATGTTTACAATTTTCCCGATTGGGGTGCTAGAGG  
 CATACAGTGGGCTACATGGCACAGCACGGCAGTGCAGAGTGAGAAAATAT  
 GACTTCACGCTCGAGGCGAGGCCACGCTTTCGAAGCTTCGAATGCCACTA  
 CCTAGACCATTTGCTGTTTGTACCTTCACGGTCCCATTTAGAGACATTTTA  
 CTTAATGCAAGATTGCCATATCCGTTGTCATGGTACCAACAGCGTAATA  
 ATTTCTAGAAATCATGATACACGTATGACATCTGGGTAACTAATCCATC  
 TGGGTAACCGATTTTTCTCTCCCTTTGCTTTCTCTTTACCACTCAGCTGA  
 CTTTATATTTTTTTTTTATATTTTTTCATTTTGACAAAATTATATAGTTAGG  
 AAGTAATCAATAGGACTGGGACAGAAACAGATAAGGGGCTCTTTTTCCTTG  
 GGGTGGGCTGCTTTTATTCAATTAATTTAAGACTCAAGTGTGCTGGGTGAA  
 ATGCTCTCATACTATGAACACAACTACTGCGTTCCAAACAAAACAAATGCCAA  
 TTCCGGTAGCAATGCCGCCACTACATACAACAGCGACGCCAATAATGATA  
 CGATCATGANTAAAAGAAAAAATCACCATTTCCAGTTTGATACACACACT  
 TTCTACCAAGATCGAAGAGAACAAAACGAGATTCCTGTAAGTACAAAGTT  
 TTCGGTCCGTTCCGGGTGTGCTAATCTTAATAACAACACACACACATCA  
 TCATCAACAACAACAACAACAACAATAATAATAATAAACCATAATCAT  
 AATAACAGCAATAATACTGCAACCTACAATAATATTCATTATAAAAAAA  
 TATCGAAATATGTCCCTGAAACCGGTTAGTATGCAACACACTATGAACA  
 GCCGCTTACTGAACGAATCTGAATCTTATCTGAAACAGAAGAGTACATG  
 ATTCTATGCTTATCTCGGTAACTAATCGGCACATAACAGGCACGAGTCC  
 TACTGGAAGTGCCTAGTATTATACAACACCGATATCATCTTCTACCATCCC  
 AAAGTATAATTCATCACAAACCACCGGTACTGCCATGCCCGCGTTGACT  
 AACAACAATATCGCTACGACTACATGGATATAGATTAA

YML053C, 212 aa (SEQ ID NO 296)

MLSYYEHNTAFQTNNCNSSGNAATTYNEDANNDTIMNKRKNDIIEFDTHIT  
 FYQRSKRTRKDSVSTKFSVSGCANLNNNNNNNIIINNNNNNNNNNNNNH  
 NNSNTATYNNIIHYKKNIEICPLKPVSMENITMNSLLNESEFYSETPLEYM  
 IHGYFGNTNRDITGTSPTGSASIIIOHYHLLFSOSIIASCAPGTAMAALT  
 NNNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)

GGTGACGCTGTTTGGGCTACTTCTGGTGGCCTATCTTTGCAACCAAAACGA  
 AATTTGGTGAATTTGTTCAAGGCTTCGACAAATACAGCTGGTCTTCGAAAGCA  
 ATGGTTTGCATATTTCAAGGCCAAAAGTTCAATGTTGTTGAGAGCTGACGAT  
 AGAAGTATCTACGGTAGACATGATGCTGAGGGTGTGTTTCTGTAGAAGC  
 TAAGCAAAACCGTTATTATTGCTCATTTATCCACCAACCGTACAAAGCCGGTG



64/251

AGCCACCAAGATTGTGAGCAATTGGCTGACTACTTGATTGGTGTCAA  
TACTAATTTATGCAGGTAAAGTTTCTTGCCCTTATACACCACCTATTCTG  
GCACTGCGGGGATTTGCGCTTCTATTTTACAAATATTTTATTGATTGACG  
CTAATTATCACTGTAAAAGGCGCACATTTTATATGTAGTCACATCCGGTA  
TTTAACATATTTACGAAACAGTCTTAAGAATATCGACATTTGATATACCT  
ATGTTTAAATTTATCTACATATTACAAATCATACGAGAAACACGCAAAAACA  
ATTACTTGAATACTTCGAAAGGAGACCAATTTGGATGTACAACCCCTTTT  
TCGCCCCTTTTCCCTTCGATATGTTATTTGATAGCTTCAAAGTCCTCAGTAGA  
CAAAGTAAATATTTTCCCTGTTCCGTTTTCGATTGATCGGGATTACAGATT  
TTCCCAAGACAAACATAACCTCTTTGGACGTGCCAGCTAATAACAACGTGT  
CCGGTTCGAACGTTATTTTCTTCGCAATTTCAAGGATAACCGGTTCCTT  
CAATAG

YORL21C, 101 aa (SEQ ID NO 356)

MFNLSTYYNHTENTQKQLLEYFERRPIWMYNPFFALFLRYVIDSFKVLRS  
QSKYFPVRPDSIGIHRPWQDNCTSLDVPANNVNSQLNVTFLRNFKDNRFL  
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTTCATCATTTTCTCTCAATTGTTCTCCATTTGGGTTACCTTTT  
TGCCAGTTGGTCTGACTTGAGGTTTTTCCAGAACTTGCAACCTTGAATT  
GTCCCTCTCTTSCCAACAACTAATTCTCAAGGTGGTCAGGAAATATTGGTC  
GGCGATGCATCTGATACTTTTCAATTGATTACTTCTTTCTGATCTAAT  
TAAGCCGATTTTGAGGCCGATTTTCAATTTTATTAATGTAGTCTGTG  
TAAATTTAAAGTCACTAAACCTTTTCATGATATTGATATAGATACTGGG  
AACACCATCCGACAACTAGAGCCGCCAAAAAAATTATCACTGTAGAAGA  
AAGACCAACACACTTACCTTTACAAGTTTTGGAAGACCGTATGGTAAACC  
CTTGATATATGGATCTATATAACTTGAABTATGCTCTATTATATCGTGAT  
TTAATGACCGCTGTTGGCATTTCCGTCCTTAACCAAGGTAGTAGCACTTGT  
ATGCTGAATGTGCGCCAGTACTATCGAACCATAGAAACCATATATTCCT  
CAATATTAATPAATTCTACTGAGAAATGGGTGAATTTTGAATAAATGTTG  
GGATTCATCTCGTGTATAAAGGCTATAAATATTAGGTATACAGAACTGACTA  
GAAGTCTCTCTCGATGATATAGGAATCCCATATATGGAATCTATATTTCT  
ATGTACCAATATTACGATTATTCCTCATTCCTATTCATATCTTTCATTAT  
CCTATTACATTTATCGATCCTTCGATTTTCAGCTTCCCTCTAAGTTGGTGAC  
AGCTTCTATAATAACTTATGTCACTATCTAACACCGTATATGATATATATA  
TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYYFTLETHIFPNINNSTEKWYNFELIVGIPSLIKAILLCIQNVL  
EVLDDIGIPIMESIFLCTNNTIIPHSISYVSLSYIILPCISASSNFCD  
SFYNNLCXYLPPYMIIV

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:  
947-1487 (SEQ ID NO 17)

CCGATGGAACGTTCTGGAAAAGAAGAATAATTAAATTAAGTTTCTCAACTAAAATCTCCA  
CAAAAAACGCAAAATCACACCTTCTAAACCTTCCGCTGTGCTTTCTTTCTAGAATGCTCTGG  
AAAGTTTACACCAATCCACAAGAACGAAAATGCCGTTCGACAATGATGAAACCATCATCCA  
CACACCGCGCACACGTGCTTTATTTCTTTTTCTGAATTTTTTTTTTCCGCCATTTCTCAC  
CAAGGAATTTTTTTTCTTAGGGCTCAGAACCTGCAGCTGAAGAAGCGCTTTAGAAATCA  
AAGCACAACGTAACAAATTCGTCGACAACCGAGCCTTTGAAGAAAAAATTTTTCACATTCG  
CGCTTCATAAATAAATAGTTTAAAGTTATCTACCCACTATATTTAGTTGGTCTTTTCTCT  
TTCCTTCTACTCTTTATCTTTTTACCTCATGCTTTCTACCTTTTACGCACTGAAGAGTCCA  
ACCGAATATATACACACATAATGGCATCCACCGATTTCTCCAAGATGAAACTTTGAAAC  
AATTAAACGCTTCTTTGGCTGACAAGTCATACATGAAAGGCTATGTTCCGATTTACTTTA

65/251

CTTTATAGATCGTTGTTTTCTTTCTTTTTTTTTTTTTCCTATGTTACATGTAAAGGGAA  
 GTTAACTAATAATGATTACTTTTTTTTCGCTATATGIGAATGATGAATTTAAATCTTTTGGTC  
 CGTETTTATGATGGGAAGTAAGACCCCCGATATGAGTGACAAAGAGATGTGGTTGACTA  
 TCACAGTATCTGACGATAGCACAGAGCAGAGTATCAATTAATAGTTATCTGTTAATTTTTT  
 TTCTTTTTTTTGTTCAAAAAAGAAAGACAGAGTCTAAAGATTGCATTACAAGAAAAAGT  
 TCTCATTACTAACAAGCAAAATGTTTTGTTTTCTCTCTTTCAAAAATAGTACTGCTGTTCTC  
 AAGCTGACGTCACGTGCTTCAAGGCTTTCCAATCTGCTTACCCAGAATTCTCCAGATGGT  
 TCAACCACATCGCTTTCCAAGGCGGATGAATTCGACTCTTTTCCAGCTGCGCTCTGCTGCCG  
 CTGCCGAAGAAGAAGAAGATGACGATGTGATTTATTCCGTTTCCGACGATGAAGAAGCTC  
 ACGCTGAAGCTGAAAAGTTGAAGGCTGAAGAATTTGCCGCATACACGCTAAGAAGGCTG  
 CTAAGCCAGCTAAGCCAGCTGCTAAGTCCATTGTCACTCTAGATGTCAAGCCATGGGATC  
 ATGAAACCAATTTGGAAGAANTGGTTGCTAACGTCAGGCCATCGAAATGGAAGCTTTCA  
 CCTGGGGTGCTCACCATTATCCCAATTGGTTTGGTATCAAGAAGTTGCAAAATTAAC  
 GTGTTGTGGAAGATGACAAGTTTTCTTGATGATGATGUAACAAAGUATTGAAGAAGACG  
 AAGACCACGTCCAATCTACCGATATTGCTGCTATGCAAAAATTATAA

>YAL003W, 206 aa (SEQ ID NO 18)

MASTDFSKIETLKQLNASLADKSYIEGTAVSQADVTVFKAFQSAYPEFSRWFNHISKAD  
 EFDSPHAASAAAAEEEEEDDVLFGSDDEWADABAEKIKAEERIAAYNAKKAAPKPAK  
 SIVTLDVKPMDDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINC VVEDDKVS  
 LDDLQQSIEEDEDHVQSTDLAAMQKL

>YAL060W, 1649 bp, CDS: 501-1649 (SEQ ID NO 19)

AAAGACTACGAGAATCAATAAACGAGGCTAAACTGCTTCACACATGATTTGUGATTGAGTA  
 CTCACGTTCTCGTETTAATCCCGCGGTCTTCTTGTTTTACTAACTTTTCTTCTCTCATA  
 GCATTCTCTTGACAGTGTTTATATACATCATATGTACATTTATCGAGCCAAATCGAGGGC  
 AGCAGTTTAAACATCAAGCCGGATTGTGCTCAGCTACTTTGACCCCTTTTCTGTTTTCGAGC  
 AGAGAAGAAACCGGTGTTTTCTATCCTTGCCATTTCTTTCTCTCTTACGGGGTCTTAGC  
 CTGTTTCTCTTGATATGATAATAGGTGGAAACGTAGAAAAAAATCGACATATAAAAGT  
 GGGGCAGATACTTCGTGTGACAATGCCCAATTAAGCCCTTTGGGCAGATGTTGCCCTTC  
 TTCTTTCTTAAAAAGTCTTAGTACCATTGACCAACTCAGAAAAAAGGAAC  
 AAAAAAAGTTTTAATTAATTATGAGAGCTTTGGCATATTTCAAGAAGGCTGATATTCACT  
 TCACATAATGATATCCCTAGGCCAGAAATCCAAACCGACGATGAGGTTATTATCCACCTCT  
 CTTGCTGTGGGATTTGTGGCTCGGATCTTCACGAGTACTTGGATGGTCCAATCTTCATGC  
 CTAAAGATGGAGAGTGCCATAAATTAACCAACGCTGCTTTACCTCTGGCAATGGGCCATG  
 AGATGTACAGGAATTCTTTCCAAGCTGGGCCCTAAGTGACAAAGGTGAAGGTGGCCGACC  
 ACGTGGTTCGTTGATGCTGCCAGCAGTTGTGGGACCTGCATTGCTGGCCACACTCCAAAT  
 TTTACCAATTCCAAACCATGTGATGCTTATGACAGGGGCAATGAATACTATGTACCCACG  
 CCGGTTTTGTAGGACTAGGTGTGATCAGTGGTGGCTTTGCTGAACAAGTGTAGTCTCTC  
 AACATCAZATTATCCCCGTTCCAAAGCAAAATTCCTCTAGATGTGGCTGCTTTAGTTGAGC  
 CTCTTTCTGTCACTGGCATGCTGTTAAGATTTCTGGTTTCAAAAAAGGCAGTTTCAGCCT  
 TGGTTCTTGGTGCAGGTCTCATTTGGGTTGTTGACCATTTTGGTACCTTAAGGGAAATGGGUG  
 CTAGTAAATTTGTAGTGTCTGAAATTGCAGAGAGAGAAATAGAAATGGCCAAGAACTGG  
 GCGTTGAGGTGTTCAATCCCTCCAAGCACGGTCTRAATCTATAGAGATACTACGTGGTT  
 TGACCAAGAGCCATGATCGCTTTGATTACAGTATGATTCCTTCTGGTATTCAGGTACCT  
 TCGAAAACCTCTTTGAAGGCATTAACATTCAAGGGGACAGCCACCAACATTGCAGTTTGGG  
 GTCCAAAACCTGTCCCATTCCAACCAATCGATGTCACTCTCCAAGAGAAAGTTATGACTG  
 GTTCGATCGGCTATGTTGTGGAAGCCTTUGAAGAAGTTGTTCTGGCCATCCACAACGGAG  
 ACATCGCCATGGAAGATTGTAAGCAACTAATCACTGGTAAGCAAAGGATTGAGGACGGTT  
 GGGAAAAGGGATTCCAAGAGTTGATGGATCACAAGGAATCCAACGTTAAGATTCTATTCA  
 CGCCTAACCAATCACGGTGAATGAAGTAA

>YAL060W, 332 aa (SEQ ID NO 20)

MRALAYFKKCDIHFTNDIPRPETQTDDEVTTDVSWGICGSDLHEYLDGFI FMPKDGEC  
 KLSNAALPLAMGHEMSGIVSKVGPVKYTKVKVDHVVDAASSCADLHCWPHSKFYNSKPC  
 DACQRGSENLC THAGFVGLGVISGGFAEQV VVSQHHITPVPKEIPLDVAALVEPLSVTH

66/251

AVKISGFYKCSSALVLCAGPIGLCTILVLKGMGASKIVVSEIAERRIEMAKKLGVEVFN  
SKIHGKSIIEILRLTKSHDGFDSYDCSGIQVTFETSLKALTFKGTATNIAVWGPKPVTF  
QPMQVTLQEKVMTGSIGYVVEAFEEVVRaihngDIAMEDCKQLITGKQRIEDGWEKGFQ  
LMDHKESNVKJLLTPNNHGEMK

>YBL058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTACATAGTGCCATTGAACACTTTTCAAGCAAACACCCAGCCCGACCCACACAA  
TAACACACACACAAAAGAGTCTTGCAGGTCTCTCTTTTAGCGGCAACGGGCATGACACTAG  
GTATATTTGGTATGGGCATCACAGGGACATGTTGGAGCTGGGAATGTTTCATCATTTTCAGG  
AACTAAACCAACCTCTGCAAAAGGCGTGCUAAACAACGAATTTGTAGTGCACAAACATGCCTC  
TGGATAAAAGAAGCCAGCAAGTAGTGGACAGCTTAGTTAAGACACACAATTCATCTCTTT  
GTAAATAGTGTTATACCATAGTAGTAGTTTCAATAATATATATCCACACTATTATATGTTGTT  
ACCCGCATTAGAACTCTTATTTGGTGGCGAAAATCGATGSCAATAAGAACGGAGGGGTT  
TAATAGTTGTATGCTTAACATATTTGGATTAAATATATAAGAAACCTCCGTAGCACAAAC  
AATTAATCATTATTTAGGTATGGCGGAAATACUUTGATGAAACUATCCAGCAGTTCAATGG  
CATTACACCAATCTCTCGCATACATAGCCGTTCAATATCTCTCTGAATTTGGAGATTAA  
ATGAAGCACTAAATTCCTATCTATGCTTCTCAAAACGGATGACCAAAAGGATAGAAGAGAGG  
AAGCACATTCGAACACACAGCAGGAGAAAGCCCTCAAGCAAGAAAGUUTCTCCACCAACT  
CTTCGAATAAAGCCATAAATACGGAGCACGTTGGTGGGTATGTCCAAAACCCAGGATCCT  
CACAAAGGTAGCAGCAGTACTTTGAAAAGGAAAGGTTCTACCTCTCTCTGAACCAACCAAGG  
GTAGTAGCCGCTCTGGAAGTGGTAACAACCTCCAGGTTTATGAGCTTPTCGGATATGGTAA  
GAGGTCAAGCTGATGATGACGATGAAGATCAACCGAGAAATACTTTTGCTGGTGGTGAAA  
CATCCGGCTTAGAGGTTACAGATCCTTCAGATCCTAATTCATTACTGAAGGATTTGCTGG  
AAAAAGCGAGAAGGGGTGGTCAAAATGGGCGCTGAAAACGGATTCCGTGATGACGAAGACC  
ATGAAATGGGTGCCAATAGGTTTACTGGAAGAGGTTTTAGATTAGGSTCAACCATCGACG  
CAGCAGATGAAGTCGTAGAAGACAACACTTCACAATCACAAACGTAGACCAGAAAAAGTCA  
CAAGAGAAATTACATTTTGGAAAGGAAGGTTTTCAAGTGGCCGATGGTCCGCTTTATCGCT  
ATGATGATCCTGCGAACAGTTTCTATTTGAGCGAGTTAATCAAGGAGGGCTCCATTAA  
AGCTCTTTAGATGTGCAATTTGGACAAGAAGTTGAAGTTAATGTATATAAAAAATTAGATG  
AGTCTTATAAAGCTCCGACGAGAAAACCTGGGCGGTTTTCAGGCCAGGGCCAAAGACTAG  
CATCTCCTATCCCGCTCAATCCTCACCTGCCGAGGTTCCAAAGAATGAGACACCCGCTG  
CTCAGGAACAACCCATCCCGGACATGAGCCAAACAAGGCGACACCTCCATCCAAATTA  
GATACGCAAAATGGCAAAAGAGAAGTTTTGCACGTCAATTCACACAGATACAGTAAAGTTTT  
TGTATGAGCATGTGACATCAAAATGCGAACACTGACCCATCGAGGAATTTCAACCTTGAAAT  
ATGCCCTTTCTATCAAAACCAATAAGCAACGATGAGACAACATTGAAGGACGCTGATCTGC  
TGAACCTCGTTGTCTGTGCAAGATGGGCATGA

>YBL058W, 423 aa (SEQ ID NO 24)

MAELPDETIIQFWALTNVSHNLAVQYLSEFGULNEALNSYYASQITDDQKDRREEAHWNKQ  
QEKALKQEAFTSNSSNKALNTEHVGLCPKFGSSQGSNEYLRKGSFSPEPTKGSRSKSS  
GKNSRFMSFSDMVRGQADDDDEDQPRNTFACGETSELEVTDPSDPSNLLKDLLEKARRGG  
QMGAEANGFRDDEHEMGANRFTGRGFRLGSTIDAADDEVVEDNTSQSQRRPEKVTREITFW  
KEGFQVADGPLYRYDDPANSFYLSELNQGRAPLEKLLDVQFGQEVENVVYKLLDESYKAPT  
RKLGGFSGQGRLGSPIPGESSPAEVPKNETPAAQEQPMPDXEPKOGDTSIQTRYANGKR  
EVLHCNSTDTVKFLYEHVTSNANTDPSRNFTLNYAFFIKPISNDETTLKDADLLNSVVVQ  
RNA

>YBR039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TDEAGATTTTCCAAGTAGTAACATCATCTTTCTGAGTGTGCTATCAAATACATACTAAGGA  
GAATAAACTCTTGTTATTACGTATCTTTCATCCTTATGGGTAGAGAGCGCACTGTTTTAG  
TACATTTTCTAGACGTGAAACGTAGAGCAATTTGTGATAAAACAAAAAAGTAAGAA  
GATATATGAATAGGACGTGTCCCTAGAACCTAGTAAGTATATGATGGAGACTATAATAAGTG  
AATTATTCGATATTTAATGAACGTTCTCATTTATTTTGAAGAAATGTTTATCACGTGAAG  
GAGAACCAATGAGCGGCGAGTAACCTACGCGAGGAACCCGGACCGCAATAACGATTAAGA  
AGGCCCCGAAGGGAGATGCTTAATGATTATCACTCAGTTAAAAAAGACAAATAAGAAAC  
TATTGAGACTGAACCGTTTGGTTAATTTTCAGGTGGAACAATTCAGACGAGCAGTAA

67/251

CATTATTTTATTAGTAGTCATGTPNTCAAQAATTGTATCAAACAAATGCAACACGCTCCG  
 CAATGTGCCACCAAGCGCAAGTGGGTATTCTTTATAAGACTAACCCAGTGAGAACTTATG  
 CTACTTTGAACCAAGTGGAAATGCGTTTGAAATCTATCAAAAATATTGAGAAGATCACAA  
 AAACATATGAAGATGTTCCTTACAAAGATTGAGTAAAGCTGAAAAGGCTAAAATTTCCG  
 CAAAGAAGATGGATGAAGCAGAGCAGTTGTTTTACAAGAAGCGCCGAAACCAAAAATTTGG  
 ATGTTGAGGCTACTGAAACAGGTGCTCCTAAAGAGTTGATTGTTGCTATCACCTCTGATA  
 AGGGGTTGTGTGGTTCTATCCACTCTCAATTGGCTAAAGCTGTGAGAAGACATTTGAATG  
 ATCAACCAAAACGCCGATATAGTCACCTATTCTGTGATAAAATTAAAATGCAGCTATTGAGAA  
 CCCATCCTAACCAACATTAAAATTGTCTATTAAATGGAATTGGTAAAGATGCCCCAACTTTUC  
 AAGAACTGCTTTGATTGCTCAATAACTTATTTAGTCTCATGAAGGCCCGCACTTACUCAA  
 AGATTTCCUATTTTCTACAAATGACCCAGTGTCTTCCCTATCTTTTGAACCATCTGAAAAAC  
 CGATCTTTAAACGCCAAGACCATTTGAACAATCCCATCATTCGGCAAATTTGAGATCGACA  
 CGGACGCCAAACGTTCCAAGACATTTCTTTGAATATACTTTGGCTAACCAATGTTGACAC  
 CAATGGCTCAAGGTTATGCTGCTGAAATTTCCGCCAGAAGAAACGCTATGGATAACGCTT  
 CCAAGAATGCCCGTGATATGATCAATCGTTACTCTATCTTGTACAACAGAACAAGACAAG  
 CTGTCAATTACCTAACTGAACCTGGTCTGATATTATTACTGGTCTCTCTCTTTGGGATGA

>YBR039W, 311 aa (SEQ ID NO 42)

MLSRIVSMNATESVMCHQAQVGILYKTNFVRTYATLKEZVEMRLKSIKNIEKITKTNKIVA  
 STRLSKAKKAKISAKKMCEAEQLFYKNAETKNLDVEATETGAPKELIVAITSDKGLCGSI  
 HSQAKAVRRRLNDQPNADIIVTIGDKIKMQLLRTHPNNIKLSINGIGKDAFTPOESALIA  
 DXLLSVMKAGTYPKISIFYNPVSLSFEPSEKPIFNAKTIEQSPSPGKFELDTDANVPR  
 DLFBYTLANQMLTAMAGQYAAEISARRNAMDNASKNAGDMINRYSLYNRTRQAVITNEL  
 VDIITGASSLG

>YBR062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGGTGACCAACTCTCCTACCCGAATTACTGTGATGATATATACTCTTCGTTTTC  
 TAGTAATGGCTTCATTTTGCCCTAAGTTGGTCAAAAATTGTTGTGGGCGGCTTTTGTTTGCA  
 CCGAGGACCGCTCAGTTCGTTATAATAACAGTTTTTGGCACTCCTAAACTACCTAAAGAAAT  
 AATTAGAAAGATATATTTCATCAAAACATAATCACAATCAAAAAAATGTCTACATATGAAGGT  
 ATGTAATGATATATTATCAAGTAAAGTTCCCTCAAAGCCCAATTAACTAACCGAATTTTAATC  
 TGCACCTCATCATTTAGATTAGAGGAACATGCCAATACAAACAATACTCAAGCGATTACCAAGA  
 AGTAGGAGGAACCTCACAGGAGGAGCAGAGAAGACAGGTCAAGATCCCAACTGCAAGGTC  
 TATTTCAAACCTTTGCTAACACCAGTCTGCTGAGGCTGATGCACATTCAGATTCAACACTAC  
 ITTTACGATTATTATCGCAAATGCTTCAGAAATCATTTACAGGAAGAATGGTTGCAAGAAA  
 TGGATAAAGGCAAGAGTCCCGGCTGCTCTGATACCTTTGACAGCCTCTTTACCACGAATCA  
 ATAAAAAAGCTCAAAACCACTGACAACCTGCTCCATTTGTTTACACTAATTATTCAACAAC  
 ATGAGTACCCCTTAGTAGTTGAATTACCTCAATTGCCATCATTAAGTTCCGACTTAGAGTGTT  
 TGTCTGTCTGGCTATCTCGAAGTACAACATGTTUATTAATGAGAGATAATGTTATGGGUC  
 ACCGAATCATTAATGAGATTGATACAACTGAAGUAGAACTGGAAGAAGATTGGGGTATGT  
 ACGGTTAA

>YBR062C, 115 aa (SEQ ID NO 46)

MLPHSLQEEWLQEMDKGKSACCPDTFAASLPRINKKKLKATDNCSICYPNYLEDEYPLVV  
 ELPHCHMKFDLECLSVWLSRSTTCFLCRDVMGHRIINEIDTTAELEEDWGMYG

>YBR101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATCAAAATGTTATCCCCAGGGTCCATTAACTCATCCAGAAAACAGATAGATGGATTG  
 AAGGCCGTAGGTTTGAATTTTGTCTACAAATTGGACGAGTTTATCAAAAAGCAACAGTGAT  
 AAAATTCGCTAAACAAGATCACAGAAAATAAACCTCACTTCAATATATATGATGTGTAGG  
 TAGGGTATATACTTATACCACTGCTGTCTGACAGTGTACTAACCTATTTCTTATTTGTAG  
 GTAAGCTTTTCAGCTACTGGTTGGTCAAGTTGGGCCCTATTAAGGTTGTAATCAGCTTAT  
 TCGTTTGAATGATATACCTCTTTGGACTGGAATCTTCTGGAAGTTTTTTGGAGGTTAGAA  
 AAGAGGAAGGCATCTCGCGCTGACAGAAATTTGCTTATAAAACCAAGGATTGGCTACATCT  
 AAAAGAGTACTCATCTCAGTCAGAAAGCCATTACCTTTCAACGAAAGAGTAAAAAGAA  
 AAAAAACACATACATAACTATGGAAAAGCTATTACAGTGGTCTATTGCGAATTTCTCAAG

68/251

GGGACAAAGAAGCTATGGCTAGGGCCGGCCAAACCTGATUCTAAATTGCTACAGCAGTTAT  
TCGGTGGTGGTGGTCTTGACGATCCAACTTAATGAAAGAATCCATGGCTGTTATTATGA  
ATCCGGAGGTTGACTTAGAAACAAAACCTCGTTGCATTTGACAACTTTGAAATGTTSATTTG  
AGAACTTAGATAATGCTAATAATATCGAAATTTAAACTTTCGGAGCCATTGTTGGATG  
TTCTTGTTCAGACGAAGGATGAAGAACTACGTCCTGCTGCTTTATCCATTATTCCGAACCG  
CTGTGCAAAACAACCTTCGGATTCGCAAAATAATTTGATGAAATACGACAATGGTCTGCGAA  
GCCTTATCGAAATAGCTAGTCACAAGACAAAGCCACTCGACCTGAGAACAAGCTTTTTT  
ACGCACATATCDAATCTAATAAGAAACCACAAAGATATCTCAGAAAAGTTMTTCAAATTAA  
ATGGGCTCGACTGCATAGCACCTGTAATAAGTGATAACACCCGCCAAACCAAACTGAAAA  
TGAGAGCCATTGCUATTATTGACCCGATATTTTCATCTGTTAAGATTGATGAAAATATAA  
TCAGTGTGCTGAGAAAGGATGGAGTAATTGAAAGTACCATTGAGTGCCTGCTCTCAGGACA  
GTAAATTGAACATCATAGATAGAGTTCTGTCTTTCTCTCTCACCTGATATCTTCCGGAA  
TAAATTTAATGAACAGGAATTGCACAAATTGAACGAAGGTTACAAACATATCGAGCCTC  
TAAAGGACAGACTTAAAGAAGACGATTATTTAGCCCTAAAGTATGTATTATGA

>YBR1D1C, 290 aa (SEQ ID NO 50)

MEKLLQWSIANSQGDKEAMARAGQPDPKLLQQLFGGGGPDPTIMKFSMAVIMNPFVDLF  
TKLVAFDNFEMLIBNLDNANNIENLKLWEPLLDVLVQTKDEELRAAALSIIGTAVQMNLD  
SQNNFMKYDNGLRSLIELASDKTKPLDVRTKAFYALSNLIRNHKDISEKFFKLNLGLDCA  
PVLSDNTAKPKLKNRATALLTAVLSSVKIDENILSVLRKDCVIESTIECLSDENLNIID  
RVLSTFLSHLISSGIKFNEQELIKLNEGYKILIEPLKDRLNEDDYLAVKYVL

>YBR139W, 2027 bp, CDS: 501-2027 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGTACGGATCCTGTAGAAATATCACTGGCAATTATACTG  
AGTTTATTGTTGGTGTGCTATTTCATATTTGAGCTGGTATTGGACGAAAGCAAGCATAT  
GAGTTTGTGTCTACTGACTCCAACACCCTAGGCTGGATTTGATCTTTCTCCATCCTTTAA  
TTTTAACCTTTTAAATTAGTGGTTGGATCAAGTTTTCGAGACTATCCCAATCTGTGACTTC  
TTGGATAAATAGTTTTTGACTCGTTTAGTATAATCCCTTTTTTCTAAAAGTGTCTTAGAGTT  
CTCTAAGATGTTCTTGTTTACAATGTGAGCGATTTAGGAAATTTCTTAAAATGGCCGAG  
GCCGGCCTAGCATTCTACGAAAGGTGAGATAACGCTTCGTTATCGAAAAATGTCCAGGGGA  
CACCGGTTTATATAAGAACGAAAATTGTCTCCTGCTATTTTTCTTTAAAAACAGCTATACA  
AAAAGTGATACCGACATACAATGAAGTATCTAACTTAGTTTTCTGCTTCAGCTTCTTA  
TTAGCATCAAAATACGCCCTCATTTGGCCCGAGCTTTTCTCTTTTTGAAGATGATACCACCT  
TTGCCAATTTGGATAAACAGCTAAAGCTTCCACAGAATACACAGCAAAACCTTAATTTGG  
ACCGTTTGAATCACGATGATCCGCTGTTTACAACCTTTATTTCTCTCTGTCGACACAGATT  
ACAGTTTGAAGCTTAGAACAGTAGATCTTCTAAACTAGGAAATGACACCGTAAAACAAT  
CGTCGGGTTACATGGACTATAAGGATTCCAAACACTTTTTTTACTGGTTTTTTTGAAGTA  
GGAACGATCCTGCTAACGACCCAATTATTCTTTTGGTTAAATGGTGGACCTGGTTGTTCCT  
CGTTTTACTGGGTTGCTATTTGAACAAAGCCCTCATCAATTTGGCCCGATATGAAACCA  
TCCACAATCCCTATTCTTGGAAATAACAACGCTCAATGATCTTCTTAGAACAGCCACTCG  
GAGTCCCTTTTTCTATGCTCATGAAAAAGTCTCCTCTACAAAATTAGCAGGCAAGATG  
CCTACATTTTTCTCGAATTGTTTTTTGAAGCTTTTCTCTATTACGCTCCAAACGATTTCC  
ACATATGCAGGCGAATCCTATGCAGGACATATATCCCTCAAATTGCACATGAGATCGTTG  
TCAAGAACCCTGAAGAAGCGTTCAATTTAACTTCAGTTATGATTGGTAATGGTATCACAG  
ACCTTTTGATTCAAGCAGATTATTATGAACCAATGGCATGCCGGAAAGGGGGCTATCAAC  
CTGTTCTCTCATCAGAAGAATGTGAGAAAATGAGTAAAGCTGCAGGTCGTTGTCTGATGGT  
TGAACAAGTTATGTTATGCTTCTAATCAAGTTTACCATGATAGTCCGCACTGCTTACT  
GTGACTCTGCACCTTTTCCAACCGTACATTAACACAGGACTCAACGCTCTATGACATTAGAG  
GGCCCTGTGAAGATAATAGTACTGATGSTATGTGTTATACAGGCTCCCGCTATGTCGACC  
AGTATATGAATTTTTCTGAAGTTCAAGAAACGCTAGGGTCCGACGTGCATAATTATTTCTG  
GCTGTGATAATGACGTGTTACCCGATTTTTGTTTTACGGGCGATGGAAGTAAACCAATTC  
AACAAATATATTGCTGAATTATTAATCACAAACATTCCTGATTAATATATGCCGCTGATA  
AGGATTAATTTGTAAATTTGGCTGGGAAACCATGCTTGGTCCAATGAGTTGGAATGGATCA  
ATAAACGTAGGTATCAGAGAAGGATGTTAAGACCATGGCTCAGTAAAGAAACAGGTCAAG  
AGTGGGACAAGTCAAGAACTATGCCCTTTCAACCTTTTTCAGCAATATACGATGCCGGTC  
ATATGTTTCCCTATGATCAACCCGAGGCAAGTTTGGAAATGGTCAACAGTTGGAATTTCCG

69/251

GTAATCGTGCCTTTTCGGATCTTTCCCACTTCGAAAATGCTAGTTAG

&gt;YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFVLQLLISIKYASFGRAFLFEDDTTFANLDKQLKLPQNTQQTLKLDRLNHDD  
 PLFTTFIISVITDYSLR/RTVDFSKLGIDTVKQWSCYMDYKDSKHEFYWPFESRNDPAND  
 PIILWLNGGPOCSSFTGGLFELGPFESIGADMKPIHNPYSWMNNASMIFFLEQPLGVGF SYG  
 DEKVSSTKLAKDAYIFLELFFFAFFHLRSNDPHIAGESYAGHYLPQIAHEIVVKNPERT  
 FHLTSVMIGNGITDPLIQADYYEPKACGKGGYHPVLSSEBCEKMSKAACRCRRLNKL CYA  
 SKSSLPCTVATAYCDSALLEPYINTGLNVYDIRCPCEDNSTDGMCTGLRYVDQYKMFPE  
 VQFTTGSQVHNYSGCDNDVFTGFLFGDGSKFPQQVIAELLNHNLPVLIYAGDKDYICNW  
 LGNHAWSNELEWINKRRYQREMLRPFVWSKETGEELGQVKVNGPFTFLRTYDAGHMVPEYDQ  
 PEASIFMVNSWISGNRAFSDLSTLENAS

&gt;YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TGCACATGTTGAGTATCCCTATTGCGCATTTTCTCTATTCTGAGAAGGAGTGTGAATAAT  
 TGGCGAGGGTTTCAGAAATGCTCTTTTAGAAATAAAAAATGAATGTAAATAGTTGGAATGTAT  
 CTCTAAGTAGACAAATGCAGGTAAGTTTACTGCGCTTTGCGGATTAACAGTATGCTCTT  
 AGTGCAAAACACGAAAGAGCTCCCAATCTTTGAAACACAATCGACCACGGAGGAACAATA  
 CACGTAGAAGGGGATAACTAATACTTTGTGCTGCAAGAGTATTGGACGACACACTAACAG  
 CAGAACTTGGCTTCTTAACCTCTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA  
 AGATGATTTATTTTTTTTTTCTTAAAAAAAGTTCTTTCTTTGAAGATCCCCCTGATAAAA  
 AAGATCAAAATAATCGAAACGCTAATCATAATCAAATCGGGAGGAGAAATAACCGCAAGAAG  
 TCTCCGTTTCTACCTGAGTAATGGTGACAGACATAGAGTGAAGTACTCTACAAATGCCC  
 CTGAGGATATCGGTAAATCATATGCGCCAAAATGACACTCATTTGACTCTTCTCTGAGGTT  
 CTGGTGTGGTTTTTACAACAAAGCTGGCTATTAGAGAGGACTGGAAGCTTTGATATAATCCT  
 TTACGAGAATCACTTGGAGGGCCAGAGCGGACCTGGCTAGAAATTTAAGCGTTATAGAAA  
 ATGAACTGAGTGTGGCTTTTTCAGTTTACTCAAAATCTTTGGATGTGCCGGAAGGTTTA  
 TTACTAACCAGTCTACAAATTCATTTACAGTGACAACTTTGACATAGAGCAGTACTTGC  
 CTCCCAGAGTAGATTGAAATCTGTCAATGGAATCCACAAGATTTTACATATGATATATCAG  
 TGGAGCCCCACACAAAATCCAAAATGTTGAATATGCTCTGTTGAAACAGGGTGAAGAATTTA  
 CAATTGCAAGAGTGAAAGATGAGAAACCTCGAAGTAGGTGTATTCTTTGTGGATGCAAGTG  
 ATGAAAGTGAATGTGATATTGGTGGAAATACCTTCTAATTGGAGGATGGACGATGGTAAAA  
 TGGAAAGATGTACAAAACATCCTTATTTGATATAAACAGGGCCATATCGCATACAATCACT  
 CGACGACTACGACATCACTATATCTGAATGAACCTATCGGTTTGCAATCCAAAATCATGA  
 TTGATCTCACAGATTTGGAAGAAGCCCCAATATGCAATGTATCTAATGCACTGCAATTTGC  
 CGTTAGAAATATTTATCGATAAATCCAACTCTCTCCCTTACTACTTTTTTGGAGAAGACG  
 ACTTAGAAATACCAGAAATCTCTCTTCGAGATAAGGCATGGGGTCTGAAAGTATCTTTG  
 AATTGAAAGCCGGCACAAATGAATGAAGTGACATTTGCATACTAGATATATTGAGCCTTCTA  
 ATAATAAAGGGGATAAATTAGAAGTTTCATTTGATCCAGAAGTTATATTAGCCTGCGACA  
 CAGGTGACAAATAACTTTCCCGTAATCCATTTTATAAAAAAGGTCTAGGATATGAATCTC  
 CTTTACAGACGATACTACATTCGCCCATTTGAACTCGACAACCTCTTCTAGTACCAATTC  
 CAGGCCTGACACAAAGGATTATTTCCAAGATCAAAAATGGTACGTTACTATCCTTACTCA  
 TCTCATATCATATATTTTCTCCAAGGTATTTGCTAACAAACAAGAAGAAAGATCAGTAA  
 AACGGGAATAA

&gt;YCL052C, 416 aa (SEQ ID NO 68)

MTRHRVTVLYNAPEDIGNHQRQNDTHLTVRCGSCVVLQQRWLLERTGSLDKSFTRITWR  
 PRADIARSLGVITENELSAFSSVSNSSDVPERFITNPVYNSFHSEKFDIEQYLPPEVDLN  
 LSWNPEDFTYDISVEPTQIQIVEYRLKQSEFTIARVKDEXLRVGVFTYDASDESVDZ  
 GGIRCNWRMDDGKMRCCQKTSLLYKQGHIAYNHSTTTSLYLNEPIGLHPKTMIDLTFE  
 ERPKCMYLMILQLPLELFDKFQSSPLLDFGEDDLPEYSLRDKAWGSESIFELKAGCM  
 NEVTLHTRYIEPSNNKGDKLEVSFLFEVILACDTGDNKVSBNPPYKKGLCYRSLFTDDTT  
 FRHLNSTLLVPTPRPDTKDYSKTKNGTLLGLTSLIIVTFSKVFGNNKQKRSVKRE

&gt;YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

70/251

CACATAAGTTTACTTTCACCTTTTTCCTGACTCCCTTACTTGTCTTCCCTGCACITTTGATT  
 TTACTTTCAGAAAAATAAGATATATGTTTCTGATAAAACTTTTtaggtTAGCGGAGAAGAT  
 GTTCCCAUGAATATCAATGTAATTGAAAGGCAACGAAAGGTCTATCGTTTGCCATTTCATAA  
 TGTGATTCCGACTTGTCTTTTTCATTGTAACAGACATGAAACGTTTCCCTTTACGTCCCTAT  
 GAATTTTGTGTTGGCTGAATCGGGCGCTGAGGGGCTGACGATCCAAATCCCCGATTTT  
 GAACAATTATGAGAATCCGAATTAAAAAGAAAGGGAAAAACAATTTAATAACAGGCAGACG  
 TGAGAGAAAGAAAGGAAACGCTGTGATATAGAAAACATATACAAATCCTATTATAAGAAGC  
 CAGAAGAAACCTGATACACATGAGTTGGGAAGGTTTAAAGAAAGCTATCAACAGAGCTG  
 GTCACAGTGTGATAAATTAAGAATGTGACACAGACCATTTGATAAAGAGTATGACATGGAG  
 AACGTCTTTATAAAGTTCTTTCAGAGAGUAGTGTAGGCUATTACAAAAGGAAGCCAAAGGTT  
 TCTTGGACTCATTGAGAGCTGTGACAGCATCACAGACTAACCATTTCCGAGGTCACTCTTA  
 ACCCTATGACGATTCAAATATGTTGTCTGTGCTGGTTTACAACGTTGGTAACTATTATT  
 TGCATCTGTTCAAGATTTTTCATAGCGAACTGTTAAGCAATTAGACGGGCCCCCTTAAGAG  
 AAACCGTACTAGATCCAATAACAAAGTTTTCGACGTATTTCAGAGAAATTGAGGAGGCCA  
 TAAAAAAGAGAGACCATATAAGAAACAAGACTTCGATGCTGCGAAGGUAAGTTTCTGATAGT  
 TACGCGACAAACCTCGCTAAAGATGCCCTCTAAACTGCCAAGGGCTGAAAAAGAATTGAGCT  
 TAGCTAAAGATATTTTCGAAATCTTAATAACCAATGAAAACTGAACTACACAGTTAG  
 TTTCAATTAAGAGTACCTTACTTTGACCCAGTTTTSAGGCTTTAATCAAGATTGAGCTAA  
 CGTTCTCTACTGATGGTTACACTCGTTTAGCGCAGATTCAACAATATTTGGACCAACAAT  
 CAAGAGACGACTATGCCAATGGGTATTAGACACTAAAATCGAAGAACTATTACGACAAA  
 TGACAAGCCTAGATATTGTGCGCTCGGGATAAAATAA

>YCR009C, 265 aa (SEQ ID NO 74)

MSWEGFKKAINRAGHSVLIKNVDKPLDKREYDMEZRRYKVLQPRAGEALQKEAKGFIQSLRA  
 VTASQITLAEVTSNLYDDSKYVAGGGYNVGNYYLQCVDFDSETFVKQLDGLPLRETVLDPI  
 TKFSTYFREIEEAIKKRDHKKQDFDAKAKVRRLLVDPKPAKDAKLPRAEKELSLAKDIFE  
 NLNNQLKTELPLVSLRVFYFDPSFEATIKIQLRPTDGYTRLAQTQQYLDQQSRDDYAK  
 GLLDTKIEELLGQMTSLDICALGIK

>YCR010C, 1352 bp, CDS: 501-1352 (SEQ ID NO 75)

GAGCTCCGTGCAATAGGCCACCGGCTCACTGGTTCTCCAAGCTACGGTTTTTTACGTGTAG  
 CCCCATGTGAGCAAGCCAAACAGGGCCCTTAAAGGCGTGACTACAAAAAGGGGCGGGTT  
 GGAAGGTCACTGCGAGCGAGATACGAAAGATTTTTTGGCCAGATTGGCGTTGGCGGCT  
 ATTTCCGTATTGTTGGGGTAACAAACGTTGGGGAAGACTGCAATTTCTTTACAGCTTTTPT  
 TCGTTATCGCGGTTGGGCGGCTATGGCGCCTTCTCCTCTGTACTCCAACCTGTGAGAGA  
 CACCAAGCTGTATATAAAGCACCTTGGTTGGATCGTATTTCCTGAGATCTTGCCTATAGG  
 TTCATTTTATATATCGTCCATAGCAATACAAATACAAACAGAACTACTAGCATCTGTTT  
 ATAAGAAAAAGGCAAAATAGTCGACAGCTAACACAGATATAACTAAACAAACCAACAAACAA  
 CTUATATACAAACAAATAATATGTCGACAAGGAACAAACGAGCTGAAACACAGACTTGG  
 AGAATGCACCAGCAGGATACTATAGTTTCUCATGATAACGACGTTAATGGCGTTGCGAGAAG  
 ATGAACCTCCATCTCATGATTCTCTCCCAAGATTTACACTGGAGGTGATAACCAATGAMT  
 ATATCTATATCTGGGCTCAAAAAGTTTTTGAAGAGCCACTTATACCAAGCCTTTGGTGCTA  
 CCTTGAATCTAGGGTTAGCTCCTGCTCCAGTGCACAAATTTGCTAATCTGCGGCCCTTAG  
 GTCCTTCAGCCTTCCCGTTGACGACATTTGTGCTGTCCATGTTCAATGCCGAGAGCSCAAG  
 GGATCACTGTTCCCTAATGTTGTGCTCGGTTGTGCTATGTTTTATGGTGGTTTGGTSCAAT  
 TGATTGCTGGTACTTTGGGAGATAGCTTTGGAAAATACTTTTGGTGGTACCSCATTATGTT  
 CTACGGTGGGTTTGGTTGAGTTTGGCTGCAATTTACATTCCTTGGTTTSETATCTTGG  
 AAGCTTACGAAGACAATGAATCTCATTTGAATAATGCTTTAGGATTTTATTTGTTGCGGT  
 GGGCCATCTTACGTTTGGTTTAACCGTTTGTACCATGAAATCCACTGTTATGTTCTTTT  
 TGTTGTTCTTCTTACTAGCATTAACCTTCCCTACTGTTGTCTATTTGGTCACTTTGCTAATA  
 GACTTGGTCTCACAGAGCTGGTGGTGTCCCTGGGAGTTGTGTTGGCTTTCATTGGTTGGT  
 ACAACGCATATGCAGGTGTTGCTACAAAGCAGAATTCTATGTACTGGCTCGTCCATTCC  
 CATTACCATCTACTGAAAGGGTAATCTTTTAA

>YCR010C, 283 aa (SEQ ID NO 76)

MSDAEQTSQNTDLNENPAGYYSSHDKNVNGVAEDERPSHDSLGKIYTGDDNNEYIYIGRQ

71/251

KFLKSDLYQAFGGTLNPG LAPAPVHK TANPAPLGLSAFALTTFVLSMPNARAQGITVENV  
 VVGCA M F Y G G L V Q L I A G I W E I A L E N T F G G T A L C S Y G G F W L S F A I Y I P W F G I L E A Y E D N E  
 S D I N N A L G F Y I L G W A T F T F G L T V C T M K S T V M F F I I S F L I A L T F L I I S T G H F A N R L G V T R A  
 G G V L G W W T A F I A W Y N A Y A G V A T K Q N S Y V L A R P F F L P S T E R V I F

>YCR021C, 1499 bp, CDS: 501-1499 (SEQ ID NO 79)

ATCGAAAGCGTGCTTTTGTAGAATATTTGGTATGGCTAAAGTAAGCAAAGCCATATCCCC  
 ATCCCGATCCCCGACTCTTACTCCGATCCCTTCGCCACATCCCTGCATGTTTATTCGAMTA  
 CCAAATTAGCTCATCTTCTCTATTTTCATCATCCCTTTCTGCTATGGCAAGGACAAGTTT  
 TTTCTAGCATCTCATCGAAAACTTTCCTCTCCCTAAATTGGCCAAAGTTTTCATATTCATC  
 ATCAGTTAGAAAAGTATAATATCAATCCCTTACCTCATTACAAGTTGTATCACACTAAAAA  
 AATCATATATAACTCTCTGCAGAGCTTCATATTATTTACCTAACACCTATTCACCTTCTA  
 ATCTTGTCTTCTTGTCTTTTACATTCTGCAATACAACACAACAATAATTAACTCGAATTA  
 TTATTATTTATAATTACAAAAACAAAACAAGTTTGAGACTTTAATATCTTTTGATTA  
 CTAAAAACAACAATTTCAAATGAACGATACCTATCAAGCTTTTAAATCGTAACGAGG  
 CTTTAGGGCTTAATCCACCACATGGCCTGGATATGCACATTACCAAGAGAGGTTCCGATT  
 GGTATGGCCACTGTTTCCAGTCTTTGGCTTTATATTGCCATGCTATGTTGTGATGTTCT  
 TCATTCCGGACAACAAGGCTCCAGATTGACTACATATGCCCTTAGCTCCGCAATTTTGA  
 TCACTTTCTTTGAATTTTCTGCTTTCTTCACTTATGCTTCTGAATTAGGTGGAGCTGGTG  
 TTCAGCTGAATTTAACCACGTCAAGGTTAGCAAGTCTATCACAGGTGAAGTTCCCGCTA  
 TTAGACAAATCTTTTACTCGAAATATATTGCCTGGTCTTGTCTGCGCAAGCCTTTTAT  
 TTTTAATCCAGTTAGCCCTAGTACTACTGGTGAGAAAGACGACATTCGCGCTTCGATA  
 TGGTACATTCGCTGTTAATTCAAATCGTGGGTACCTTATCTGCGGTGTTTCTGCTATTAG  
 TTGGTTTCATTGATCAAGTCCACCTACAAGTGGGGTTATTAACACUATGGTCTCTGCTA  
 TSTTGGTTACCCAACTGTGCATATGCCAACCTCAATTCCTCAATTCGAAAACAGAGGGT  
 TCAATGCACCTTATGCTGTGTACCTGCATGGTAATCGTTTGGTTGTACTTTATCTGTGGG  
 GTCTAAGTATGGTGGTAACCGTATTCAACCAGACGGTGAGGCTATCTTTTATGTGTTT  
 TGGATTTATGTGATTTTGGCAATTATCCATGTTACTTGCTAATTGCAGTCAGCGTGATG  
 GCAAATTGCCAAGGCTATCTTTGACAGGAGGATTCTCTCAACCATGCTACCGACGATG  
 TCGAAGATGCGGCTCCTGAAACAAAAGAAGCTGTTCCAGAGAGCCCAAGAGCATCTGGAG  
 AGACTGCAATCCACCAACCCGAACCTGAAGCAGAGCAAGCTGTGGAAGATACTGCTTAG

>YCR021C, 332 aa (SEQ ID NO 80)

MNDTLSSFLNRNEALGLNPPHGLDMHITKRGSDMLWAVFAVFGFILLCYVVMFFIAENKG  
 SRLTRYALAPAFLLTFEFEFAFTYASDLGWTGVQAEFNHVKVSKEITGEVPGIRQIFYS  
 KYIAWFLSWPCLLFLIELAASTTGENDDISALDMVHSELLIQIVCTLFWVSLLVGSLTKS  
 TYKWKGVYTTGAVAMIVTQGVICQRQFFNLKTRGFNALMLCTCMVIVWL YFICWGLSDGGN  
 RIQPDGEALFYGVLDLCVFAIYPUYLLIAVSRDGKLPRLSLTGGFSHHHATDDVEDAAPE  
 TKEAVPESPRASGETAIHEPEPEAKQAVEDTA

>YDR073W, 1010 bp, CDS: 501-1010 (SEQ ID NO 91)

GTTAGCTTGCCCTTGCAATTTCCCAAGCGCTCTCGAAAGGAATTATTCAAGATGGATTATT  
 GGCATTTACGAGTAACCAAGGATAACCCCGCTGTGGGTGAACCAACCTCTTTTTCACCTT  
 TCTTCAAGGCCAGTGCAAAACGCGAATAAACATATCTACGCTATATATAGATATGACGTTT  
 CTCAGGCAACAGAAAGTAGATAAAGCAGCCAGGAGGTAGAGAGTGTTCAAATTATAGCA  
 AGCCTTCTTCTACCTGTTTTTTTTTGTATGATTGTTTTGGCGGGTAACAATCGACTTTCCG  
 CCAAAATTTTTTCTCTTTTCTCTCTAACAGTATATACGGAGTGGAGAACAGACTTCCCA  
 TAAAGCATATTACGTGGGGTCTGTAGTAAGATTGCCGTTTATGATAACCTCTATTTAGGG  
 CTCAGAGCGCATCACGATCGGGAGTGTAATTCATGTGCATATAAGCAAAACACACAGA  
 TTTCTCTTTTTTCCAGAAAATGAGCAGTCAAAATTGCCTACTCGAATACCAACACCAACA  
 CTGAAAACGAGAACCGCAATACTGGCGCTGGCGTAGATGTAANTACAAATGCAATGCAA  
 ATGCAAAATGCAACTGCAATGCAACTGCAAAATGCAACTGCAAAATGCAACTGCAAGCTGA  
 ACCTCCCCACGGTCGATGAGCAAAAGACAGTATAAGGTACAACCTGCTATTCGATATCAACA  
 GCATATTACTTGCTAGAGTTATTACAGATGAATAATAGTTTACAAAACAATCTACAGAAUA  
 ATATAAATAATAGCAATAACAATAACATCATCAGGATACAGCAACTTATATCTCAGTTCC  
 TAAAAAGGGTTTCATGCCAATCTTCAATGCATATCTCAGATAAACCAAGGAGTGGCCCTCAG



72/251

CGAAACCACTGATCCCTCAGCGCTCCCTCAGCTAGCCCAACCAGCAGCAACCTCCACAGGATA  
TTCTTTCTAAACTCTATCTTCTCTCTGGCAAGAGTGTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)  
MSSEIAYSNNTNTNENENPNTGAGVDVNTNANANANA'ANATANATANATAELNLPVDE  
QRQYKVQLLLHINSILLARVIQMNNSLQNNLQNNINMSNNNNIIRIQQLISQFLKRVHAN  
LQCISQLNQGVPSAKPLILTPPQLANQOQPPQDILSKLYLLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)  
ACGAATTAGGCGTCAAGTCCTTAGACCCCCAATGACAAACAACACAGCCAAACCGTATCATCGA  
GGAAATTGTTGAAGTGAATAGATATAAAAAAAAAACGCAUCAAAGTAAGTAAGTAAATAAAGAA  
TAAATAAACTATATCAGTAAACACCAAGCGAGGATGTTTTCATTGTGCATCCGTGTTCTT  
GATGATCACATAACTGTAAAGAATAATACGGCACGTTAAATGTTATTTTAGAATATATA  
AACACCTTATGTCCCATAGCATTGAGCCCAATCGCTGCTGTTTTCCTTATTCGGGGGCAC  
CTTCGGGAAGAACACAGCGCGCAATTTASTTATATAAGGAGAAGCCCTCGAGCGATCAGGGG  
ACCGACTGCGGATCGCTTTAAGGCAAAGATAGAAGGATAAATATCTGCTTTTGGAGGATAG  
TCGTAATCTAATTTCCCATTCGTGTGTTTCTTGTATCTTTCTACGCTTTTCGACTTTCTTC  
CTACGGGCTTTATATAGCTTATGATCTTTCCTCAAGATCCATGAAATTTATGACTGGAAGGA  
GAATTTTCCATACTGCCACAGTAAGGGCTTTCAGTCTACCGCTAAGAAGAGCTTAACTA  
TCCCATTTTTCGGCGTATTACCCCAAGAAACAGGTTGGTGTAGCGGCACTCCCAATGATG  
CCTACGTCUCCCCCUUTGAGAA'AAATAGAGGGCTTCATACCACTGGTATATGGAAAAAA  
TCTTTGCCCTGTCCGTCCGTTCATGGCTACGACGGCTATCTCACAACCGGTCCCTTAT  
CCACTGCAGCTGATTCTTTCTTTCTGTGCATGCTTTTGGCATATTCTTACATCGATTTA  
ACTCTTGTATCACCGATTATATTTCTGAAAGAGTTTATGGTGTTTGGCACAAGTACGCCA  
TGTATAATGTTGGGCGCTTCGTTCTCCGCTCTCCCTTTTGGGAATCTATAAATAGMAACCG  
AGAAATGATGGTGTGTTGCTTTATGTAAAGAGTCTATGGGATTCCTTCGAGAAAGACAACA  
GTCAAAACATTCGAAGCCAGAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)  
MMLPRSMKFMTGRRIFHTATVRAFQSTARKSLTIPFLPVLPQKPGGVKGTENDAYVFPPE  
NKLEGSYHWMKIFALSVVFLAIPFAMLTTHGFLSTAADSFPFVMLLGVCYMEFNSCIITDY  
ISERVYGVWIKYAMMYMLCLGSVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQRIEAK  
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)  
CAATTCCAACCGGAAATTGCAAACAGCAGCAATTTCTCGTACCGATGAAGGGGAACATGG  
CCGTGTGTACCGAGGTTCCATTGGCCGAGTATTAGCCAGGGCCCTAATACGTAACTCGGTA  
CGCTCTTCAGCTTCTTTTCGATAATCAACGTTCTTGTATATGTAAC'ACACCAAGTTCCATG  
GCATCCGCCAAACCTTGCTTCCTTACCAATATTAATGAGCCCTAAGGTGTACATTGCCGCC  
GCAGGTAATATTAGCCCAAGCAGCTTGGCATTTCACTGCGAAAGTAGCTGCTTGATCTCACT  
AAAGATAACCTCAACATACTCTTTTACTTGTCTCTTTTGTAGCTAATTGCTTTCTCTCCC  
CTTCTTTTCCACAAACUGCAACTATTTTCTCTCAAAAGTTATATGAAGTATATATACTC  
AATGGAGCAATTCCGGGTTGAGTGAATTACAAAATTATAGTATCTGATCAACCACACACT  
GGAAGTGCCTCGAAAARCAATATGAGTGTGTGATTTGTTTCCAAATGATAGATTGGTGACG  
AAGATAAA'ACCGACAAC'ITTAAGGAAGCCGTAAAAGAAATGCTCCTGGCTCATCGAAGAAA  
TCGTCAAACCGCAATTACCCCAACATTTATGACAACTTTTCTAAATCCCTAGAGATGCTAG  
AGAGTGACCAAAATATTCAAAATGCCTGTATCTAATCGGTATTCCCAACCGAAAGTAACAAAC  
AAAACGACTCTCCGACGGTAAGGGTGTTATCACAAAGATAAGGCCAATACATGTGTGACT  
TTACATTTGTTGTGATGATTTCCACAAATTTCAAAGGGGTAAACAAGTTATGTTCCGAATGA  
ATACGGGCACTGAATTTCTTACTTATTCATTTCAAGTAGATAATGACCCACTTGAAAAATA  
TTTTTGGAAAT'ACTGAATCAACTTCAAGTAGCTACAGATGTGAGCGAATTCGTATCCAAAT  
TTGGCGTCCGCAATGCAACTTTTGAACCAATCTCTAAAT'ACTTTTACAAAATCCT'CTTAGAG  
ACCTGCTATCTCCAGAGATAACAACCTTGTCTATGAAGGAAATGTTCCAGGATTGTACT  
CAGTCTGCGAATCCACAGCTCAGATCTT'GGAAGTGGAACT'ATACGCTTTGTAGGAATGAGC  
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTAAAAAACCTTGGTGCGAGATTGATA  
GTAAAACTGGCAGGTCAATTTTCGACCAAAATAGAAATCAAGTGACAAATCAAAACAAACA

73/251

AAACCTTTATCTAAGATCCTCTCAGAAAACGGTGTACAGTCCAGGATTCCACATTACTTA  
 ACCACATAATTTCTTCTTTTCAAAGTGAAGCTATAACACTTCCAGAAGCTCAGCAATTAT  
 TAAGAAGGGGGCGTTACTTTCCGATAATAGGGTAGTCATGGAATCTGAAAACCTTAATAGTAT  
 CTACAAGTGAATCCAACCTTTCATCAGTATAAGCGCCAAATTGAACAGTCTCAAAGCTTCGA  
 TGGCGAACCATCAAGCAAATTTGGTAGCTAGCBAACAGTTAAGTACATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGAEDKYDNFKDAVKESWLTERIVKPQLPNIIDNFSKCLEMLESDDQIEK  
 MPVSNIGIPNESNKQNDSPYKGVITRCQYIVDFHIVVRFPPQPRGKQVMFRMNTGILNPT.  
 LIQFSKIMTHLKNILEILNQLQVATDVSEFVSXFGVAMELLNHSLLILLQNPFRDLVFPED  
 NMFAMKEMFQDCYSVCESTAHILGLELTLCRNELCIELRNLIKVTKKPWCBIDSKTGRSF  
 CDQIRNQVTNERNKTLSKILSENGVQVQDSTLLNHIISFQSEAITLPEAQELLRGGVTF  
 DNRVVMCECKLIVSTSDPTLLISISAKLNSLKASMANHQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACCAAGAGATGTTATCGGCTCGGAGAGTTTGTAAAAGCGAAATAGATTGCGTGC  
 AAGTPTTGTGAAGAAACCATCGACAGAATTACAAAGTTATTCTGATGAAAAGCTGCTAA  
 CTAATATTTTAAAGAGAAAGTTGACAGAGGAAGAAAAAGCTCTGTCAAAAGCTCCTTGGG  
 TGAAGAAGTGAGCGGTTCGTCTAACCACTATTTTAAAGCCGCAATTAGTAATGCCAAAAGT  
 TGGCCCGGAATTAGCCCGCGCAAGTTGGTGGGGTCCCTTAATCCGAAAAAGGACCGGCTTTAA  
 CAAATATAAACTCCGAAATCCCCACAGTGACAGAAATTGACAAAACAACCACTTTTGATA  
 TCGCCATACATATAAAGAGATGTAGAAAGCACTCTCTCACTGTAATGTCCAAATCGTACAT  
 TTGAATTTCTTTGTAGGTTTATTTTAAAGGTAAGTTAAATAAATATAATAGTACTTACAAA  
 TAAATTTTGAACCCTAGAAGATGTCGAAATTCGGACAAGAAAAAATGAAGTAAATTACT  
 CTGATGTAAGAGAGGATAGAGTTGTGACAACTCCACTGGTAATCCAATCAATGAACCAT  
 TTGTCACCCCAACGTATTTGGGAACATGGCCCTTTGCTTTTGTCAAGATTATAACTTAATTG  
 ATTCCTTTGGCTCATTTTCAACAGGGGAAAATATTCCTTAAAGGAATCCACATGCTCATGGT  
 CTGGTGCCTTCGGCTATCTTGAAGTAACCGATGACATTACTGATATCTCGCGGTCTGCTGTA  
 TGTTTAGTAAAATTGGGAAAAGAACGAAATGTTTAAACAAGATTTTTCGACTGTGGGTGGTG  
 ATAAAGGTAGTGGCAGACACGGTTCTGTATCCAAGGGGCTTTGCCACCAAATTCCTACACAG  
 AAGAAGGTAATTTAGATTGGGTCTACAATAATACACCGGTATTCTTTATCAGAGACCCCT  
 CCAAGTTCCTCTACTTTATCCACACACACAAGAGAAACCCACAAACCAACCTTACGGATG  
 CTGACATGTTTTTGGGATTTCTCTACCACTCCTGAAAATCAGGTGGCCATTCTATCAAGTAA  
 TGATCCTTTTTTTCAGACCGTGGTACCCCTGCCAACTACCGTAGTATGCAAGGTATTCTG  
 GTCATACCTATAAATCGTCCAATMAAACGGAGATTGGCATTATGTGCAAGTTCCATATCA  
 AAACCGATCAAGGAATAAAGAATTTGACCATAGAAGAGGCTACCAAAATTCGGGATCCA  
 ATCCAGATTACTGCCAGCAGGATTTATTTGAGGCTATTTGAGAAATGAAACTATCCCTTCT  
 GGACAGTTTATATTCAAACAATGACCGAACCGATGCCAAAAAATPACCATTTTCAGTCT  
 TTGAATTTGACTAAAGTATGGCTCAGGGGCAATTCCTTTACGGCTGTGGGTAAAGATTG  
 TTTTGAACGAGAATCCACTGAACCTCTTCGCACAGGTGGAACAAGCTGCCTTCGCCCCCA  
 GTACCACCGTTCTTACCAAGAAGCAAGCGCTGATCCAGTATTACAGGCCCGTTTGTCTT  
 CATATCGGGATGCTCATAGATACAGGCTAGGTCTTAACCTCCATCAAATACCCGTAAACT  
 GTCCATATGCATCTAAATTTTTCAATCCCGCTATCAGAGATCGACCGATGAATCTTAACC  
 GCAACTTCGGCTCAGAACCTACATATTTGGCCAACGATAAATCGTACACGTATATCCAAC  
 AGGACAGACCCATTCAACAAACACCAAGAGGTATGGAATGGGCCAGCTATCCCTTATCATT  
 CGGCAACATCCCGCTGACTCTAGATTTCTGTCAACCAAGAAATCTCTACCGGCTTTTGG  
 GTAAACAACCTGGACAGCAAAAGAACTTGGCATATAACATCGGCATTCTATGTAGAAGCG  
 CTTGTCTCTCAAATACAGCAGCGCGTTTATGATATGTTTGTCTGTGTGATAAGGGACTAT  
 CTGAGGCAATTAAGTAAGTAGCTGAGGCAAAACATGCTTCAGAGCTTTGAGTAACCTCCA  
 AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNYSVDVREDRVVENSTGNPINEPVTQRIGPHGPLLLQDYNLCDSLAHFN  
 RENLPRNPHAHGSGAFGYFEVTDOUTDICGSAMFSKIGKRTKCLTRFSTVGGDKSSADP  
 VRDPRGFATKFYTEEGNLDWVYNNCFVFFIRDPKFPFHITQKRNPQTNLRDADMFWD  
 LTTPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSKNKGDWIHYVQVHLKTDQGEK

74/251

NLTIEEATKIAGSNPDYCCQDLFEALQNGNYPSWTVYIQMTTERDAKKLPFSVFBLTKVW  
 PQGQFLRRVVGKIVLNENPLNFPAQVEQAAFPSTTVPYQEASADPVLQARLFSYADAGR  
 YRLGPNFHQIPVNCOPYASKFFNPARDGPMNVNGMFGSEPTYLANDKSYTYIQDDRPIQQ  
 HQEVWNGPAIPYHWATSPGDVDFVQARNLYKVLGKQPGQOKNLAVNIGIHVEGACFQIQQ  
 RVYDMFARVDEKCLSEAIKKVAEAKHASELSSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

ACCATTCGTCACTTCTCCATTGAGATTTCGAAAAACCCCTCGGCTCTTCTTAGAACTAAATT  
 ACCTTCATAGGGGTGGGATTTATATTGTAATTTCGCGAGGTTTACACGAAAAGATATCTCA  
 ACTCTAGCCGCACATCCATTCCGGTATGTACTCTCCACCATTGGGTATTATAGAATGTA  
 ATACGTTTCAAGCGGATATCTTTTGGCCCGTGAGTTCTTACTTTTTCATTTCGAGCAATG  
 AAGTACATTCTAGAAGTTCTTAGAACCTPATGGAAGCACCAAGAAAAAAGGAAGTTAAAC  
 AAAACACTGATTCAATAAGCAAGGGGGGAAGCTCCTTAGTTTGACGACAGTAACAAAATG  
 TTCTTATAAATTGAACGAAACTCAAGCCAATAAAGCACTTTTCAGAGGCCATCTCTTCT  
 TTTCTCCACAACCTTTTCGAATTAATAACCACTAATAAAAAAGTAAATAACAAAAACAAGAAAA  
 AAATAAACAACAAATAATCAATGTCAAAAAGCTGTTGGTATTGACTTAGGTACAACTATT  
 CATGTGTTGCTCATTTTGCAAACGATACCGTTGAAATTATCGCTAACGATCAACCTAATA  
 GAACGACGCCCTTTCTTATGTGGCTTTTACTGACACAGAAAGGCTAATTGGTGACGCTGCCA  
 AGAATCAAGCTGCGATGAACCCACATAATACAGTATTCGATGCTAAGCGCTCTGATCGGAC  
 CTAAATTCCTATGATCCACAAGTGACCAACGATGCTAAGCATTACCCATTCAAAGTGATTG  
 ACAAGGGAGGTAACCGGTAGTGCAAGTGAATATAAAGGCGAGACAAAGACATTTACTC  
 CAGAAGAAATTTCTCTCAATGATCTTGACAAAGATGAAGGAGACTGCTGAGAACTTTTATG  
 GAACAGAAAGTGAAAGATGCTGTAGTAACGGTTCAGGCTATTTCAACGATTCCACAAAGGC  
 AAGCAACAAGATGCGGGTACAATCGCGGGCTTGAAAGTTCTTCTGTAATCATTAATGAAC  
 CTACAGCTGCCGCTATTGCGTATGGGCTGGACAAGAAATCGCAGAAGGAGCACAAAGCTCT  
 TGATCTTTGATTTAGGTGGTGCTACTTTTGATGTCTCTCTGCTATCCATAGATGAAGGTG  
 TCTTTCAAGTTAACCTACTCTCTGCTGACACTCACTTGGCTGCTGAACATTTCCATACTA  
 GGCTGGTTAACTTTCTAGCCAGGAGTTCAAAACAAAAAATAAAACCATCTAACCACTA  
 ACCAAGTTGCCCTAAGGAGGTTAAGGACCGCCGCTGAAAGGGCCAAGAGAATCTGTCTT  
 CGTCTGCTCAGACATCTATAGAAATAGATTCATTATTTGAGGGTATCGATTTCATACTT  
 CCATTACAAGGGCAAGATTTGAAGAATTATGTGCTGATTTGTTTAGATCTACATTGGAGC  
 CACTCGAAAAAGTTTGGCTGATTCAAAATTAGATAAGTCACAAATTGATGAAATTGTAC  
 TTGTTGGTGGTTCAACAAGAAATTCBAAAAGTACAAAAACTGGTTTCTGATTTTTCACAC  
 GTAAAGAACCAACCGTTTCGATTAAACCTGATGAGGCGGTGGCTTATGGTGCTGCCGTAC  
 AGGCTGCCATCTTAACGGGTGACCACTGCTCGACCAACCAACATTTACTGTTGCTGGATG  
 TTGCACCATTATCTCTAGGTATTCGAACTGCAAGTGGTATTATGACAAAGTTGATCCCAA  
 GAAATTCGACTATCCCAACAAAAAATCGGAAGTGTTTTCCACCTACGCTGACAAACCAAC  
 CTGGTGTGTTGATACAACTTTTTCAGCGTCAAAAGCAACAGACAAAACACAACTCTAC  
 TGGGTAAATTTGAGTTGAGCGGTATTCCACCCGCTCCCAAGAGGCGTACCACAAATTGAAAG  
 TTACATTTGATATCGATGCAATGGTATTCTGAACGTATCTGCCGTTGAAAAAGGTACTG  
 GTAAATCTAACAAAGATTACAATTACTAACGATAAAGGAAGATTATCGAAGGAAGATATCG  
 ATAAAAATGGTTGCTGAGGCAGAAAGTTCAAGGCCAAGATGAACAAGAGCTCAACGTC  
 TTTCAAGCTAAGAAATCAGCTAGAACTCGTACGCGTTTACTTTGAAAAATTCTGTGAGCGAAA  
 ATAACTTTCAAGGAGAAGCTGGGTGAAGAGGATGCUAGGAAATTGGAAGCCGCGCCCAAG  
 ATGCTATAAATTGCTTAGATGCTTCGCAAGCGCCCTCCACCGAGGAATACAAGGAAGGC  
 AAAAGCAACTACAAGCTCTTCCAAACCCCATTTATGACTAAATTTTACGGAGCTCCAGGTG  
 GTGCCCCAGGAGCAGGCCAGTTCCGGGTGCTTGAGCAGGCCCCACTGGAGCAACAGACA  
 ACGGCCCCAACGGTTGAAGAGGTTGATTAG

>YER103W, 642 aa (SEQ ID NO 146)

MSKAVGIDLGTTYSCVAHFANDRVEIIANDQCNRTTPSYVAFEDTERLIGDAKNQAAMN  
 PHNTVFDKRLTGKFFDDPEVTNDKEYPFKVTDKGGKPVVQVEYKGETRTFTPEEISSM  
 ILTKMKETAENFLGTEVKDAVVTVFAYFNDSQRQATKDAGTIAGLNVLRINEPTAAAAIA  
 YGLDKKSQKEHNVLIIFDLGGGTDFVSLLSIDEGVFEVKATAGDTHLGGEDFDSPLEVNFLA  
 EEFKRKNKKDLTTNQRLRLRTAERAKRTLSSAQISIEIDSLFECIDPYTSTCRARF  
 EELCADLPRSTLEPVEKVLADSKLDKSLQIDELVLVGGSTRIPKVQXLVSDFFNGKEPNRS

75/251

INPDEAVAYGAAVCAALLTGDQSSTTQDLLLLDVAPLSLGIETAGGTMTKLTFRNSTLPT  
 KKSEVFSTYADNQPGVLIQVFEGERTRTKDNLLGKFEISGIPPAPRGVPIEVTFDIDA  
 NGILNVSAVEKGTGKENKTITNDKGRLSKEDIDKMVAEAEKFKAEDEQEQRVQAKNQL  
 ESYAFTLKNSVSENNFKEKVGEEDARKLEAAQCAINWLDASQAASTEYKERQKELEGV  
 ANPIMSKPHYGAACGAPGAGPVPGAGAGPTGAPDNGPTVEEVD

>YER150W, 947 bp, CDS: 501-947 (SEQ ID NO 149)

ATACCGCGGGAAGAAGAAATATCATATTCAAGCTAATTCATTGAAATTAGTGTCTGCTC  
 ATCTAGCCCTTTAGTCCCTTAATCTCTCGAGCAGCACATATGCCCTTAAACCCATGCCCGGA  
 CTGGGGGGCCCCATCGGGGCTCGAACCCGAATCCCCGCGAGTATTTATTTGAAGTCCCGG  
 ACGCAAGTTACCTAATCTGGTTAATTGATATCCCATTTAGGCGATGAUGTTCTTCCCT  
 CACCCCTCGGCTTCTTACAAGATCTATTCTTATAGCCCTCCCTCTGGAAGAATTTATGCCAG  
 ATPAAAGAAAAAACTTCTCGAAGTTCCCGAGATGCCCAAATGAGGGCTTTCCATCCCTGTT  
 AGCTGCAAACTCTAAGTATATCTATATAAAAAGTCCGCTTACTTTTGGCAGGTTCCGTCT  
 TTCACFTGCACCTCTCTTGATCTTACTTTCTACTCAAAAACAATCCAATACACAAAATAA  
 AATCAGTACTATTACTAATAATGTTGTCTAACGCTAAGCTCCCTTCTATCATTGGCCATGG  
 CCTCTACGGCTCTCGGATTGGTATCTAATTCTAGTTCCCTCTGTAATCGTGGTACCATCAA  
 CGGATCTTACTATTCCCCGTAACGATACAGCCACCCCAAGCACCAGAGCCATCATCCGCCG  
 CTCCAAATATTCTACAACTCGACTGCTACTGCAACACAGTACGAAGTTGTCAGTGAATTCA  
 CTACTTACTGCCAGAACCAACGACTTTTGTAAAGAAATGGCGCTACATTCACCTGTTACTG  
 CCCCAACTACGTTAACAATTACCAACTGTCTTGCCTATCGAGAAGCCTACTTTCAGAAA  
 CATCGSTTTCTTCTACACATGATGTGGAGACAAATTCTAATGCTGCTAACGCAAGAGCAA  
 TCCCAAGAGCCCTAGGTTTGGCTGGTGCAGTTATGATGCTTTTATGA

>YER150W, 148 aa (SEQ ID NO 150)

MLSNAKLLLLSLMASTALGLVSNSSSVIVVPSSDATIAGNDTATPAPEPSSAAPIFYNS  
 TATATQYEVVSEFTTYCPEPTTFVCTNGATFTVTAPTTLTITNCPCTIEKPTSETSVSSTH  
 DVETNSNAANARAIPCALCLAGVMMLL

>YFR033C, 944 bp, CDS: 501-944 (SEQ ID NO 155)

ATCGAGCCATTTCGCGGTCTGCTGAGTAAGCGACGGTCATCGGGCGCGCTCGTGGACGATGA  
 CAACCGCGGAATCACACAACCATCCACACCAAGCACGGCGTAAATCGATTAGCGCTCGCGCT  
 GCACGAACCTGGCGTCTTTAATCCCCGCGGCACTGGAAACAGCAAAATCTGTGGCGCGCGCC  
 GTCCAAAGCGATCACCGTGGAGGGCGGCTTCCCGGTACATCCGTCACCTACAGCAGAACGT  
 GAGCAAGTTGACCGTTGCACCAATGGGAAGCACGTTCCCGGGCATATCGGACTGGGGCGCGCC  
 TCCCTTGGCGGCTGCTTCTTATAAGAGCGGCTTTGCTGGAAAGTGGCCACACCGGGTTT  
 TCGAGATTAGGACCTACTCAGTCTTAAGGGCAGTATTGGTTGGCGCTTATTTGCACATAT  
 TGTATACAGGCACTCACATTAACAGAAGCACACATATACACTTACACCTACACACACCGGA  
 TAAAGAAAAAGAAATAGAAAATGGGCATGTTGGAAGTAGTTGGTGAGTACTGGGAACAAC  
 TAAAGATAAACCGTTGTGCTGTGTGTGGCGCGGCGCGAAGATGACGATAACGAGCAGCATG  
 AAGAAAAGGCAGCAGAGGAGAAGAAAAAGAAGAAGAAAATGGGGATGAAGATGAGGATG  
 AAGACGAAGACGAAGATGATGATGATGATGACGACGAAGAAGAGGAAGAGAGGAAGAAG  
 TCACTGATCAGTTGGAAGATTTCAGAGAACATTTCAAGAACACGGAGGAGGGTAAGGCCC  
 TTGTGCACCACTACGAGCGAGTGTGCTGAGAGACTCAAGATACAGCAACAACAACCCGGCT  
 ACAGCGGATCTTGAAACAAAGGAGGACTGTGTGGAGGAGTTTTCATCTACAGCACTATT  
 TGGACACTGCCACGGCACCTAGATTATTTGACAAATTAAAGTAG

>YFR033C, 147 aa (SEQ ID NO 156)

MQMLELVGEYWEQLKITVVPVVAADDDNEQHFEKAAEGEKEKEENGDEDEDEDEDEDD  
 DDDDDDEDEEEBEVTDQLEDLREHFNTZEGKALVHHYBBAERVKIQQQQPGYADLEHK  
 EDCVEEFPHLQHYLDATAPRLFDKX

>YCR086C, 1520 bp, CDS: 501-1520 (SEQ ID NO 175)

GTTGAATATTTACCAATTEGGAAAAAGAACTCGTATTTTCATTCCCCTTTTTTGAAGGGG  
 TGGGGAGAGACTGTTGTTTCAGCCACGTCAATTATTATTTTTTCTTTGGCCCTGCGCTTGT  
 CTTATAAAATTCGGCAGCCCGCTCTTATTTTTTTTTTTTTCCATTTTGGCCCCACAGGTC

76/251

ATATFGCAAAAACCGAATGGCCGCGCCCCCTCAGGCACTGGACGGGAAGAGGGGCGCGT  
 CCCCCTGTTTCTTCTGCTTGGGCTCAGCTCTTGGGCTCCGACGGACGAAAGACGGGATCCCC  
 CTTCCCGTGTCTTTTATAAATAACAAGTGCCTATTCTGCATCCTTCCTTGTTCCTCGTC  
 GFTTGGGTACAATGCGTTGATTATCCCAACCCAAAGAAAGAAAATTTGTCTCACATCTGCA  
 TCTGCACATTTATTTACCTATACTTTTCCATTGTTACCAGCTATTGCAAAGTCAAGAATAT  
 ATCAGCATCAAGTATATACTATGCACAGAAGTTACTCTTTAAGAAATTCAGGGCACCCTA  
 CCGCTCTCAATTACAGAACCCACCGCCACCACCCTCTACAACCAAAGGTAGATTCTTTTG  
 GGAAGGGTGGTCTAGCTTACAGCTTTAGGACAAGTGGTGGTGGAGCTTTTGGCCCGAAT  
 TATCCAGAAAAGTTGTTCAATTGGTTAAGATTGAAAAGAAATGTTTGGAGTCCATGGAAAT  
 TGACAGCCAAACGAAAGACGTGACGCTGCTAAGCAATTCTCTATTTGGGGGTTGGAAAACG  
 ATCAGCATCTTTCCGACATCACTGATAAATTAGGTCCTCTTGATCTATGAAGTTAGTGAAT  
 TAGACGACCAATTTATCGATCGTTATGACCAATACAGATTGACTCTAAGTCCATCAGAG  
 ATATCGAAGGTTCTGTTCAACCATCTAGAGACCGTAAGGACAAGATCACCGACAAAATCG  
 CCTACTTGAAAATACAAAGNTCCTCAATCACTAACATTGAGGCTCTGGAAACAAGATTGG  
 TCGTGGTGGGCTGAATCTTTGGTGGTGAAGCTCAATTATCTAATATCACAGGTCAA  
 AGTTGAGAGCTGCTTTCAACTACCAATTGACTCCATCATCGAACATTACAGAGAAAATTG  
 CTTTAATCGCTGGTTACGGTAAGGCTCTCTTGGAACTATTGGACGACTCTCTGTCTACTC  
 CAGGTGAAACCAGGCTGCTTACGATGGGTATGAAGCCTCTAAACAAATCATTATTGATG  
 CTGAAAGCGCACTGAATGAATGGACACTAGACTCTGCCCCAAGTCAAGCCTACTTTAGTT  
 TCAAGCAGGATTACGAAGACTTCGAACCTGAAGAGGCGAACAACAGGAAGAGGAAGACG  
 GTCAAGGCAGGTGGTCCGAGACCAACACACATCCACAAATTGAAGAACCTGAACAAG  
 AAGAAGAAGGTGCTGTTGAAGAACATGAACAAGTGGACACCAGCAAAGTGAGTCTCTTC  
 CCCAACAAACAACAGUTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MIRTYSLRNSRAPTASQLQNPPPPFSTTKGRIFGKGGLAYSFRRSAAGAFGPPELSRKLSQ  
 LVKIEKNVLRSMELTANERRDAKQLSLIENDDVSDITDXLGVLTVEVSELDNQFTD  
 RYDQYRLTLKSIRDIEGSVQPSRDRDKITDKIAYLKVKDFQSPKIEVLNQHGVRAEAE  
 LVAAEQLSNITRSKLRAAFNYQFDSIIHSEKIALIAGYGKALLELLDDSPVTPGETRPA  
 YDGYEASKQIILIDAESALNEWTLDSAQVKPTLSFKQDYEDFEPEEGEEEEEDGQGRWSE  
 DEQEDGQIEEPQREZGAVEEHEQVGHQQSESLPQQTAA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATTATGCCTTGCACACCTAAAGCACATATTTTCGTTATTTTTTAC  
 CACAATAGGTGGATCTCGAAAAGGATGGAAAATCAGGAAAAGAAATGTTCCACAAAAAA  
 TAAACCGATTCCCCTTTAGTTTCTCTCTATTTCCGTTATATGCGTGGTTATTGCTTTTC  
 GAATCCTTTTATGAATGTCCGAGGAGGTGTTACAATCCGAAATAGACTAAAGAAAAGCGA  
 AAGUCGTGAGTTTGTGTTGATGATAGATGACTCCGAGCTTTCTCATCAACGGGGCCACCTA  
 TTCCAGAAGAGGAATGGAAAACGGACTGGCGTAGTCAATAAGCGTCTTCATATCTTAGCA  
 TTGTTGAGAGATACATAGTGTACTCCATATCGTTCTTTTTTTTTTGTATATATCAAGCCAC  
 ATATCCTGTTCCTTTAATCTTTTAACGUCGTAAGAATCGGGTACTGACATAAGTGTAAAG  
 TAGCCGTACAGAGAACAATATGACTAATCGGTTGGTGTATGAAGACTCACAGTACATTTG  
 AGGACCTTAGTTTTGACAGCAGCAGCTGCATTTACTGGCGGCAGGGACGGGGTTCTGTAQA  
 CTAAATCAGCCATTTCCTGAGCGTTCCCGCCATTCTTTCTGACTTAGCAAAGTCAATTGAAG  
 ACTATCGGCCCTCTGATGAAAAGCCGCTCTCATTTGTCATCTGTGGCCGACGCTGGCCCTA  
 ATGAGGAAGACAACGGCGGTAAAGACGGCGGTCCCTTGGCAAGAATTCAAACAGGGCTTT  
 TTTCTCCAAGACTGCGAAATCATAGGAAAAGATTCTCTGGAAGTTTGTTTTGAACAACCT  
 TCTTCATTGCTTGTGTGTGTATCGCTCATATCGATTACTGGGGTGCCTCTTACCGAA  
 CACATCCTTACTTTTTCAAAGTGAATAATATTGTTGTATTGCAGGATGCGCCATCTAATA  
 CTTCAGTTCAATCTATTTCCGCGATCATACCTCATTTGTTAGCGTCTGTCCCGGGACAT  
 GGCATATATACAACGCAACATCAATTTTCATAGGAAATTTGGTACGACGAATCCACCGAAA  
 TTGACAGAAAGATAGTCGATTAAATTTACGATGAGAGATACTGGCTGGCGTTAAACGTPA  
 AACCTAATGCTACAGACACTTTGTATAATTCTTTGATTAGCCAAGACGCAAACTCGGAGT  
 TCAATTCATCAATTTTTTTTGAATCCGTGTTTGAAGTGGTGGTGAACCATCGAGTGTTA  
 AATCGACATTCTTACCACATGCAACAATTGGAGTCCGCTTCAGAAATATTACGTCA  
 AGGAATATCTTCCCTCATTGATGAGCAACATCACTTCTAATGACAGAGATCTTAATATAA

77/251

ACATGGGAGAACTGGGUGATTGCAGGACAGTTGTGTTCACCTACAACGATTATCGTCCCT  
 TTGCTGATCGTATTTCTAATGGCCCCCTCTGCAGGTCGGTCTGATTTATTGTATTTTGTAA  
 CCGCTTTACAACTGTCATTATATGGTAAGCTGCACGGAGAAATGGCCACAGTTCTGAAGC  
 CAAAGCATATTTAATCTACAGGUTTTCTAATTTCTCTGGGCAACTATTTTCTTCTTTCCA  
 TTGGATTCTCTACCCCTATCTGCAATTTTATAGGATCGATTTCACCCCCGCCTTTGGCAGAG  
 GAGGATTCTGTAGTATATTGGATGTCTACGTGGTTTCTAATGATCGCTCTTGGTGGTGCCA  
 ATGAAAACCTTCTCAGCTTAGTTATAGCTTACTGCCCTCCATACCTCAGTATTTGSETTGA  
 TGACGTGGATCATATTTAAATATTTCTCTCTTCAATCTACCCAATGGTTTTGAACAACGAAT  
 TTTCACAGGTACGGCTACATAATGCCAATCCATAATGCCGTGGATATCTATAAAGTGAATTT  
 TTTTGAATTTTAAACAAAAGAAAAATCGGAAGAAATTACGGTATTCTCGTGGCATGGGTTG  
 CCGTCAATACATCTTTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAAA  
 ATGCTATGCAAGCAGCAGAAGCCGCTGTGCGCAGCAGCTACCCAGCGTGTAGTCCCCCGG  
 CAGAGGCCAATACTGATAAAAAATAACAACCCGCCCCGAAATTAA

&gt;YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGDDEESQYLRPSFAAAAAATGGRDGVSYSNQRFAEGSGHSSDLAKSLEDYRPPDE  
 KPSSTSSVGEGCANEFKGCNDGGPLARIQTGLFSPLRLNHRKKILSKFVLNNFFIACVC  
 VSLISLYWGACYGIDRYFFKVNINIVLQDAPSNSTSVQISAIIPSLLASVPGTWHIYNAT  
 SFHRKFGPTNSTEIDRKIVDLIYDERYWLALNVKPNATDTLYNSLSQDANSEFNSSIFW  
 KSVFESGRDPSSVKSTILPLMQLEVRLOKYYVKEYLPSLMSNITSNDRDLNINMENWAL  
 AGQLLPYNDYRPFADRIILMAPLQVGLIYCILLTVLQISLYGKLHGEMARVLKPKHILY  
 KLLISWATYFLLSIGPTVSAIFRIDFTPAFGGGFVYWMSTWLVMMAVGGANENVLSL  
 VLAACPYPVLSIWLMTWILLINISASFYPMVLNNEFYRYGYIMPIHNAVDIYKVIPLNLTKR  
 KMGRNYGILVAVVALNISTMPFCKMPAGKKMQKNAMQAAEAAVAATQRASRPAAENTDK  
 NNNPPGN

&gt;YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCTTGTGTACGTACGATGTTTCTCCCCGTGATCCGATTACTAGCCGAAGACGTAAAAATTG  
 GCGCTTGATTCAATTTATGCCCTTCCCGGAATAGTTGACCAAAGGGCAAAAAAATTACAG  
 TCGGAGATTCCCTATTGCGCGGAATTTAGTAGATCTCTTTCCGTGCATAACCCCTGCCCG  
 TTAGTCGTTATTTACGTTAACATTTTCTTGCCCACTGCGCTATATAAATAAATACATAT  
 ATATATGTCAAGCACAAATAAGAAACTTCCCTTAAATATTGAATAACTAAATAATAGTTG  
 AAAAGTGGCTTTTCTTCCGAAGGATTAGAGTGTCTTAATTTTAGTTCTGTTCAACGGTCTC  
 AAAAAAGTGTGAACAAGTAAAGCATAGCACACATCCCAAATTACAAGGCACCCCTGATTA  
 AAAATCCAAAAATAAACCATTAATTTTATTTTACTAAAAACATTATACGTGAAAGACAAA  
 CCGCATCAGAAGTTTCGAGGATGAATATTCCAGAAGAACCATCAGATGAAGTAATATCTA  
 GTGGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGAGCGCAGAAGCTGGAG  
 ACCAATCAATAAAAAATTGAAAGGAAAACCTCCACTGGTCTTCAACTGGAACAATTGGCCA  
 ACACAAATTTATTAACCATTAAGATTAATATGGCAGTTACAAAGAAGAAGAAGATGATCACT  
 GCAACTCTAGAATAACCGATCAATAATGGACACAATACAGCACTACAAAGGTATCTCCG  
 TTACAACTCTGATACAGAAACATATGAATTTCTTCCGGATACAAGGAGGTTACAGGTTT  
 TCCAAACAAAATAAAGACATCTATCTTTACGAGCATGGAAGTCAAGAGTATGAGAAATCTT  
 ACAAGATAACGAAGAGGAAGATGATTTGGAGATACGATACCGTTTTTGCAACCACAATTCA  
 AGTACCCCAAGTCATTAGAAAAATGCATGTAACAGATATCTCGGAATTACTCAAGAGCGAAC  
 CTATTTGGTCAGCATATTGATAAATGGTCTATCGGTCTGMAACAAGCATGCCTAACCTATC  
 CTGGAAATATTTTTTGTCCGGCGAATAGCAAAGACCCCTTTCTATTCCCTCAACTAAGTTTCT  
 TATTTTCAAAATATGGACCAATTTTATCAATGAATTTGATATATGATAAAACGAAAGGCG  
 AACCTAACGGATACGGGTTTATCTCTTACCCCTTGGGTTCTCAAGCTTCACTTTGCATCA  
 AGGAACCTAATGGAAGGACCCGTAATGGCTCCACACTATTTATCAACTATCACGTTGAGC  
 GAAAGGAGAGAGAAAGAATCCATTGGGACCATGTCAAAGAAACACAACATGATGATAACT  
 TCAGGTGTCTCTTTACAGGCAACTTGCCTTATCAAAATCCTGAAAAAGTAGAGACTTTGA  
 TTACACCTAAAGCAAGTCTATCAAGTAATCAAGAAAGAGTTATCAAAAAAGTTTCCCGGAC  
 TTGATATCATTTTATATTACTTTCCCAAGAGAGTAATCAAGAAAGCAGTACGTTACAGTAA  
 GTTTCAATGAGGAGGGGTCAGTAGAATCAACAAATCTTCCAATAATACTAATGGAATG  
 CCCAAGATGAAGATATCTTGAACGGTTATGGTTTCATCAAGCTTATCAACCATGAACAAG  
 CACTAGCAGCCATCGAGACCTCAATGGGTTTATGTGGCATGGAAACAGGCTCGTTGTTA

78/251

ATAAGGCGGTTCAACATAAAGTTTACACAAACCACAATAGCCATGACAGGCACCCCTTCCA  
 TCAGTAACCACAAATGATATGGAGCTTTTGGAAATTTGCAAAATAACCCAATGTATGATTACA  
 ATAATTATACATATGATAGATATTACTTCAACAAATAATAAAAACGGGAACAGCAACCATA  
 CCTCCAAATGTACGGTATTTTGTATTCTGTAAAGATCAACCCCTGTGGCAGAGAAAATGGATC  
 TGTTCIATCCTCAAAGGGGAATCTTTCAAGTGAAGGTCGTGCTCAACGGTGTCCCTAGATTCA  
 TGGGCAACAAGTTTGACATGTACCAGTACCCATCAACTTCTTACAGCTTACCTATAACCAA  
 TGAGTAATCAGCAAGAATCAAAUCTATA'GTCAAGCACATCCCTCTTCTTGCACAGATG  
 AAGATTTATATGATTTCTACAAATCTTTCCGGTGAAATAATCAGCGTTAAGGTCATTACTG  
 TTGGGGGTAGTAAGAACAAGTATCGTCAACAAATCGAATGATAGCTCATCAGATAATGATC  
 TGCCAGTGGGATCATCAAGAGGTTATGGT'PTTGT'PTCT'PTTGAAGCCCATTAAGATGCTG  
 CTAAGCCAATTTTGAATACAGACGGGTATCAAGTGAGCAAGATCAAGTGTATCTGTTT  
 CTTTCGCTCAGAAACGGTGGTAATTTATCTTCAAGTGAATCATCATCAATCCCAAACCTC  
 ATAACTATCAAAAGTTCCAAAATTTTTCAGCCACATAATGATTATCATAAGGCTTATCCAA  
 CAAAGTATAATAAGAAAATCTATCAATGCCCTTGATGACTTACGAACCAATCCCAACAGCAAG  
 TCTCGAGGGGAAAATTAATTCATACCACATGCAATACCTTAATACCAACACAAAGCCCGTGA  
 ACAGTTACAACCTAATAAGTGCAACCAAAATAACGCTAACTGGATGATGCCAATGTTCC  
 CATCATTTGGGTTTATTCCACAGGTGCCGCCAGTCCCTATAT'ATAAATCCTCCGCAGAAATC  
 CTGCAGCAAAATCATATTCCTATAATGGCAACCGTAGTAATGAAGAGGAAGAATTTTCTA  
 GTGGT'GAT'PA'PTTATGGAATACTAG

>YCR250C, 781 aa (SEQ ID NO 192)

MNIAEEPSDEVISSGPEDTDICISQOTSASAEACDQSIKIERKTSTCLQLEQLANTNLLTI  
 RIKWQLQEREDDHCHNSRI TDQIMDTLQHYKGISVANSDDTETYEFLPDTRRLQVLEQNKDI  
 YLYEHC SQEYEKSYKDNNEEDDWRYDTVLQAQPKYPKSLENACTDISELLKSEPIGQHID  
 KWSIGVNHALTYPGNIFVGGIAKSLSIGELSFLFSKYGPTLSMKLIYDKTKGE'PNGYGF  
 ISYPLGSQASLCIKELNGRTVNGSTLFINYHVERKERERIHWDHVKENNDNDMFRCLFIG  
 NLPYHNPEKVETLITPKEVIEVIKKELSKKFPDFCLISYYPKRSNTRSSSSVS'NEEGS  
 VESNKSNNNTNGNAQDEDMIKGYGFTXILNHFGALAAIFTFNGFPMWGNRLVFNKAVQHX  
 VYNNHNSHDRHPSISNHNDMEVLEFANNPXYDYNNYTYERYYPNNNKNNGNSNDTSNVYF  
 DSVRSTPVAEKMDLFYPQRESFSEGRGQKVRPRFMGNKFDMYQYPSTSYSLPIPMNQQES  
 NLYVKHIPLSWTDEDLYDFYKSFGEIISVKVITVGGSKNKYRQQSNDSSENNDLPVGSRR  
 GYGFSVSFESPLDAAKATLNTIGYQVSKDQVLSVSFAQKRGNLSSDDDDQSQTDNSSKFQ  
 NFQPHNDYHKAYPTKYWKKFINALMTQNSQQQVSSENYFIPLOYPNTNTKPVNSYNTIS  
 ANONNNANMMMPHFFSFGFIPQVPPVPYLIIPPQNPAANILPIMANGSNEEEBFS SGGVSMO  
 Y

>YHR001W-A, 797 bp, exon1: 501-506, intron1: 507-569, exon2:  
 570-797 (SEQ ID NO 195)

TTCTATTCGGGCTTATAAAAAGCAAGGAATCCAAAAGAATTAGGCTTCTCATTCATTTT  
 AATTATACTAGTAGCATTTCTCACCTCTGTAATTTAATATCAGTGTAAATATGCACCTAGTT  
 ATCGGTAGTTTTTGTCTAACCTTACGAGCCGCGAAACTGTCTCTCAATCTTCACCACTACCT  
 CTAATGACTGAAGAATGCTATGCCGATATAACGCTGTGCGACTT'NGAATAT'ATCTTA'AT  
 TTACATAGTTTTTCAAGTGCGTATTACCTATTGCAAAGTAGTA'TTTTGTUACGTGATTTTGA  
 TCCAATCAAACTAAATATGGTTCAACCCGTTGTTTCCGCATCAAAAAACCATACCATTT  
 ATCAAGGGGACGGGATATATCACATAACAGTTTGAA'AGCATAA'TTGT'TATAGATA'K'UT  
 CTGGAATAATCTTCACAGCAAAAGCGCAAGTGAATAATATATCGATAAATACAATCCAT  
 AAGACTTAAACTAACCTCAATGGCGGTAAAGTATCCTATCATATTTATGTGAGCTAGAACC  
 GAATTAGTATACTAACATTTATAATACAGTACACT'PTCTCATCTGTCTTCAAAAAC'GTGTC  
 TACATTTCCGTAGACTTTCTTTAAGAAGTTTACAGCTTATGCTCCGAATTTAATGTTAT  
 GGGGTGGTGTAGCATGCTTGGGCTATTTGTATTCACAGAGGATGCCCTAACTTTTCAAC  
 ATACGCTATACAAAAGATTCGGTTGTTAGGACCTACATTGGAAGATCATACTCCACCAG  
 AAGATAAAACCTAATTGA

>YHR001W-A, 77 aa (SEQ ID NO 196)

MAYTSHLSSKTGLEHFGRLSLRSLTAYAPNLMMLWGGASMLGLFVFTEGWFKFQDTLYKKIP  
 LLGPTLEDHTPPEDKPY

79/251

&gt;YJL142C, 893 bp, CDS: 501-893 (SEQ ID NO 225)

TGCTGAATTAATTTTGGGTATACCGATCTTCCCAGGCGCTTCTGAATATAACCAATTAAC  
AACAATAATACACCGCTTGGATATCTCCATCGTGGATGATAGATATGGGTAAAACTC  
TGGAAAATTTATGAAGAAATGGGCACCAGAAGAAAGTTCTTCTTCTACACAAAAGCATCG  
TATGAAAACATATTGAAGAGTTCTGCAGAGAATACAAATATAGTGGAAAAGCCCAGTAAACA  
ATATTTTAAAGTCCAGAAACATTACCAGATATTTATTAGAACTACAGGTATCCTAAAAGCAT  
ACAGAAGTCCCAAGAACTTATCGACCAAGAAATGCAGAATAGGGAGTGTTCATCCACTT  
TTTAGGGCGGTGTGCTAAATTTGAACCCGTTAGAAAAGATCGACACCACAACAAGCTATGCT  
ACACCCCTTCTAAACAAAGCAGGAGTTTACAGGTGAGTGGTTTCTCCAGGATCGTCTTT  
ACCGGGTCTCTCAGAAAACATGACGATGCAAAAGGCCAGCAAGTGAATATGGAAGTGC  
GAACGACTCTAGTAACAATGCLAGGUCACAACTATGTCTATATAATCCTAGCTCTGCCACTGG  
TGGTGTCTGATAGCGTCCGACATTTGGTGGTATCAGTAAAGGAAGGAGAATACATCTGGCGA  
CATCTCCAATAAATTTTGGTGTCTTACTCATCTCTGTTCCAGAAAGGCCCAACAAGCCCGTTCAA  
TAAACTTCACATTTGTGGAAGAAATAATCGTTATTTTGTCTGACTTTTCTTAAGTACCCAT  
TTCTATTTTATTACGGCTTGGTGGCATAATGATATACTAAATAAATATGAATTTTGCCCTTT  
CTTTAAATTTCTTTATACGTATAGTCAATTACAAATTAATAAAGTAAACAATTATAA

&gt;YJL142C, 130 aa (SEQ ID NO 226)

MTNQKASKVNMEVRTTLVTMQATTMSIILALPLVVLIASTLVLSVKRRRIHLATSPIILL  
LLILFKKQQQARSINFLLSKNKSFLCLPLNYPFHFITAWCHNDILNKYEFCLFLIFLIR  
LVITINKVTL

&gt;YJL144W, 815 bp, CDS: 501-815 (SEQ ID NO 227)

AGAAAGAAGTTTCGTGGTATTAACCGACGGCAGCAAGTTGGGTCAATACTTGAAAGCATTCG  
CCATATGAAGGGTATGUGUGGGAAGATAAGAAGAACAATCTGAUUAAGCAAAATGTCAACA  
AATGTCCATCCAACAGAAACACGGCCTTTACATTTTACAAAAACAAATCATCCAGGACCTT  
GAGTCATTTGTTGGCATGATCTAATAATAGTCTCTTATATAAACCTATAATAATTTCTT  
ATTTTTCCCTTATATTTCAGGTAAATCACCATCTAACTGTATTATCTCTCAGGTACTTCA  
CTTATATGGCTCAGAAAACACCGTACGAAACGAAGGGGCTGGGAAAATGTTTCTAGAAGG  
TAATGGCAATAATAAGGATACAGATCCGATCAGATCCGCTTATATAAAGACAACGCACCG  
AAGGTGAACAAGATCGCAGATAAAGGTATTTACAAGGGAAAAAAGTCAACAAAAACAAGA  
GATAAGATAAACAAGAAGAGATGTTAAGGAGGGAAACTTCAACAATATACAGGACACACA  
AAAAAAGCAACAGTAGTATACTCAGGAGCCAGCGGGACCAGACTAGAGTGGATTCTCTGG  
TAGAGGAGTCTCCCATGGCCGATTTCCGGATCAATAACCAGCTTACACAGCTTCCCGTGA  
TATACTACTTTGTAGAGCTGACTAATTTAGGCATACAGGAAACACAAGCAGTAATAATA  
ACAACAACAATAATCATGGTGACGATGAAAACGGCAGTCCGATACGGCCACGGCAGCAGTC  
TGGGTGGAGACCTTCACTCTCGCCCTTCTTCATGA

&gt;YJL144W, 104 aa (SEQ ID NO 228)

MLRRETSTIYRTHKKSNSILRSQRDQTRVDSLVEESPMGLFGINNQPTQPGVIYYFVZL  
TNLGIQENTSSNNNNNNNHGDDENGSRYGHSIAGGVHSHRCS

&gt;YJL166W, 785 bp, CDS: 501-785 (SEQ ID NO 231)

TGAACAGCTATACCACGAAATGAAGAGTCTATTTGCCAAGGATTTGAAGGCCAAAAATTC  
TCAGGTCCATGAGTCTCGTGGCTTCAAAGCTGATGTCTTAACTCGCTTCTTGAACAAAGT  
TTACAAGAGAAGCAATAGAACTAACGCTAATCGATAAAPACATTAGATTTCAAACTAGAT  
AAGGACCATGTATAAGAAGTATATACCTCCAATATAATATAGTATAAGCTTTAAGATAGT  
ATCTCTCGATCTACCGTTCCACGTGACTAGTCCAAGGATTTTCTTTTAAAGCCAAATGAAAAT  
GAAGAAAATGUGTGTATCGGAAATTAAGGGTAGTACGAGAAGGAAATTTGAGCCACCCCCCA  
AATTTTATTATATAATAATAGGAAAAGCAACGACCTCATCTCTCGAACATTGTTTACTT  
GAGCAACTCCGATTAACAGTAAGTCTCTGTACGTTAAATACAATAATCAACAAAACACT  
ACACAAAAAATTTCTACGATAATGGGTCTCTCAAGCGGTAAAACCTTACATGGGATGGTGGG  
GTCACATGGGTGGTCCAAAGCAAAAAGGTATAACCTCATATGCTGTGTCTCCATATGCTC  
AAAAGCCATTACAAGCTATTTTCCATAACCGTGTATTCAATAGTTTATAGAAGATTAAAGT  
CTCAATTTCTATATGATTAATACCTGCGGGAATTTATTGGTACTGGTGGGAAGAACGGTA  
ACGAGTATAATGAATTTCTGTACAGCAAGGCTGGTAGAGAAGAGCTCGAAAGAGTTAATG



80/251

TTTAA

&gt;YJL166W, 94 aa (SEQ ID NO 232)

MGPPSGKTYMGWNGHMGSPKQKGI'ISYAVSPYAQKPLQGIFINAVTNSFRFPKSSQFLYVL  
IPAGIYWYWKNNGNEYNEFLYSKAGREBLERVNV

&gt;YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATACAACTGTTTTATGTTTTAAAAGAGCTTGTATAGTAATCTAAGTGGAAATACACT  
AACAGTAAATAGGGCGTGTGGCGTAGTCGGTAGCGCGCTCCCTTAGCATGGGAGAGGTCT  
CCGGTTGCGATTUCCGACTCGTCCAACTCTTTTATACUATTATTAATAATTTT'TTCTGCGG  
TTACTTGCCTTTTAAAATAACTGCCCTTTATGAATACAGAGTATAATTTTGTATATACAAA  
EAGGTTGACTGTGATAATCAATACTTAATTTGTGGTTATTGTTACACATATACCTACAAA  
AGTTACCAACAACTGTTUGACTTTTAATGCTACCCGCCCTTCCGAGTGT'TTTTGAAGGGG  
CCGACACGAGCGGCAAGAATTAGCATGGAAAAAAGCATAAAAAGACCAAAATCGGTGGCAA  
TGTAATTAACCTTGTTTCGAGAAACCTAGTGGACTCAATTCAATTAACAACAAGTTTCCCAAG  
ATCATCGATTTCATAATAGTCATGTCCGATAAAGTTATTAAACCTCAAGTGGCATGGGCTC  
AAACCTCTACTACTACTGATCCAGAAAGAAATTATGTCTTAATAACTGTGTCAACTGCAG  
ACTGTGATGCCCTGAGTCAACCAATTAAGCCATCATACATCGAATTAAAGGCTCAATCAA  
AGCCTCATGTTTGGGATGAAAATGTUATUAT'PAICAAITACACAT'GATCTATACAAAGG  
AAATTACACTGAAAAAACAAATGCATAAGGTTGCTAATGGCCAGCACTACTTTT'GAAAAT'  
TGTATAAAAAGGATTTAGAATCTGAATACTGCCACGTTTGACAAACGAAAACCTGAAGT  
ACCCTTACATCAAAACTGATTTGATATAATCGGTTGATGAAGATGAACAGACCAACTTC  
AAGCTGAAGGTAATGATGCCGCTCAAGGAATGGATTTACGCCAAATGATGGGAGGTGCTG  
GAGTTCTGGAGGTGCTGGAGGCATGGACTTCAGCCAAATGATGCGAGGTGCTGGTGGCG  
CTGGTTCTCCAGATATGGCTCAATTCAGCAAT'TATTTGGCTCAAAGCGGTGGTAATTTGG  
ACATGGGAGATTTCAAAGAAAACGATGAAGAAGATGAAGAAGAGGAATAGAGCCCGAAG  
TCAAACCTTAA

&gt;YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINPQVAWAQRSSSTDPERNYVLITVSIADQDAPELTIKPSYIELKAQSKPHVGDE  
NVLHYQLHIDLYKEIIPKTMHKVANGQHYFLKLYKKOLESEYWPRLTKEKVKYPYIKTD  
FDKVVDEDEQDEVEAEGNDAAQCMDFSQMMCGAGGAGGAGGMDFSQMMGGAGGAGSPDMA  
QLQLLAQSGGNLDMGDFKENDEDEEEIEPEVKA

&gt;YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACAGAAATGCCGTAGCCGGAAAAACCGAAAGCGGGGGACAGTGAAGCGTGAGAGGG  
GCCAGACAGUGGGAACCTTGAATGGGGTATTTTGTCTTTTGTCTGCATTTT'TTCCGCTGGTAC  
CTCTATCTTTTAGGCGACCGGAAAAATTCATTTTCTCATCTTTTPPTTTT'TTTCTGTTCCG  
ACTCGATACTCTTTTAAAGAAACCCCCGCGGGAAATGTTAGATTTGAGCTTTT'TCCGC  
CAGGAAAAGAAAAACCTGGGGACATTAATCTTTGTTTTTCTTTCTTCTTTTGTCTTCC  
TTGGATGACTGCAGAAAAAGTACAGTTACCGGCTCTTAGCAAAAACAAACATATATATAT  
ATATATATGAAGCGTATGGTCAACACGGTTTTATAGGTTTTACTTTT'TGCATTCAAGTTC  
AACTTTTCCCTTTCTCTTATCGCATTCAGATACTACACACAAGTGTTCATACACACACA  
AATAGATACATATACAGAAAATGACTAGTTTGGACGATACAATAATTTTCTGACCAGAATA  
TAATCTTACTGGATAACATGACCAACTACAACAAGCCTGGGATTGACTATTTCCATCATG  
AATTTAATGATGCAAGCTTCCAAACATCGGCTTCATGGACACTACTATTCAGATGCCCA  
AACATAAACTACTTCCGATTACCAAGTTGCTCTTCAGAGGACGTGCTAGATTACAACATGT  
ACCTCGTTAGGCTACATCATTTGCCCTTGGAGGCGTTGGTCCATAAATCACTATGTTTTAC  
ACAACTCCAAATCCAAATCCACTGTCCATCAACTGGAACAAAGAAACCGATGTAACGGTGT  
TGTACGGTCCAGATTTGACTAACATAGATAGTAATGAAAACGAATATCGCCGGTCCAGA  
ACCAAAATTSACCAGAAACAAACAAAAAATCTAAAATCTGCTTTTAAAGAAAAATACGGAAT  
GCTGGGTAAACCGAGGAGGTGGATGAGATTAACGCTTCTATAGACAGCAATGACAACGCTT  
TGGTGAATTAGAAGACATTTTATGCCCATTCGTTCTGTGATTTCT'UACACGTCCTTCCATTT'  
TUGACUAGCATTTCTACATGCACTAAAATTTCCCTCCATAGATGAAGATTCTGAAGACCTTJA  
TGAACGAAAAGAAGGAACAAATTTCCCGAGGAAGTTGAAGTTTAAACCAAGCCGTGATGAAGA  
GGAGATCGACTCAAAGGGGACTATCCGCGAATCCCTCATCAACATAAACGATATCCAAC

81/251

ACTCCCGCCACCATCGCCGTCACCATCGTCGCCATCATCACCATCACCATCAAAATAGTT  
CTCATTTCTGATGAAACAATAAAAGAAGCTCATTTATGAGTTTACCAACTATACATTTGGCA  
CTATCGAAGACACATTTTTTATAGGAACGAGGTTGTTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTIISVQNIMLLDNKTNYNKFAIDYFHHEFNDALEISASWTLILLKMRKIILRL  
PSCSSSDVLDYNYMYLVRLLHICLWRRWSINHYGLQNSKSNPLSINWNKETDVTVLVYGPDLT  
NIDSNENEISPVQNGIDQKQTKNLKSALKKNTCEWVTEEVDEINASIESNDNALVKLENY  
SCPSSVDSHTSSIFDQHSCTCKISSIEDSEDLNNEKKEQFPKRLKFNQAVMKREIDSKG  
TIRRESLININDIQHSRRHRRHRRHHHHHQQSSHSDETIKEAHYEFSNYTFGTMEEDIF  
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGAATACAAAGAGGTCCAAGAAGACGAAGACUUGGATGTGTGGGACACGAGAATATCC  
AAGACCGGATGCTACGTAGAGAACCTCGCATTACAGCTGTGCCATGCCGAAACAGGTGAC  
TGGAGGCAGTGCTTCAACGAGATGGCGTTATTTAGGAAGTGTGGGAAAAGAATGGTAAT  
AGAGAGCGCGTAAGCACAGTGGACGTCCATGGGACGACCAGTAAAGATTCCGAAAAGAAG  
AAATGAAAATCTAAATCTCGTGATCTATAACTTGATATAATAGACAGCTGCAAGTGATCG  
AAACACATTTGTTCCCTTTATAGAACATAACTGTTACCGCTTTTGAACGGCATTTCATGA  
GCTTCTAGAATATTTTTCCGCCCTAGCTGGAGAAAGTTCAGACAGAAAATTTATTAAGTA  
AGTCCAATATCAGAGGTGCTGATGCGCTCACATCACATAGAAAACCTGGTAAGACAATACT  
CAGGCCATCAAGGACTAAATGACTAGACCTAAAACTTTTTTTGATATTTCTATTGGAG  
GTAAACCCCCAAGGCCGTATAGTTTTTTGAGTTGTACAAATGACATAGTGCCATAAACCGGCTG  
AAAATTTTTTGAAGTTGTGTGAAGGAAATGCTGGPATGGCAAAGACTAAAACCTGATGTAC  
CATTTGTGCTACAAGGGTCCATTTTCCACAGAGTGATCAAAGACTTCATGTGTCAATTTG  
GTGATTTTACCAATTTTAATGGTACTGGCGGTGAGAGCATATACGATGAAAAATTCGAGG  
ATGAAAAATTTACATGTGTTAAACATGATAAACCATTCCTTCTATCCATGGCCAAACCGCGGTC  
CAAAATACCAATAGGATCTCAAGCTTTCAATAACCTGTGTTCCTACACCTCATTTGGACGGGA  
AGCACCTTGTCTTTGCTGAAGTGATTCAAGGTAAAAAGAATTTGTTCTGTTGATTGAAAAAC  
AACAAATGTGACCAAGAAAACAACAAGCCATTGCGTGATGTAAGGATTGATGACTGTGCGC  
TGTTACCTGACGATTATCAAGTGUUAGAGAATGCCGAAGCTACACCAACACAGATGAGTACG  
GCGATAATTTACGAAGATGCTTTAAAACAAGACGAAAAAGTTGACTTGAAGAATTTGACAC  
CCGTCTTGAAAGCTATCGAAACGGTAAAGAACATTGCTACTGAAACAGTTCAAGAACAGA  
ACTATTTCCGTGGCTTTAGAAAAATATGTCAATGTGATAAATTTCTTGAAGAGTATTTCC  
CAGAAGATTTGGAGAAGGAACAAATGAAAAAATCAATCAATTGAAAGTGTCATTTCCAT  
TGAATATTGCCATCTGTGCTCTTAAATTAAGATTACAAGCAAGTATTAGTAGCCTCAT  
CGGAGGTGTTATATGCCGAAGCGGCTGACGAAAAGGCCAAGGCCAAAGCTTTTGTACCGTC  
GTGGCCTGGCCTATTACCATGTTAATGACACAGATATGGCTCTCAATGACCAGAAAATGG  
CCACTACTTTCCAGCCAAATGACGCTGCCATTTTGAAGCTATTCATAATACTAAATTA  
AAGGAAGCAACAAAACGAAAAAGCTAAAAGTCTCTTTGGAAGATGTTCTCTCTGA

>YLR216C, 371 aa (SEQ ID NO 280)

MTRPKTFFDISIGGKPGGRIVFEIYNDIVPKTAENFLKLCENAGMAKTKPDVPLSYKGS  
IFHRVIKDFMCQFGDFTNFNGTGGESIYDEKFEDENFTVKHDKPFLSMANAGPNTNGSQ  
AFITCVPTPHLDGKHVVFGEVIQGKRIVRLIENQQCDQENKPLRDVKIDDCGVLPDDYQ  
VPENAEATPTDEYGDNYEDVLKQDEKVDLKNFDTVLKAIETVKNIGTEQFKQNYVALE  
KYVKCDKFKLYFPEDAREKQTEKINQLKVSIPLNIAICALKLDYKQVLVASSEVLYAE  
AADEKAKAKALYRRGLAYYHVMDTDMALNDLEMATTFQPNDAAILKAIINTKLKRKQQNE  
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGGTACCCATAATTTCAACCATCUTTAGCTTTUCATTA AAAACACAAATGAGT  
TGCGTTACTAGCCAAACCGGCTTATCTGTTAATCTTGCTTGCAAACATCTTAGCTGAAAG  
TGAAAAGGCACAGCGCACCTGCTGAATGCTCAACGTTTTGTAATAATCCGCCTATTTCCGC  
GGAATCAATAGGGCTCCTAGCAGCGCCCATCAATTTTACGCTGCCCATTAATAATAT  
ATTACCAAGATTTTCATTTCCCGGCTCATTCCTATCAATATTAAGTAATCAATCTTTTC

82/251

CTCGTGATTCTTGTGATGCTCATTACAGAGGACTAATTAAGACATGTAGCACAATATA  
 TTCATATAAAAGTTGGTGACGTTAATGATTAATTGCAATTGTTTTCCTTGTTCCTTCTGT  
 TATACCTGTGCAATTAAACATAAAGTGTATATGAATTTTAACGGGCACAAATAACAAAGG  
 ATTATTTATCACCTTTAATAATGCAATCGATCAGTAATTTGCCATCCGCTTAGTTTCAA  
 AAAACACAATCAATTCAGCTTCCACTATTGACAGGTGGGTAGCATGTCCATGGAAATATA  
 TCAACGTTGTTGGTTCAGGCAGATATGTCAGCAATAAACCTCATATAAATTACAGATATG  
 ATTTACTCAAGGCTGCCAGGAAGCGGAAATGCAGGAGTTGCTTACAAGAAATGATATGA  
 AAGGTAGACATAAACGTAATAAGAAAAGTAAGATAGCATTCGAGACTATACCCGAAGAAA  
 ACTCTTCAACTCAAAGCCTTTTTTTAA

>YLR346C, 101 aa (SEQ ID NO 290)

MQSIENCPICLVSKNTINSASTIAEWVACPWKYINLVGSGRYVSNKPKITRYDLLKAAQ  
 EAEMQELLTRNDMKGRHKRNKSKIALETIAEENSSTESLF

>YML129C, 713 bp, CDS: 501-713 (SEQ ID NO 297)

TAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTUGGCACTGTAAAGGAGCCTGCCTT  
 ACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACTAAT  
 GATTGGGGTGTCAACCTAATGTACTTTTCTCCCAATTTTCTTTTCATCCGTATATTTT  
 ACCCTAAAAATCGACAAGCTAATAGCAAAACGAAAAACACCGTTGTCACTTCTATATAACT  
 TTGCTTAAGTAAGTATTTTCTTTTAAATGTTACATACTGTGAAATACACTCTTTAGAA  
 AACACTATTTCTTCACTCTUGGAAGCAGATTTCGAAGTACTTCTTACTTCTGAGCTTTG  
 CTTCTCTCTTCTTGGGATTAAATGTTACCGCTTATACGAAATCGGAGAGGATCAGAATAAA  
 TGCATTGAAAGGAGCATAAACTTATACAGCGCTTTCGCAATCGTCAGAGCAACGAGAACAA  
 AAAATAGAACGCAGATAGTCATGTCCAAATACGCTTGGTATACCAGAGTTACAGATACAT  
 TACATCGTCTAACGGTACTCACGTTGGTTGGTTGGTACGTTATACATGTCCGGTGGCTTAG  
 CTTTACACTTTTATACATGAACGGTAAGAAGTACGPAACAACAAGTGACCCAAACAAAAGCCAC  
 TTGAAGAAGACAATCAACAACCTGCRAAGTCCTACTGCACCTCCTACCGAGTAA

>YML129C, 70 aa (SEQ ID NO 298)

MSKYAWYTRVTDTLHRLTVLTLVGGTLYMSGGLAYTLYMNGKKYEQQVTQQKALEEDNQ  
 LQSFTAPPTL

>YML132W, 1640 bp, CDS: 501-1640 (SEQ ID NO 299)

GTAACCTGGTCTTATCAATCTTCATGTACAGATAAGTAGGACAGACTCTTTCCCTGTGTAAA  
 TATTITGTCACAGCTAAGTCTATTTTCTACTAGATGTTTACACAGTTTGTGCACAGGAAAT  
 CTACGCTTAAAAATATGTATTTCAATTCAAGCGGTAACCGCTGTACGAGCAGTGACATTGCT  
 GGTCCGACCCCTAAATGTGAACCAACGTACGGGCACACCGTGATGTACCCGCATTAAAGTTT  
 TTGTAAATTCGTTATTACGATTATCGAGTTGGCTAGATAGAAAACCGGAAATGTAATGGA  
 TCCCTTTTTCGAATAGCTGAGTTTCTTTGCCTAAATAGCCCAATATTGTTGCCCTTTT  
 CTATCACGAGGTTACTGAGCCATTGCATGAACCCGCGCGCCTCCGCGGCTTTTTTTTCT  
 GCTGTGCTGTATAAAAGCGAAAAGCCAGAAGTTACTATCTCGAATAAAAAACCCCTCGAA  
 CTGUCATCTCACTACCGAAAATGAAACGGAATGAACCTTAAAAATGGAAGAGTGTAGATG  
 TATTATCCTTCAAACAGCTCGAATCCCAAAACATTGTTCTACCTCAAGATCTTTTCAGAA  
 GCAGCTTTACCTGGTTTGTATGAAATTTACAAGTCTTTAGCGTTTTCGATCTGGAATGC  
 TATTATGGCTACCACTTAGCGTCTGGTGGAAACTTTCCAACAATGTATTTACCCACTTA  
 TAGTTTCACTCTGTGCTCTGTTTCTGGGACCAATATTTGTCTTGTATTGTTGGACTTT  
 CTCGTAAOCCTTCCCTTATCGAACAACCTCMTTCAGTTTTCGAAGAGATTACTGAAAACA  
 CAQCAAGTTCTGATCCTCATEATTGGGAGTTGTGTCAGCAATCTAAATTCGTACTTAT  
 ATGAAAATAACGTTTGGAACTACTAAGTACTTTTTTTTCAATGCCATGGTCTGTCAAGAAG  
 CGTTACAGAACACCCCTTCTCGAACCATTTCCTTTGAAAAAAGATAAAGCTGCCAAGGTTA  
 AGTCATTTAAGGATTCGGTCCCTTACATTGAAGAAGCATTCACACTTTATTTTACACAC  
 TTGAAAAACAATGGAAATGTCTTAATACTGAAAAATCATGGAGCCCTGTTGGCCTGGAAG  
 ATCCTAAACTTCCCAAGGAAGCTTACCGATTTAAGCTTACTTGGTTTTTAAAGAGGATTT  
 CCAATATTTTTATGTTGATACCATTCCTTAAATTTTTCCTCTGCATATATGCTCACGGC  
 GAATGTGCCTTCTATTACGCACCTTGTATCTCGGGTGGATTCTTTTCATGTTGGTACAAG  
 GTTTCCAAATATAAGCGTTTTCATTATGAGCATGGAACACAAAGATGCAGTTCTTGTCGA

83/251

CTATTATAAATCAGCAAGAAASTGGTGCGAATGGATGGGACGAAATTGCAAGGAAATEA  
 ATAGGTACTTGTGAGAAAAAGCCTGCAAGAATGAAGAGTTTTCTTCGACGGGATTC  
 ACTGTGAATGGTTTTTAACCACTTCTTCTACCGGTTCTATCTCGCAAGAAATCTATGT  
 GGCCTTTACCATTGAATGTGGAATATGCCATACATTAAAGAAGCGCAA'TATCCGCA  
 GTGAGGTGCTCT'TAG'CTAG

>YML132W, 379 aa (SEQ ID NO 300)

MKENELKNEKSVTVLSFKQLESQKIVLPQDLFRSSFTWFCYBIYKSLAFRWMLLWLP  
 VVWKLNNCLYPLIVSLLVLEFLGPLFVLVICGLSRKRLSKQLIQFCKEITENTPSSDPH  
 DWEVVAANLNSYLYENMVWNTKYFF:NAMVCQEA'RTTLLLEPFSLLKKDKAAKVKSPKDSV  
 PYTEALGVYFTEVEKQWKLFNTEKSWSPVGLRDAXL>KEAYRFKLTFWFLKRISNIPMLT  
 PFLNFLCCLYVSRGMCLLLRTLYLQWILFMLVQGFQNIKVLIMSMEIKMQFLSTIINEQE  
 SGANGWDEIARKMNRYLEFKKAWKNEEFPFDGIDCEWFFNFHFFYRVLSAKKSMMLPLNV  
 ELWPHYKEAQLSRSEVLLV

>YMR009W, 1640 bp, CDS: 501-1640 (SEQ ID NO 301)

ACCGGTATTTTCATCTCTTCTAGATCAAGACTAACTGCTCGTTCACTACAAGTATTTTAC  
 GATAGTCCATATTACTCT'CAAT'CAATPA'PTTTT'PTATATTCTGGCCCCGTTTTTGACA  
 CAATTTTTTCCCTTCTCTTTTTCTCCCTATAAACTATGCAGAAGTAGCGATAATCACCATC  
 'T'G'P'AAATGAT'TCACAT'G'GCGCAAGTCTGATTGCTCTCTCTAGATAGTGAGATGCCCTTCT  
 AAATAACAGGAGAGAGCGCAAGACAGCATAACGGCGCAATGAAGGTAATTTCTGCCAGTTT  
 TCT'P'TGCAAT'GACGACT'GAAAGGGGCCCTTGTAAGAGCCGCTCGACAGGGCGACGCCACAG  
 TAGAGTCCGCTAACACCGAAATATGCATATTGAAAAACATCABAGTATAAAAGAACAAAGA  
 GGGTGGCATCTGCAGATCAAAAAAACAAATAAACCACCAACAAAGACACTAAAAAAGGTCTG  
 TAAAAAGGTCAAAAGTTAGAATGGTTAAGGTATATATTTCATGACAACAAGGTTGACTCCG  
 AT'ATATCGCGCCAUCCCAATTTCTGGAAACAGAACT'PTCCCTGGATGAATTAGCCAAAGTTAG  
 GAGTGATTTATAAAATACTCTTGCAAAATGACCAAGCAACTGAATGAAATTCCTACGCCAAGAG  
 AATATAAAAAATAGAGATGTGGTCAACATCTCGCAAGCTTCCCTTCAAAACTCAAGCAGACT  
 TTAATGAAAAAACTAGCAACATTTCTACCAAGAGCATTTACATGAAGACGAAGAAATAAGAT  
 ACTGTCTCGAGGGTCTGGATACCTTTGACCTCAGGGATGCTTCCACACCCAGAGAACTGGGA  
 TTAGGTGTTTTGGTAGAGTCAGGTGATTTACTGATTCCTTCCACCAGGCATCTATCATCGTT  
 TCACCTTGACAACCTAGCAACCACATCAAGGCCCTTGAGACTGTTTAAGGACGAGGCCAAAT  
 GCGAAGCTATCAACAGTFLCAAAT'CAAGGCTGAT'CA'FGCCCTTACGCAAGGACTACATTG  
 CCC'GATCAAT'CACTACTAA

>YMR009W, 179 aa (SEQ ID NO 302)

MVKVYIHDNKVDSYRAPHNSGTSLDELAKLGVLYKYCANEEVMEIARQREYKNRDV  
 VNICEGCSFKSEAEFNEKLATFYQEHLEDEEIRYCLEGAGYFDVRDASTPENWIRCLVES  
 GDLLILPPGIYHRETLT'SNHEKALRLFKDEPKWQAINRSNQADSLPVRKDYIALNQY

>YMR011W, 2126 bp, CDS: 501-2126 (SEQ ID NO 303)

GCACCTTCACCTTTTAAAGTTTCTTTTTCTCCTCAGCGCGCAACCGCTAACTTAAGCTAATC  
 CTTATGAATCCGGAGAAAAGCGGGCTCTTTTAACTCAATAAAATTTTCGAAATCCCTTTT  
 TCC'ACGCGT'PTTCTTCGGGAAGTAGATAGGTGGCTCTTCCACCTGTTTTTCCATCATTT  
 TAG'TTTTTCGCAAGCCATGCGTGCCTTTTCTGT'PTTTCGGATCGCGAAGCAGGGCTGGAAA  
 AAT'CAAGGTACGCGCGCTAACGATAGTAATAGGCCACGCCAAGTGGCGTGACGACAACA  
 ATAAGTCGCGCA'PTT'PTATG'PTT'CAAAACCTAGCAACCCCCACCAAAC'PTG'CATCGT  
 TCCCGGATTCACAAATGATATAAAAAAGCGATTACAATTCATATTCTAACCAGATTTGAG  
 ACC'CCCTC'PTCTCAATTCCTCTTATACTAGATTATAAGCAACAACAAATTAATTAACAA  
 AAGACTTATAAAGCAACATAATGTCTGAATTCGCTACTAGCCCGCT'GAAAGTGCTCT'CT  
 AACAAACTTCTATCCACTCTACTCCGATAGTCCAGAAATTAGAGACGGATGAATCTCCTA  
 TCCAAACCAATCTCAATACACTAACGCTCAACTCCCAGCAAAGCCAAATCCCGCATATT  
 GGACTGTTATCTGTTTATGTCTAATGATTCATTTGGTGGGTTTGTCTTTGGTTGGGATA  
 CCGGTACCATCTCTGGTTTGTGTTAATCAAAACGATTTCAAAGAGAGATTTGCTCAAATGA  
 AACTGATGCTACCTATTATCTTTCCGACGTCGGCACTGCTTTGATCGTTGCTATCT'CA  
 A'AT'GTGTTGTGCCCTTTGGTGGGTTAACCTTAGGACGCTCTGGG'GATA'GTATGGACGTA

84/251

GAATTGTTTTGATGTGGCTCGTTCTGGTATACATCGTTGGTATTGTGATTCAAATTGCTT  
 CTAGTGACAAATGGTACCAATATTTTCATTGGTAGAATTATCTCTGCTATCGGCTCTCGGTC  
 GTATTGCTGTCTATCTCCAACCTTTGATTTCGGAAACAGCACCAAAACACATTAGAGGTA  
 CTTGTGTTTTCTTTCTATCAGTTAATGATCACTCTAGGTATTTCCTTAGGTTACCTGTAACCA  
 ACTATGGTACTAAAGACTACTCCAATTCAGTTCAATGGAGAGTGCCCTTTGGGTCTGAACT  
 TTGCGCTCGCTATTTTCATGATCGCTGGTATGCTAATGGTTCAGAAATCTCCAAGATTCT  
 TACTCGAAAAAGGCACATACGAAGACGCTAAACGTTCTTTGGUAAAATCTAACAAAGTCA  
 CCATTGAAGATCCAAGTATTGTTGCTGAAATCGATACAATTATGGCCAACTTTGAAACTG  
 AAAGATTAGCCGGTAACGCTTCTTGGGGTGAGTTATTCTCCAACAAAGGTGCTATTTTTAC  
 CTCGTGTGATTATGGGTATTATGATTCAATCCTTACAACAATTAACGTGTAACAATTAAT  
 TCTTCTATTATGGTACTACTATTTTCAACGCCGTCGGTATGAAAGATTCTTTCCAACTT  
 CCATCGTTTATAGGTATAGTCAACTTCGCATCCACTTTCGTGGCCCTATACACTGTTGATA  
 AATTTGGTCGTGTAAGTGTCTATIGGGTGGTTCGTTCCTATGGCCATTGTTTGTGTA  
 TCTTCTCTACTGTCCGTGTACAAAGCTTATATCCAAATGGTAAAGATCAACCATCTTCCA  
 AGCTGCGCGGTAAAGTCAATGATTGCTTTTACCTGCTTATTCATTTCCTTCTCGCTATTA  
 GTTGGGCCCAATTGCTTACGTTATTGTTGCCGAATCCTATCCTTTGCGTGTCAAAAATC  
 CTGCTATGGCTATTGCTGTTGGTGCCAACTCGATTGTTGGGCTTCTTCATTCGCTTCTTCA  
 CTCCTTTCATTACAAGTGCAATTGGATTTCATACGGGTATGCTCTCATGCGCTGTTTGG  
 TATTTTCACTTCTTCTACGTGTTTTCTTTGTCTGTGAAAUCAAGGCTTAACATTAGAGG  
 AAGTTAATGAATCTATGTTGAAGGTGTCAAACCATGGAATCTGGTAGCTGGATCTCAA  
 AAGAAAAAGAGTTTCCGAGGAATAA

>YMR011W, 541 aa (SEQ ID NO 304)

MSEFATSRVFSGSQQTSIHSTPIVQKLRTDRSPIQTKSEYTNAEI.PAKPTAAYVTVICLC  
 LMIAPGGFVFGWDTGTISGFVNQTDFKRRPFGQMKSDGTYXLSVVRTGLIVGIIFNIGCAFQ  
 GLTLGRLGDMYGRKIGLMCVVLVYIVGIVIQIASSDKWYQYFIGNIISGMGVGGIAVLSP  
 TLISETAPKHIRCTCVSPYQLMITLGIPLCYCTNYCTKDYNSVQWRVPLCLNEFAFIEM  
 IAGMLMVPSPRPLVEKORYEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA  
 SWGELEFSNKGAILPRVIMGIMIQLQLTGNNYFFYYGTTIFNAVGMKDSFQTSIVLGIV  
 NFASTFVALYTVDKFGRRKCLLGGSASMAICFVIFSTVGVTSLYPNGKDQPSKAAAGNVM  
 IVFTCLFIFFFAISWAPIAYVIVAESYPLRVKNFAMAIAGVANWINGFLIGFTTPTTSA  
 IGFSYGYVFMGCLVPSFFYVFFVFCETKGLTLEEVNEMYVEGVKPKSGSWISKEKRVSE  
 K

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTACCTCGATCTACATATACTTCAATGCGAGAATGACTAATCTTTGCCATTGAC  
 AAACAACCCCTTTTACTGCCAGCGCCCTTTCATAACCATGTAGTTTATATGCCCTAATTATA  
 ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTAACTTGAAACCGAGATTCT  
 ATCTATTGCACCAGGAAAGTGCCCTTCTTCTTAAACATAAGTTACGTCCCGACCATTTCA  
 TCTAAACGGCATCAATCATTGCAGCAGAAGAAATAGTGTGTAGATGTCCTCGTTCCGCTAG  
 ACGCAGTCAATGATAACAAGGTCTTTCTTCAAGCTGTCTTTCCATAAAAAGGTATCGCAA  
 ATGGGGTCACCAATGGCCCTTTTATTTTTCACGCCGAAAGAAAACCTTAGTAGGTCCTCTAG  
 AAATGAATAAAGAGGTGATTCTGAGGTTCAATTATAAGCCCTTTGGTAAAACCTTGAACCAAG  
 AAAGATTAAAAACACAAAGCCATGCCTATCAAAGAACTGATAAAGAAGTTGTTTGGACTC  
 ATCCAGCTCATGAGACCAACACCGCTTCATATTCTAAGTACCCCTGCTACAGTTTATTCTT  
 GGAAATTCAAACTCTGAAGAACTCTGTGGTTGTCTACTGCTCTAAATTTGGATCGTAGCA  
 AACCTGTGAGAGGTGGTATACCTTTGGTCTTTCTTGTATTGGGAAAAAAGCACCGATG  
 AACATTTGAGTAAATTACCTCAACATGGTCTTGCAAGAAATTCTACTTGGGAGTTTTTGG  
 GTCAAACTAAGGAAAACCCACCCACCTACAATTTGCCCTCAAAACAGAAATTGCTAACC  
 CAGAATTGACCAAAATGTGGCCAATGGATTATCTTTTGATTTTGACTGTTGAATTAGGCT  
 CCGATTATTTGAAAACAGCCATAGAAATACAAAACACATCTACTTCCAACGAATTAAAGT  
 TCAACTCGTTCTTCCATACTACTTCCCTATCGAAGATATTGAACGAACATGCTCTCTA  
 ATCTAGCTGGCATGAAACTTTATGACCAACTGTTGAAGGAATCTTACGTCCACAAGCACC  
 CAGTCTGTACCTTCAATCAAGAAACCGATGTAATTTATCAGAATGTCAGCCCGAAGCGG  
 CCATTCAAAATAGTTGACAAGGGCGTTCAAAATTCACACTCTAAAAAGATACAACCTTCCCG  
 AACCTGTTGTTTTGGAATCCATGGATTGAGAAGTCTCAAGGATGGCCGATTTTCAACCAA

85/251

AAACTGGTTACCAACAAATGATATGTATTGAACTGGTCATGTCATGATTTTATTTCCT  
TGGCTCCTCGTAAAAAATGGAATGCTTATCAATTACTTTGCAAACAACAATCGAATATC  
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MPKETDKENVLTHPADETTSVHILKYGATVYSWKLKSEEQLWLSTAAKLDGSKPVRGGI  
PLVFPVFGKNSTDEHLSKLPQHGLARNSTWEFLGQTKENPZTVQFGLKPELANFELTKLW  
PMDYLLILTVELGSDYLKTAIEVENTSSSKELKFNWLPHTYFRIEDIECTMVSNLACMKL  
YDQLLKESYVDIHPVVTFNQETDVIYQNVSAERAIQIVDKGVQIHTLKRYNLPTDVTWNP  
WIEKSQGMADFEPKTYQQKICIEPGHVHDFISLAPGKKAMAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAAGCTAGATTATCATTACAGCAGCCACATAGTATACCAAATTCCAGTACAG  
GCACACCAGAACATGATCAACACACTTAGAGGAAATGCCAACACGAATTTCCAGCCAAAA  
ATTCCGAGTAGTTCAAGATGAAAGATTTTACATGCAATTTATATATAAATATATACCGT  
CCTATATGGAATTTCAAGCCAACAGGGTATATAAATAGACAATTACCGGTGTACTGATATAT  
CAACTATCCACTCCAGCCCTTTTATCTATCACTCAATTTTACATCAAGATCCCACTTTTA  
GATAGGTTCCAAAAATCAATCTAATATTTAGTGAATTTAATTAGATGGTGGATTGCTTACCC  
TTTTTTTTGTCTGTTTGGAGGAGATTCTTCGGATTTTAGGGATAAACGGATACTCCATA  
TATAAAAAACAAAACCTTCACCCATATGATTTATCTAAAAGGAATATTCTAAAACCATAGC  
CATAGTAATTTATCACCACATGTCAAACGACGGCTCAAAAATATTGAATTATACCCCGAG  
TGTCTAAAATAGATGAAATAGCTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAATTGA  
AATTGTCCACGAAAAATAACCCAAAGGAAAAAGATCTAGAAATTCAGGCAGTTGCAGTTGA  
AAAACTCTATTATGCGCTCAAGATCATGAGGAAGAACTGATCGATGCTATGTACAAGG  
ACTTTCATCGGAACAAAATTGAATCGGTCTCGAATGAAACGACCAAACTTATGAACGATA  
TACTTCACCTAATTGAGATTTTACCAAAATTGATCAAACTTCGGAGAGTATCTGATTCTT  
CTCCTCCATTTATCTTTGCTAAAACAATCGTCCAGAAAATATCAAGGGCCACTCTCTTCA  
TTATTGCTCTCTTTCAATTTTCCCTTACTTTTACCAATTTGCCCTTATGCGCAGCAGCTCTG  
CTGACGGTAACACCATTGTTCTGGAAGCCAAGTGAACCTAACACCACACACTGCTGTGTTTA  
TGGAAAAATTTGTTAACCCACAGCTGGTTTCCCTGATGATTTGATTCAAGTAGTTTCAGGGAG  
CTATAGATGAAACTACAAGACTACTAGATTGTCGAAAAATTTGACCTAATATTCTACACAG  
GTTCTCCCCGTGTCGGATCAATAGTTGCTGAGAAACGAGCAAAAAGTCTAACACCTTGTG  
TACTTGAACCTTGTGCTAAATCACCTACCTTTTATTACAGAAAAATTTCAAAGCAAGTAACA  
TAAAAAATTGCTTTGAAAAGGATTTTTTTTGGTGCTTTCCGAAATTTCTGGCCAGATTGTG  
TTTCACCACATTATTTCTTACTACATAAATCTATCTATCCAAAAGTCATTAAAGACTGTG  
AATCAGTACTAAATGAATTTTATCCAAAGCTTTGATGAACAAACAGATTTCACTCGTATGA  
TTCATGAGCCTGCTTACAAAAAGGCCGTTGCAAGTATAAACTCAAGTAACGGCTCCAAAG  
TTGTGCCTTCAAAAATTTCTATCAATTTCAGATACTGAGGATCTATGCCTTGTACCCCAA  
CCATAGTTTATAACATTTGTTGGGATGATCCTTTGATGAAACAGGAAAACTTTGCTCCTG  
TATTGCCCATCATTTAGTACGAGGATCTTGATGAGACCATTAACAAGATAATAGAAGAAC  
ATGACACTCCATTTGGTGCAATACATATTCTCTGATAGCCAACTGAAATAAATCGTATCT  
TGACGCGCTTAAGATCTGGTGACTGTGTGTCGGTGATACAGTGATTCATGTAGGAATTA  
CCGACGCTCCATTTGGAGGGATCGGTACTTTCAGGTTATGGTAACCTATGGTGGATATTATG  
GATTCAATACCTTTAGTCAATGAAAGAACAAATTTTAAACCAACCATATTGGAAATGATTTTA  
CCCTTTTTATGAGATACCTTCAAATAGCCGACAAAAAGGAAAGCTCGTCCGTTTTTGGGA  
TGCACAAACAAACCTTGCCTTTGACAGAAATGCCAATAACAAGTGGGGCTTACGCCAATATT  
TTTCATTATCTGCCGCCGTTATTTTAATTAGTACCATTTACGCTCATTTGTTCTTCCCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNYTFVSKIDEIVEISRNFEEFKQLKLSHENNPRKIDLEFRQLQLKKLYYAV  
KDHEEELIDAMYKDFHRNKIESVLNETTKLMNDLHLIEILPKLIKPRRVSDSSPPPMFC  
KTIYEKTSRGSVLTAPFNPPIILAFAPLAATAAGNTIIVLKPSELTPHTAVVMENLLTT

86/251

AGFPDGLQVVGGAIDETFRLLDCGKFLIPYTGSPRVGSIVAEGAASLTPTCVLELGCK  
 SPTFITENFKASNIKALXPLIFFGANGNSGQICVSPDYLLVHKSIYPKVIKECESVLNEF  
 Y?SPDEQCTDFTRMIHEPAYKAVASINSTNGSKI VPSKISINSDTEDLCLVPPTIVYNIG  
 WDDPLMKQENFAPVLPFIEYEDLDETINKIIEHDTPLVQYIPSDSQTEINRILTLRSG  
 DCVVCETVIHVGITDAPFGGIGTSGYGNYGYYGFNTFSHERTIHKQPYWWDFTLPMRYF  
 PMSAQKEKLVRFAMERKPMFDRNGNNKWLGRQYFSLSAAVLLISTIYAHCS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

AAAAAACCACTCCGAAGGTTCCACCATGACAAATCGCCCCCTAGCTGTGGCCATACAAGC  
 TTGGCACCGACGAAAAAGGGAAAAAGGAAAAGAAATGTCGTACAGAACTCTTACAACTAC  
 GTTGAGATTTTCATTTAACAAUGUCCCCCTTTTCATPATATAAGAAGGCATTAATTTTAT  
 GTAATAAAAAAGAATTTCTCGAAPTGTCTTACAAATTAATTTTTTCTTTTGTAGAGTAG  
 GGCTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCAATGGGTCT  
 ATTTGATAAAGTGAAGCAATTTGCTAACAGCAATTAATAAUAUAATGATTCTGGCAATAA  
 CAATCAAGGCGATTATGTTACCAACCTGACAATATGATCCCCAAGATAGAGTCAATCA  
 ATTCAAAAGCAAAATCGGAGAGGACAGATTTGATAAGATGGAGTCCAAGGTTCTGTCAACA  
 ATTTCTTAATACCTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAA  
 TAACAACGATTCATATGGTTCTAACAACAATGATTTCATATGGCTCTAACAAACAATGATTC  
 ATATGGCTCCAACAACAATGATTCATATGGCTCTAACAAACGATGATTCCTACGGTTCTTC  
 CAACAAGAAGAAGAGCTCTTATGGTTCTAACCAATGACGATTCCTACGGCTCCAGCAACAA  
 CAATGACTCTTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAACAATGACTCTTA  
 CGGTTCACAACAATGACGACTCTTACGGTTCTGTCAAACAACAATAAGAGCTCTTACGGTTC  
 CAACAATGACGATTCCTATGGCTCTAACCAATGATGATTTCATATGCTCTTCCAACAAGAA  
 GAAGAGTTCTTATGGTTCCAAGCAACAACGATTCGTATGGTTCTAACCAACGATGATTCATA  
 TGCTTCTAACAAACAATGATTCATATGCTCTAACCAACCAATGATTCCTACGGTTCTTCCAA  
 CAAGAAGAAGAGCTCTTATGGTTCTAACCAATGACGATTCGTACGGCTCCAGCAACAACAA  
 TGACTCTTACGGTTCCAACAATGACGACTCTTACGGTTCTGTCAAACAAGAATAAGAGCTC  
 TTACGGTTCTTCTAGCAACGATGATTCCTTACGGATCTTCCAATAAGGACGACTCTTACGG  
 TTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAACAATGACGATTCCTATGGCTCTAA  
 CAATGATGATTCATATGCTCTTCCAACAAGAAGAAGAGTTCTTATGGTTCCAAGCAACAA  
 CGATTCGTATGGTTCTAACCAACGATGATTCCTACGGTTCTTCTAACAAAAAGAGGTTCT  
 TTATGGTTCCAACAACGATGATTCATACGGCTCCAGCAACAACAATGACTCTTACGGTTC  
 CAACAATGACGACTCTTACGGTTCTCTTAATAGAAACAAGAACCTCTATGGGTCTTCCAA  
 CTACGGTTCTATCCAACAATGATGACTCTTATGGTTCTATCTTAATAGAGGCGCTCGTAATCA  
 ATACGGTGTGTGACGACGATTACTAAGTTTTTGGATGTCTTCCGAAAAAAAATATATTAT  
 TGTGTTTAGACTTAAGTATGAAAATTTTATGTATGAGCTGTGGCTATGTATCCGCTGGCA  
 AATAG

>YMR173W-A, 394 aa (SEQ ID NO 692)

MTTTPPTTTTHMVLTTTHMVLTTMIMHMLTTMIMHAPTMMIMHMLTMMIPTVLPTRRRL  
 MVLTMITRTAPATMTTLTVPTMTTLTVPTMTTLTVPTMTTLTVRQTRIRALTVPTMTILM  
 ALTMMIMHMLPTRRRVLMVPATTIRMVLTMMIMHMLTMMIMHMLTMMIPTVLPTRRRALM  
 VLTMTIRTAPATMTTLTVPTMTTLTVRQTRIRALTVLLATMILTDLPTTTTLTVLPTRRR  
 VLMVPTMTILMALTMIMHMLPTRRRVLMVPATTIRMVLTMMIPTVLTKRRVLMVPTMT  
 LHTAPATMTTLTVPTMTTLTVPLIETRTPMGLPTTVHPTMYTLMVHLIEAVVINTVVTTI  
 TKFLDVFDKKNILLCLDLSMKILCMSCGYVSAGK

>YNL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CAACAGUCCAGGCGCGAGTGAACAACATATTAATTAACGCCCTTCTTGTUAGTGTGTTTT  
 GTTCTGGTCTGGTCTGCATTCGCGCCCGAAAAAGCTTGAGACGCGAAGCTCCCGAAGC  
 TCCTGCCATACAAATGCGAAACTCTCGGTCTAGTACCCTTTCCCGGTGCCAAACGACCA  
 CAGTTGTCCGTTCGAGCAGCTCGCATTAAGCGCGTGAACCTATGGCACGCCCTTAAGGG  
 GCTCCCTACGGATGGGAGTTGGTCAATTAGCGTTCATTATCGGCCAATGTGACGCACAATC  
 ACUGCTATGGCTCGGTGTCAAAACATAGTTTGGGTGATAACAGCGTGTGTTGTTCTCTCC  
 CGTTGCTCTTGTGACCGCAGTTGTATATAAATAATCTTTTCTTGTCTTTTATATAGG  
 ACCACTGTTTTGTGACTTCCACTTTGGCCCTTCCAACCTGTTCTTCCCCTTTTACTAAGG

87/251

ATCCAAGCAACACTCCACANTGGCCAGAACTAAACAACAGCTAGAAAATCCACTGGTG  
GTAAAGCCCCAAGAAAACAATTAGCCTCCAAGGCTGCCAGAAAATCCGCCCCATCTACCG  
GTGGTGTTAAGAAGCCTCACAGATATAAGCCAGGTACTGTTGCCCTTGAGAGAAATTAGAA  
GATTCCAAAAATCTACTGAACTGTTGATCAGAAAGTTACCTTTCCAAAGATTGGTCAGAG  
AAATCCTCAAGATTTCAGACCGACCTGAGATTCAATCTTCTCCTATCGCTCCTTTGC  
AAGAATCCGTCGAAGCATACTTAGTCTCTTTGTGTGAAGACACTAATCTGGCTGCTATTC  
ACGCTAAGCGTGTACTATCCAAAAGAAGGATATCAAATTGCCACAGACTAAGAGGTG  
AAGATCATGA

>YNL031C, 136 aa (SEQ ID NO 326)

MARTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFQKSTR  
LLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFEDTNLAALIAKRVTI  
QKKDIKLARRURGRS

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AAACTCGGAAACTCTTTTCTATTTCATCTTCCTTCTCCTACGTGCCACCGGAAGCAATA  
AAAAGAACCGAAATAACCAACACCCCGTAACGTCAAAAGCATTTCATGCTTAGAATGGAACCC  
ATTTCTGCGAATGAAATGGCAATTGATCACAATTGATTGCTCGTTCCACCTACCTGTGTCC  
GCAATTTTTTAATGGTCATCAGAGCCCTGCTGACTAAAGTTCTCGGATCCGCTTACGG  
TTGTGCGGCGTTTCCGCCCTGCGTACCTCTTACGTAATGATATCGGCTCCCTCCGTTG  
GATTGGCATCGATTAGTAAGGACAGATGTTAAGGATTTAAGACCGTTTCTTAAGGTATTTTC  
GGCAATGCTTCGATTCTAAAAGGAGAGAGTTTCTTTTGTGCCGTTTCTTCTCCTCTCACTTC  
TTGATTAGTACTGTAAATTCTAGTTGAAAAAAATCGTTAACTATACACAGCAAAAAGCAA  
TATCATACTGCATATCAAGCATGTCCGCTCGATTCCAGAAAACCATGAAAGCCGTGTCTCA  
TTGAAAATGGCAAGGCTGTAGTCAAACAGGACATTCCAATTCTGAAATTAGAAGAAGGAT  
TTGTTCTAATTAAGACTGTCCCGTTGCCGGTAACCTTACCGATTGGAAACATATTGATT  
TCAAGATTGGTCTCTAAGGTGCCCTCTTAGGCTGTGATGCAGCCCCCAAAATCCTAAAGT  
TGGGCCCAAAATGTTGATGCTGCGCCGCTTTGCCATTGCTGATTACATTTATCGGCTTATTC  
ACGATGCTTTCAGTGAGGTTCCTCCCAAAACGGTTCCTTTGCTGAGTACTCTCCCACTTCAT  
CCGAGACTGCTTATAAAACCAGCCAGAGAGTTTAGATTGTGCGGTAAAGACAAGCTACCCAG  
AAGCCCCCGTAAATCTTTAGAACGGCCAGTATCCCTCCCACTCTCATTTGACCACGGCTG  
GTATCATCTTACACATAGTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAAA  
GAGATCAACCCATCTTATTTTGGGTGGTGGCACTGCCTGTTCGCCAGATGCTTATTCAA  
TGGCAAAAAAACTAAACGGTTTTCAGCAAGATCAATGCTGCTTCTTCGTAAACATGAAA  
AATTGTTGAAAGAGTACGGTGCAGATGAACCTTTTGACTACCAAGATGCTGACCTTATCG  
AACAGATAAAAAAGAAGTACAACACATTCCTTACTTGGTGGACTGTGTCTCCAACACAG  
AACTATTCAACAGGTGTACAAATGTGCCGCTGATGACTTAGACCGCTACGGTCGTTCAAT  
TGACCGTTTTTAACCGAAAAAGATATCAAGGAGGAAGACAGGACCCAAAACGTCATTTTC  
AAGGAACCTTCTATATTTGATAGGAGGTAAAGACGCTCCCATTTGGCACGTTTACTTTGC  
CAGCAGACCTTGAATACAAGGAAGCCGCCATAAAATTTATTAAAGTTTCATCAATCCAAAA  
TCAATCATGCTGAAATCCACCACATCCCAAGTGAAAGTTTACAAGAACGGGTAGATGATA  
TCCACAGTTACTTGATGATATTAAGCACGCCAGCAATTCCTCGCGAAAACCTTGCTTCCCC  
TCTTGAAACAA

>YNL134C, 376 aa (SEQ ID NO 332)

MGASIFETMKAVVIENGKAVVKQDIPITPELEEGFVLKTVAVAGNPTDWKHIDFKIGPQG  
ALLGCDAAAGQIVKLGPNVDAARFAIGDYIYGVVHGASVRFPSNGAFAYSAISSSETAYKP  
AREFRLCGKDKLPECPVKSLEGAVSLPVSLTTAGMILTHSFGLDMTWKPSSKAQRDQPILF  
WGGATAVGOMLIOLAKKLNGFSKTIIVVASRKHKKLKEYGABELFDYHDADVIEQIKKKY  
NNIPYLVDCVSNTEITQQVYKCAADPLDATVVQLTVLTKDKIKEEBRRQNVSLGFTLLYL  
IGGNDVPFGTFTLPADPEYKKAATKFIKFINPKINDGEIHHPVKVYKNGLLDDIPQLDD  
IKHGRNSGEKLVAVLK

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

ATGGACAATTTGAAGTTCTTGACTACCCCTATCTCACACIAGTACGTAATTCAATGTATC  
ATTCGTATTGTAAGTAGATAGAGACGCAATACAGGAAAGCTGACCTTCCTTCCAATCAAC



88/251

ACGGCTGAAACGCTTTGTGACCAATTACGGACGCTTAAGAGCGGACGCGGCTGGAAACGG  
 CTCCATCCCTAAATCGCGGAGGGAGAACTCCGATACCAGCCGACATGGCAATAATAGTGA  
 CAGTAGATGCTACCAGCCCCCAATAATTTTACAGTAGATCATCAACAGTCTCTCATTTT  
 CTGGAAATGATCAGCAACTTCGACGGATT(TAACTCTCAAGCAGTACCGCAC(TCGGAGAAC  
 AGCCGTGATCATCTTTGAACAAGCAAAATATATAAAGCAGGAGAACTGTCTTACCTAGAG  
 CTACAATAGCCATAACTAACTATGTAACATTCTACAGATCAATCAAAAACAATCTTCAAT  
 CACAGAAAAAATAAAAGCCATGCTCTGACAGAGAAACAAAGCAGCGGCAACACCGCTTTTG  
 AGAACCCCTAAGGCACCTCGATTCTTCCGAGGG(TGAGTTTCATCTCTGAAAAACAACGATCAGA  
 GCGGCCACTCCCAACAGTCCATATGCCAAATATATACTGCGGGCAAAAAACAACGAGTATA  
 TTTTACATCGGCGCTCAAAAAATTTTAAAGGGATGATTTGTTTCGAGGCATTGGGTGGTACTC  
 TGAATCCCGGTTTAGCCCCCGCGCCAGTCCATAAATTGGCAATCTGTCTCCACTAGGAC  
 TTTCCGGTTTTGCCCTCACTACGTTTGTCTTATCCATCTTCAATGCCAAGAGCCCCAAGCCA  
 TCACATACCCCTAATGTTGTTG(TGGGTGTGCCATGTTTTACGGTGGCCCTCGTTCAACTCA  
 TTGCTGGTATTTGGGAAATCGCTTTACAGAACACTTTGGGTGGTACAGCCCTGTGTTTCTT  
 TCGGCGGTTTTTGGTTAAGCTTCGGTGTATATACATCCCTTGGTTTTGGAATTTACATG  
 CCTATAAGGACAAGGAATCCGACCTTGGAAATGCGCTAGGGTTTTTACCTCCTAGGATGGG  
 CACTCTTCACCTTCGGTCTTTTCGGTCTGCACCTTCGAAATCAACTATAATGTTTTTCCCT  
 TATTCTTCTCTTAGCAGTGACCTTCTTACTTCTATCCATTGCCAACTTCACACGCCAAG  
 TTGGCCTCACTAGAGCTGGTGGGGTCTTGGTGTGATAGTAGCCTTCATTGCTTGGTACA  
 ACGCTTACGCAGGIATTGCCACAAGACAAAACCTGTACATPATGGTCCATCCATTGGCAT  
 TACCTAGCAATGATAAGGTGTTCTTCTAA

&gt;YNR002C, 282 aa (SEQ ID NO 340)

MSDREQSSGNTAFENPKALDSSEGEFISENNDQSRHSQESLCKLYTAGKNMAYIYIGRQK  
 FLRDDLFEEAFGGTILNPLAPAPVHKFANPAPLCLSCFALTTPVLSMPNARAQGITIPNVV  
 VGCAMFYGGLVQLIAGIWEIALENTFGGTALCSFGGFWLSFGAIYIPWFGILDAYKDXES  
 DLGNALGFYLLGNALFTFGLSVCTMKSTIMFFALFPLLAFTFLLLSIANFTGEVGVTRAG  
 GVLGVIVAFIAWYNAYAGIATRQNSYIMVHPFALPSNDKVFF

&gt;YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGGATACCTGGTATTGTGACTCTTGTGAAGAAGAAGAAATACATCTTGTTGTTCTAT  
 GTGAAGACCATTAAAGAAACTGACCATGGTCATCTTCCCCCTGTGGACACGAAGGTCACCT  
 TCCAGTGCATACAAGAATGGTTTCTCCATCAGAATCAACAAGAATGTCCCCGGCGCTTGCC  
 CCGGTGTTGCCATTTCATCTAGGTTCTCCACATAATGTATAGTTTAAACATATCATCACCATT  
 GTTTAGTTAAATCGTTTAGAGTAATATTACCCGTCAAAAAGCTCGGCTAAAAATTTATTTA  
 CCCTCTCCGAAAAGAAAAATTTTTTCCCTCCGTCAATAGACTTTAATCCCAATACCTGATAAA  
 GAGAGTTTTACATTCGAAGAGGTAGTGTTAACTCTGGATTATATCTGTACATATGTGTTTT  
 GTGTTAGTGCTTGAGTACTTCCTAGGAGTTTACGAAAAATAAAAGCAATTTTTGTCTGAA  
 AACTAGTGAAAGGAAGAAAAATGTCCGTTGAAGAAGTTAGCAAGAGTTTGAAGAAACCG  
 TTTCAGTCGATGATACCAACAGCTACTCCAAAGACTGTTTTAAGTGACAGTGCCTCACTCG  
 ATGTCAAGCACCCATTGAACACCAATGGGACTTTATGGTACACAAAGCCAGCCGTCGATA  
 AATCTGAGTCGTGGTCTGATCTATTACGTCCCGTCAC(TTCATTCCAAAC(TGTGAAGAAT  
 TTTGGGCTATCATTTCAAAATATTCTCTGAGCCACACGAAC(TACCATTGAAATCAGATTACC  
 ACGTCTTCCGTAATGACGTTAGACCTGAATGGGAAGATGAAGCCAATGCTAAAGGTGSTA  
 AATCGTCTTTTCCAACCTTAGAGGAAAAGGTGCTGATATTGATGAATTTATGGCTAAGAAC(TT  
 TACTAGCAGTTATTGGTGAAACAATTGATGAAGACGACTCCCAATTAACGGTGTCTGTTT  
 TAAGCATTAGAAAAGGTGGTAACAAGTTTGCTTTATGGACTAAATCTGAAGACAAAGAAC  
 CACTATTGAGAATTTGGTGGTAAATTCGAAGCAAGTTTAAAAATTAACCGATTGACGGGCAATT  
 TGGAAATCTTTCCACATTCAGTGCCAATGGTAGACACCCTCAACCATCAATCACCTTGT  
 AA

&gt;YOL139C, 213 aa (SEQ ID NO 348)

MSVEEVSKKFEENVSVDDTITATPKTVLSDSAHFVVKHPLNTKWTLWYTKPAVDKSESWSD  
 LLRPVTSFQTVSEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGKWSFQLR  
 CKGADIDELWLRLLAVIGETIDEDDSQINGVWLSIRKGCNKFALWTKSEDKEPLLRIGG  
 KFKQVLKLTDDGHLFFPHSSANGRHPQPSITL

89/251

&gt;YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)

TGTCTTACATATTGCAATGGATATGCTTGGGTGATCATACTTCTGGCTTTAGATATTTG  
 AAACCTAACTCTTCTCAACAACTTCTATCGAGTGTATAAACAATTGTAAAGTTATAACAC  
 CCGCGAACAATCGGGGCAGACTATTCCGGGGAAGAACAAGGAAGGGCGCTCTTTTCTCCC  
 TCATTGTCAATAGCAAGGTCAATTTCCGCTTCTCAGAAAGGGGTAGAATCAATCTAGCACGC  
 AGATTGCAAAACACGGCTTAAATAATATGCCCTATCAGCCATTACCCCGTGTGACGAATCGCA  
 CACCGCTGCTCTCCTTAATTCCTTAGAGTAGAAAACCGAGCTTTCAGGAAAAGACTACGGC  
 AGTAAAGAATTGCTTTACTGGGCGTATAAAACCGGAGAAATCAACACATTCTAATGACTT  
 GATTACCCATGACAGCTTAATAGGTGCATCTTAGCAAGCTAAAATTTGGACAGCTCTCAT  
 TACTAAATTAAGATAGAAAATTCCTCTCTACTTTAATGATTCTACCAAAATCTCTTCTC  
 TAAATACTGGAGCCCCAATUUCTCAAATAGGTTTAGGTACCTTGGCAGTCCGAAAGAGAAAG  
 ATGCTTATAAGGCTGTTTTAACCGCTTTGAAAGATGGCTACCGACACATTGATACTGCTG  
 CTATTTACCGTAATGAAGACCAAGTCGGTCAAGCCATCAAGGATTCAGGTGTTCTCTCCC  
 AAGAAATCTTTGTTACTACAAAGTTATGGTGTACACAAACCCACGAAACCTGAAGTAGCGC  
 TGGATCAATCACTAAAGAGGTTAGGATTGGACTACCTAGACTTATATTTGATGCATTGGC  
 CTGCCAGATTAGATCCAGCCTACATCAAAAATGAAGACATCTTGAGTGTGCCAACAAAGA  
 AGGATGGTTCTCGTGCAGTGGATATCACCAATTGGAATTTCAATCAAAACCTGGCAATTA  
 TGCACGAACACCAAAGACTGGTAAACTAAGGCCGTTGGAGTCTCCAACTTTTCTATAA  
 ATACCTGAAAGATCTATTAGCATCTCAAGGTAATAAGCTTAAGCCAGCTGCTAACCAAG  
 TCGAAATACATCCATTACTACCTCAAGACGAATTTGATTAATTTTTGTAAAAGTAAAGGCA  
 TTGTGTTTGAAGCTTATTTCTCGTTTAGGTAGTACCGATGCTTCACTATCGAAGCAACCGG  
 TTATCTTTGAAATTCGGAAGAAAAATAACGTTCAACCCGACACCTTGTATTAGCTGGC  
 ACGTCCAAAGAGGTTATGTTGCTCTTGCCAAAATCTCTGAATCCCGATCGAATCAAAACCA  
 ACAGGAAAAATATTTACTTTGTCTACTGAGGACTTTTGAAGCTATCAATAACATATCGAAGG  
 AAAAGCGCCAAAAAAGGGTTGTACATCCAAATTGGTCTCTCTTTGGAAGTATTCGAAGTAA

&gt;YOR120W, 312 aa (SEQ ID NO 354)

MPNTLHDSTKILSLNTGAQIPQIGLGTWQSKENDAYKAVLTALKDGYRHIDTAIYRNRD  
 QVGNALIKDSGVRRRTFVETKLNCTQHHEPEVALDQSLKRLGLDYVDLYLMHWPARLDPA  
 YIKNEDILSVPTKKDGSRAVDITWNFIKTMWELMQELPKTKTKAVGVSNFSINHLKDLL  
 ASQGNKLTFAANQVELIHPLLPQDELINFCKSKGIVVEAYSPLGSTDAPLLKEPVILEIAK  
 IKNVQPGHVVISWHVQRGYVVLPKSVNPDRIKTNRKIFTLSTEDFEAINNISKEKGEKRV  
 VH?NWSPFVFK

&gt;YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2: 723-1090 (SEQ ID NO 357)

AGGAAGAGGAGGCTGCGTTTGACGACGAAGAGGATGATAATGAGCAAGAAGAAGAAGAAG  
 AGGACCGCGATGAAGAGAACGCCCTCTCGTCTAAGAAATTTAAAAAGAGAAGSAGCAGCAA  
 TGTACAGAGAAGAGGAAGAAGAAGAAAAAGATAGGAGCGAGACAAAAAGAGAAGSGTTG  
 CGGTCAATCGAGGACGACGAAGACGAGGATTACAGCAGACCTTACTTTGTTTATATATATT  
 AGTATGTACAATCGCAAAGAAATGGAGTGTATGACATGTTGTAGTATTTAGTATGAGGTTA  
 CTGTGTGGGAGGTTTTTACCATGATTTTTTCCGACAAACACCCCATCAAAATGCTCTTTGACG  
 AAACCTATTACCGCATTAATATTTTTTTCTTTTTAAAGCTCAGTTGACCCCTTCTCAT  
 TCTCTTTCTTAAAAACAACCTGCTGATCTTTGAGAAAAAGATAAAATTACATACACAAUATAAA  
 CCAACTACGATCGCAAATTATGCTCTGGCAAGGTATGTGAACGAGACAATTATCAATTG  
 ATTAAGAAAGAAATCAGTCGGAGGCTAGCTTGTGTGACAATGTTTGGCAATGCCCGATTT  
 TTCTTGATGCGCCCTAATTTTCAAGATTAAACACTCAGAGTAAATTAATACTGGAAATATC  
 AAAAAACATATGAAATTTCAAACATGAACCTCTTTTCGGTTTTTTTCTCTCTACTTTTAAAC  
 AGCATACACTGATAACTTAATAGGAACCGGTAAAGTACAAAGCTGTUATCTACTCGAG  
 ACCAGGTGACGCTGTTTGGGCTACTTCTGGTGGCTATCTTTGCAACCAAACGAABTTGG  
 TGAATTTTCAAGGCTTCGACAATCCAGCTGGTTTGCAAAGCAATGGTTTGCATATTCA  
 ACGCCAAAAGTTTCATGTTTGTGAGAGCTGACGATAGAAGTATCTACGGTAGACATGATGC  
 TCAGGGTGTGTTTGTGTAAGAACTAAGCAAAACCGTTATTATTGCTCATTATCCACCAAC  
 CETACAAAGCCGGTGAAGGCCACCAAGATTGTCCAGCAATTGGCTGACTACCTGATTTGGTGT  
 TCAATACFAA

90/251

&gt;YOR122C, 126 aa (SEQ ID NO 358)

MSWQAYTDNLTGTCVKDKAVIYSRAGDAVWATSCGLSLQPNBICEIVQGFDNPAGLQSNGLHIQGGQKFMLLRADDRSIYGRHDAEGVVCVTRTKQTVIIAHYPPTVQAGEATKIVEQLADY  
LIGVQY

&gt;YOR261C, 1517 bp, CDS: 501-1517 (SEQ ID NO 361)

GTAAGGTAAGGCATCATTAGCAGGATCCATATTCACCTACCTGGGAATGTCTTCCCATGGC  
ATTGAAGAAGCTGTGAGCAGCCGTTGCCAATAGGTTGACTTCCCTGAACCTGGTGGACCAAT  
AACAATCTGAGCGAAGGGCATTATCTGACTCTCTAGTAGAAAAATCAAACTATTGACACA  
ACAACAATCAAAATGAAAAACAACCATTCTATTACGGTAAGTAGTGAAAGACTCACAAATGCA  
ATCTTTCAATGAGCATCACTTACTTTAAGTAGCAATATTCTTAATCACTTATTACGAAAT  
TTGATTTTACTAAAGTTCGGGGATACCTCAGTGGCAAAATCGTTACTCAAGCTTCCACGTAA  
UGTAGAATCTACAATGAAATAATTGTGAAGCCAACAGCTAAGCAATCTATAGTGTAAACGT  
TGGCTTTTCTGTACAACGTGCTAGCTGAGCGGCATTTTTCGAATTTAAAAAAGCAAAAGAAA  
GAAAGGAAATCAAAATACAAATGTCTCTACAACACGAGAAAAGTTACCATTGCACCACTAG  
TTTGTCTATCTGCTTTGGATCATTATGAGCGTACGCAGACAAAAGAAAAACAAAAGATGCG  
TTGGTGTCTATCTTAGGTGATGCTAACAGTTCCACTATCAGAGTCACTAATTCTTTGCTT  
TACCGTTTGAAGAAGATGAGAAAACTCTGACGTTGTGGTTTTTAGACCATAATATATTTG  
AAAAATGAATGAAAATGTTTAAAAAGATTTAATGCCAAGGAAAAATCATTGGATCGGTATC  
ATAGTGGTCTTAAATTAAGGGCTTCTGACCTCAAGATTAATGAGCTGTTTAAAAAATATA  
CTCAGAATAATCCGCTATTATTAATTGTTGATGTCAAACAACAAGGTGTTGGTTTACCAA  
CAGATGCATATGTCGGGATTGAGCAAGTTAAGGATGATGCTACCTCTACACAAAAAGACCT  
TTCTTCATTTGCTTGTACTATTGAGGCCGAAGAAGCTGAAGAAATTTGGTGTAGAACACT  
TATTGACACAGTACCTGATCAAGCAGCAGCTCGCTTATCTATCCGGTTGACCAACCAAT  
TAAATCTTTGAAAGGATTACAAAGCAAACTAAAAAGACGTTTTCGAGTACTTAGACAAAAG  
TCATTAATAAGGAATTACCGATAAACCCACACTATATTGGGCAAGCTACAAGATGTTTTCA  
ACUTTTTACCAAAATCTGGGAACCCCTGATGATGACGAAATAGATGTGGAGAATCATGACA  
GAATTAATATCTTCAAATAACTTACCAAAAGGCTTTAACTGTGAAAACATAATGATGAATTA  
TGGTTATATATATAAGCAATTTGGTTTAGGTCAAAATATCGCGTTTGTATGATTTTCAATGAAA  
ACAAAAATCAAATAAAAAAATCAAGAACAAAGAGTAAAGGACAAAACAAATCAAAAGTCT  
CTGATGACAGTGAGAGTGAGAGTGGTGACAAAGAAGCAACTGCGCCATTGATCCAACGAA  
AGACAAAGAAAAATTA

&gt;YOR261C, 338 aa (SEQ ID NO 362)

MSLQHEKVTHAFLVLLSALDHYERTQTKENKRCVGVILGDANSSTIRVTNSFALPFEEDE  
KNSDVWFLDHNVTENMNEMCKKINAKKKTGWYHSGPKIRASDLKTNELFKKYTQNNIDLL  
LIVDVXKQQGVGLPTDAYVALEQVKDDGTSTFKTFLHLPTTBAEEAEELGVEHLLRDVVD  
QAAGGLSIRETNQLKSLKGLQSKLKDVEYLDKVINKELPINHTILGKLQDVFNLLPNLG  
TPDDDEIDVENHDRINISNNLQKALTVKTNDELMVIYISNLVRSIIAFCDLIENKIQNKK  
IQBQRVKDKQSKVSDDESESGDKEATAPLIQRKNKK

&gt;YPL271W, 689 bp, CDS: 501-689 (SEQ ID NO 391)

CAGCAGCCACAACCTCAGAGTGCTTACAAAAAAGAGTTGATCCCGCTAAAGAAAGTCT  
TGATTTACGTATTTATCCAGGTTCAAACGGATTGCCAAAAATAGTCGATAACCTCGGAGT  
AAGCAAAGCAACAATATACTTGTCTTCGAAAAGGTAACCTCTTAACTTCTATAGAAGC  
ATTCTACTAGTTCTCTCGAAGAAAAAACTAAGAAAGCTATAGCTGTATCTTACCAAGCC  
ATGAACCTTGAGGAATTGGTAATCTTATTAGGAAATAAGCTAAACTAGGTAATAGCAGAT  
GATTTACTAGCTTACTATCTCAUACTAAGTCTGGCAAGCGCTTATTTTTTAATACTTTT  
ATACGAACCAATGAAATTTGATCCTCCCCCTTTTTCGTCTAGTTAAATGAAGAGATACAAG  
TAGGCCCTTTCTATTGAGTACTTAGCAAGATATGTATTTCTAAGAAACATCAACAGTTTCA  
GUCCACAACCGATTTCATAAAATGTCGTGCTGAGGAAAGCTGGTATATCATATGCTGCAAT  
ATTTGAATGTGGCGGCTCAGGCTATCCGTTCTTCATTGAAAACCTGAATTAACAACCGCTA  
GTGTTCTTTAACAGATCGCAACAGATGCTTTTATATACCCAAATATAAAATCGCACTGCAAG  
CTTCTGAACCCACTCCAAATACAAAAATAG

91/251

&gt;YPL271W, 62 aa (SEQ ID NO 392)

MSAWRKAGLSYAAYLNVAAQAIRSSLKTEIQTA5VLNRSQTDAFYTQYKNCTMSEPTPI  
TK

&gt;YPR035W, 1613 bp, CDS: 501-1613 (SEQ ID NO 395)

TAGTGCCATTGTGTCATTATTATTATCCCAAATATGCGAAAATAGTACACTATTTTTTGG  
 CAGGAGACTAGGCTGATATGCCGCATTGATGTCTGTGTAGCGAAACACAAACAAAAAA  
 GAAAAAGCTAGGATGAAAAAAGAAAAAGTAATATGAAAAAAGAGTCAAAAAATTAATTCATT  
 TGTTAGTGTAAAGCGGTACGGTGTAAAGTAGTAGGCTTGATAATGAATTAAGATGACTCCG  
 ACGCATATGTGTTCGCATGTATTATTTTAGTTTGTAGATTTCTTTTTTTTGTAAATATATA  
 AGGGAGTGATTCCTATATATCGAATTCTCAGGCTTCCTTGGTTTGGTAGCTTGTCTCTCTT  
 TGTATTTCGTTAGGTAAGAACATCACACAAAGATAACTATAGAATCACATACATATTTGTG  
 AGAAATTAACTTTCAATTTATAGAGAAGTTCAACCGAAACAAAAATTAACATAAT  
 ATAATATAATATAATCAAAAAATGGCTGAAGCAAGCATCGAAAAGACTCAAAATTTTACAAA  
 AATATCTAGAACCTGGACCAAGAGGTAGAAATAATTGCGGAATACGTTTGGATCGATGGTA  
 CTGGTAACTTACGTTCCAAAGGTAGAACTTTGAAGAAAGAGAATCACATCCATTCAGCAAT  
 TGCCAGAATGGAACTTCGACGGTTCTTCTACCAACCAAGCCCCAGGCCACGACTCTCACA  
 TCTATTTGAAACCCGTTGCTTACTACCCAGATCCCCTTCAGGAGAGGTGACAACATTGTCTG  
 TCTTGGCCGCATGTTACAACAATGACGGTACTCCAAACAAGTTCAACCCACAGACACGAAG  
 CTGCAACAGCTATTTGCTTCCTCATTAACCATGAAGAAATCTGCTTTGGTCTAGAACAGAAT  
 ACACTCTATTTGACATGTATGACGATGTTTACGGATGGCCAAAGGGTGGGTACCCAGCTC  
 CACAAGGTCCCTTACTACTGTGTGGTGTGTGGTGGCGGTAAAGGTTTATGCCAGAGACATGATCG  
 AAGCTCACTACAGAGCTTGTCTTTGTATGCCGGATTAGAAATTTCTGTATTAACGCTGAAG  
 TCATGCCATCTCAATGGGAATTCGAAGTCCGTTCCATGTACCGGTATTTGACATGGGTAAC  
 AATTATGGATGGCCAGATACCTTTTTCACACAGAGTGGCCAGAAAGATTTTGGTATCAAGATCT  
 CATTCOCATUCAAAGUCATTGPAAGGTGACTGGAAACGGTGGCCGTTTGTACCGCTAACGTTT  
 CCACCAAGCAAAATCAGACAACCAGCTCTACGAAATACATCCAAACAAGCCATCCAGAACT  
 TATCCCAAGACACAGCTGAACACATTAAGTTGTACGGTAGCGATAACGACATGACATTAA  
 CTGGTAGACATGAAGACCGCTTCCATGACTGCCCTTTTCTTCTGGTGTGGCCAAACAGGTA  
 GCTCAATTAGAATCCCAAGATCCGTCGCCAAGGAAGGTTACGGTTACTTTTGAAGACCGTA  
 GACCAGCTTCCAAACATCGACCCATACTTGGTTACAGGTATCATGTGTGAAACTGTTTCCG  
 GTGCTATTGACAATGCTGACATGACGAAGGAATTTGAAAGAGAATCTTCATAA

&gt;YPR035W, 370 aa (SEQ ID NO 396)

MAEASLEKTLQLQKYLELDQREGRLAEYVWLDGTVGNLRSKGRFLKKRITSLEQLPEWNFD  
 GSSTNQAPGHDSDIYLPVAYYPDPEFRGDNIVVLAACYNNDGTPNKENHRHEAAKLFAA  
 HKDEEIWFGLEQEVTLFDMDYDDVYGWPKGGYPAPQGPYYCGVAGAKVYARDMIEAHYRAC  
 LYA5LEISGINAEVMP5QWLEFQVGPCTGIDMGDQLWMARYFLHRVAEEFGIKISFHPKPL  
 KGDWNGAGCHAMVSTKEMRQPGGTXYIEQAIEXLSKRHAETHIKLYGSDNDMRLTGRIHETA  
 SMTAFSSGVANRGSSIRIPRSVAKEGYGYFEDRRPASNIDPYLVTGIMCETVCGAIDNAD  
 MTKFERESS

&gt;YBR133C, 2984 bp, CDS: 501-2984 (SEQ ID NO 53)

AACTTACGACAGAGTTGTAATGAATGCTACTGATGTCTGCTCTACTGCCA  
 TCCGCTGTCCCTTCATGCGATAAAAGCTCCATTCTTTATTTATCTCATACC  
 ACGAGAAAAAAATTCACCTGACATATTTTATTAACCCGCCCTTTTGAAGCC  
 CTAAAACAGATCTCAGGGCTCGAGTACTGTTTTATCTGAAAAATCTTCGA  
 GCCCTCGTTTTCGACTGAGCTAAACCAAAAGAAAAATAAACAAATCAGAAA  
 TGGAACCCGAAACAGCACGCTGCCGAGTGTTTTATATTTTCTTGAAACA  
 AATGGCTTTATACAAATGTGTATGTCTGATAGAAAAATGCTATATTTTGA  
 GTGACTTGTGATCCTATTCCCAAGCCCTATAGGAGCTATTTCAATTTGCC  
 TGTGTGAAAGCGTGTTGTGTGTGTGTGTGTGTGGAATTGTCCGGACGTTCC  
 TCTTCTTTTATACATATAATTTTTATATATACAAAGGGTTCAGTTTGCAT  
 ATGCATAGCAACGTATTTCTTGGTGTCAAAACAGGCTTTAATCMTAAACA  
 GCACAGCAAAAAGTCAGTTTCTTAGAAAATGTCTCTAGTCATTCCACAG

92/251

AACTGCCTAGTAACTATGATTACGTTTTCCTTCCATATAACACGCCAAGA  
 TATAAGGAAATAGTTGGGCAAGTTTTCAAAGATTTCCAAACACAAATCCAT  
 ACAGAACTGGAAACCGCTTCAATTCCTGAACCGCACTTGCAGCATATCT  
 GTATACCCCGGTTCAAGCTCAGAGCTCAGACAACTACCAATACCGCGTCT  
 TACATAGGGCTGTATCCTCTTGGCTGGAGCTGGAGCTCGCGATCCAAA  
 TGTAAGAGATCTTGGCTTAAAGGTCCCTCTAAACGAATCTAACTACCCGA  
 GGTTCGTTGGGAATCAATAAGCTAATATTGGCGCTCCACGGACCTGTCC  
 AACCTGCAATCTGTATGGACAGATGATTTACAGGCTCCTGCAAAATCGCAT  
 CGTCTTTGCTGGCGCTGCGTTAACCATACTCCATTTCTCTGCCACTTCAAG  
 AAGACAGCGATCCATTGGCCACTTGGGAAGCTGTGGAATACCGTGGCGAAA  
 CAATGCGAATCATCTCCCTCTTTGACTATCTCTTTGGCTTTGCCAAGAAC  
 CAGGACTCCTTCGTATGTGCTGAATAGATGGTTAGCCGAACCGTCTCGT  
 GTCTTTTGGTATCTTCATCCATCTTTGCCAGTAATCAGTACGATTAATCC  
 GTTTTACACAAGTTTAAACAGAAATTTGATTTTAAAGTTCCAAAAGCTTAA  
 TGGAGATTCACAAAATTTGGGTAAATGAATTAATGCGTGATATTGCATGGGA  
 TCGAGAAATTAACCAATAATGTTAAGGGCGGAGAAATCTGCCATTTTGGAA  
 TATATAAATCTATTATTGAAAAAGGGCGACAAAGTATTAAATTCCAATAG  
 TAATCACCAACTTTTGCTCCAAGAGGACTCTCGGATAATGCCGCTCTGA  
 AACCTCATTCAGATAATTTAATTAATTCACAAATATTGACCTTTGAAAAA  
 GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGGCGCTTCA  
 AGATCTTGCTCCTCGAGCGAGTGCCTAAGAGACCGTTGCTGATCTACTAG  
 CCGGTGCGGGAAGAGGACCTTTAGTGGATCGAATTTTAAAGATAATATCA  
 ATGTTGTTTTATGGAATAGTAAGGTTTCTATAATTGCCATGAAAAAATCC  
 ACAGGCATATCTGTACTTCAAAAAAGAAATTTGACTCTTGGCATAATA  
 GAGTGAATTAATCAAGGAGGATATGACCAATGGCAATCAACGAGCCG  
 TCGGAAAAAGCGTATTCAGATAGATCTGTGCATAAGTGAATGCTGGGTTT  
 GTTCGCTTGCAATGAATTATCACCAAGATGCTCTGCTGCTATTTGAAAAAT  
 ATCATTCACCAATGACACAAATTTTCATACCGAGGTCATACTCTTCATAC  
 ATAGCAATCCATTTCTACCAATTAATTCACCAAAATCTCACAAACAAA  
 TCGCTCTTTGGAGGCGCCCTCGATAGTCCATAGAGTGCCATCTGTATAT  
 TATCCTCAAGGGTAATGAAGTGTGGCGGTTGAGCATCCCATGCCCCAA  
 AAACATACTCTCCAAGACGAAGATCATTTTACAGTTGAATTTCTCAAAAG  
 TTCATTAAATGAGTTCAGATAAAGCAACCGCGCGAAATCCATGGCTTTA  
 TCGGATCTCTCTCGGCRAACTTATATAACAATATATTTCTGTCACTTTG  
 CCCAATCACAGCACAGTCCGTTTAAATTTAGCGAAGAAACGTTGATGAA  
 TACCAGACGAGAAGAAATCTAATCAAGAAATGTGACCATAACCCAAATA  
 TGACCTCGTGGTCTCCAATTAATCTTTCTTTGAAGCAACCAATATCTTT  
 ATAGATGACTCCGAACCTTTCTGTGCTGATGCTCTCGGATACACTCCGATAC  
 AGAACAAAAAGTTTGGTATGAATGCTCTTTCCAGACTTTTCATATACCTTA  
 TGTGTGCAAAATTACACTTCGGCGGTAACGCTGCAAGCATGACTATTCGG  
 AGGTCTATAGTTACAGATCACACTAAAACPTTAGCCCNATATCGACATTA  
 TTCAGCGACTACCAATCAAAAGCTAGATAATCAAAATTGATCTTGACCAAG  
 ACATTGAAAACGAAGAAGAACAGGGATTCTTATCCAATCTAGAAACTGGT  
 TGGCAAAAGCGTACAAGATATTCACGGACTCAGCGAAACCGCCAAACCGGA  
 CCATTTAGATTCTATCAATAAGCCATGTTTGATCTCAAATCTACTAAAG  
 CCGTTGAACCCCTCTAACGAATTGCCAAGCCACCAAGACCTCGAGGAAGAT  
 GTTCCAGAASTTCATGTACAGCTCAAGACTAGTGTTCACAGCTACATAA  
 TGTCTGTGGCAGAGCCTTTTCCCTGUCTCTGTGA

YER133C, 827 aa (SEQ ID NO 54)

MHSNVFVGVKPGFNHKQHSKKSRLFNVSSSHPELPSNYDYVLLFITTFR  
 YKRTVGGVFKDQQRQS(QNNKPLQIPEPQLQDICIPFNVVKILNDQTPS  
 YIGLLSSWLELRSRDENVRIHGLKVLNECKYARFVGINKLI)AFPHHS  
 NLQLYGOMLYRLDQNRIVFAAPALPISISLPLYEDSDPLATWELWNIVRK  
 QCEYHPSLTISLALPRTRTPSYVLNRWLAEPVSCLLVSSSIFAENQYDYF  
 VLHKFNQNLILKFKQKVGDSQILGNELCVILHGMEKYANNVKGESAYLE

93/251

YINYLLKKGDKVLNSNSNHQFLLOEDSRIMFPLKPHSDNLLNSTYLTFEK  
 DLVKYDLYESAILEALQDLAPRASAKRPLVILVAGAGRGPLVDRTFKIIS  
 MGFMDSKVSIIEKNPQAYLYLQKRNFDCTDNRVKLIKEDMTKMQINBP  
 SEKRIQIDLCISELLGSFGCNELSPECLEWSIEKYHSINDTIPTPRSYSSY  
 IAPISSPLFYQKLSQTNRSLEAPWIVHRVFYCILSSRVNEVWRFEHPMAQ  
 KDTVQDEDDFTVEFSQSSSLNEFKIKHRGEIHGFIGFFSANLYKNIFLSTL  
 FNDSTVRLKFPSEETLMNTRREENLIKCDHTPNMTSWSPLIIFPLKQFLSF  
 IDDEELSVLMSRIHSDTEQKVWYEWLSLEFIYLMLSNYTSAVTAASMTIP  
 RSTVTDCTFKTLAHRHYSATTNQKIDNQIDIXQDTENEEFQGFLENLETC  
 WQSVODIHGLSETAKPDHLDSEINKPMFDLKSITKALEPSNELPRHEDLEBD  
 VPEVHVVRVKTSTVSTLHNVCGRFSLPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)  
 AAAGGGGAAGTATGGCATGCCAGAAATCTTTCTGGAAACTTTGAAGCAT  
 ATCATATAATTGTATGAACCTGTCCCTCAAAGATGTTACCAAATATTCA  
 AGAGTATGTGAGCTTTCTATCTATTGACGCGTAAGAAAGGCTATCACGT  
 GTGGGGGGGAGAGCTCAGCCACATTGCCACTACTTTTGGAAACCGCTAGTC  
 GGAAACGACATTCCCCCGTACCAAACAAACGAAAGGACGTGAAAGGTAA  
 ATGAATAACATGGCACTAAAAATTTGGCAGAAAACGAAAAAAGGAA  
 AAGGAAACTGAAAACATACCGCTTCCCTTAGGATACCTTCTGATTTACAT  
 CCGAAGAATTGGGTGCCTCAATTAAAGGCAATTCTTCCCTCTATCAAGCA  
 GTTTTACTGCGTCTCTCTAAACAAACAAATTCTTTTACTGAAATTTCAACAA  
 AGTTCTAACTCGAGGTGACCGGAGGCCACTGTAATAATAAAAAATAGAAG  
 ATGAGTCTTGAAGGAAATACCCCTAGGCAAGGGGCCAAATCTTTTCTCTCT  
 GTATATTGCGGTAAATCAGTACTCTAAACGAATGGAGGACGAGCTCAATA  
 TGAACACAGGTGATAAAATTAAGTCATTAAGTATGATGGGGASTACAAT  
 GACCGCTGGTATTTATGGGCGCAATTTGAGAACCAAGAGGAAGSTTTATA  
 GCCAGCGGTATTTACCAAAGAATAGCAATAGAAAAACCTAGAGAACCTGC  
 ACAAAATCACCAACCCCAAGAGAGTGGAAATTTCTGGCTGTAAATAATGGAAAT  
 TTAAATGATTCTGCGAGTAACATAGGTAAAGTCTCCTCGCATCAACAGGA  
 GAACAGATATACATCATTGAAAAGTACAATGAGCGATATAGACAAAGCCT  
 TGGAAAGAGCTAAGAAGTGGTTCAAGTGAACAAGAGGTATCAAAATCGCCC  
 ACACGCGTGGCCGAGTTAGCACTCCACAGTTGCAAGATGAACAGACTTT  
 GATTCAAGAAAAACAGAAATGAGGAAAACAGACACATGACTCGTTAT  
 ITTCTAGCACAGCGGATTTAAACTTAAGTTCTGAATCTTTGAAGAATATA  
 ACTAAGTCAAAATATATCAACAAAATCCCTAGAACCAGATTCCGGAATCAGT  
 TCGTCAATTAGATTTGAAAATGGCTAAAAGTTGGAGCCACAGAAGAGGTTA  
 CTGATTACTTTAGCTTGGTTGGATTGATCAATCCACTTGCAATAAATTC  
 AAGAGCATCAAGTCTCCGGAAAATACTACTCGAATTAGAACTCGAACA  
 CCTAAAAGAATTGGAAATAAATTCCTTTGGTATAAGATTTGAGATATCA  
 AAGAAATAAGGAACATCAAGTCTGCAATTGATTCCGTCTCAAAATAAACCTG  
 GACGCGGACTACTCTACCTTTGCTTTTGAAAACCAAGCTGCCCAACTAAT  
 GCCTGACGCCACTGTAAATAGAGACGAATUCACCAACAAATTTCCCTCCA  
 AGTGTAACAAGTTGTCAAGTGAAAGCTCTGATAGAAATCATCTTCGGTC  
 ACCACAGAATTGCAAGACCAAGCTCGGTTGTTGTTAATCCCAATTTTAA  
 ACTTCACGACCCAGCTGAGCAGATCCTAGATATGACAGAAGTTCCCTAATT  
 TGTTTTGCTGATAAAGATATTTTCAAAACACCGGGGAGGGCTCCAAAACCA  
 UATCATATCCAAGTTCAGTTCAACCTTCACAATTCGCTCTTTTAAATAA  
 CAGGTACACAAATAATAACGCAAGGTTTCCCTCCTCAAACAACATATCCAC  
 CTAAAAACAACAACCAACCGTTTATTCAAATCGGGCTAATTTCCAAATTCT  
 TCGACATCTTCCGATAAATTCAAACGGGCAAGTTCAAATTCCTTGGCATGAA  
 TGGTCATGACTCGAACTCTAGGAAAACAACACTGACATCTCCTACTATAAC  
 CTCTATTAAACACCGTAAACACACATCAATCTCTACCCGCAATTTCAAAAT  
 ACATCTTCAAATGCTACATCTCATCATCCGAACAGAAATTCGGTTGTTTA  
 CAATAACCATAAGAGGACCGAATCCCGAAGCTCATTGTTGATTGTTCA  
 ACAGGATTTCAATCTCTATCCCGAGTCAAGTCAAGTTTCGACGAAGAAGAA

94/251

ACGAAACAACCTTCCAAAAGCTAGCAGAGCAGTCTTTTGACTCAGCAGCGCAG  
 AAGTTCGTCTTACGGACATTTCAAGAGATGCCTCAGTTCTGAAATGAAAA  
 AGCATAGGAGAAACTCTTCTATATTATCTTTTTTTTTCTTCAAAAAGTCAG  
 TCTAATCCAAACGTCACCAACCAACAACCTTTCACTATCGATCCCGCAAA  
 GATGACTTCCCATTCTCGTTCTCAGTCGAATTCCTATTGCGATGCAAGAT  
 CACAATCTTACTCCCATAGTAGAAAACTCTCGTTAGTTACCAGCCCCCTTG  
 AAACTTCTTTAAGUCCATATAAAATCCAAATCCAATATTGCTTTAGCGCA  
 TAGCGAAACTCCTACTAGTAGTAATAATAAGGAGGCAGTATCACAAUCAA  
 GTGAAGGGGAAGCACAAGCACAAGCACAAGCACAAGCACAAGCACAAGCACA  
 AAGAACAGTAGCTCCAAAGATGGCTCTTCCGAAGAAAAAACA AAAAGAA  
 ATTATTTAGTAGCACCAAAGAATCATTTGTAGGAAGCAAGGAATTCAAAA  
 GATCTCCCAAGTGAACCTTACCCAAAPATCTACCAAATCGATACTTCCCAGG  
 TCGAATGCTAAAAAGCAACAAACATCTGCTTTTACCGAAGGTATACGCTC  
 TATCACAGCAAAGGAATCTATGCAAACTCCCGACTCTTCAGSCTGGATGA  
 GCAAAAAGGTACCGCTGCTATGGGGACTTGGAAACAACGGTTTTCACA  
 CTTTCATGGAACAAGGCTTTCTTATTTTACGAATACCAATGATGAGAAGGA  
 GCTGTCGGCTGATAGATATAACGGCACATAGGGTCTTACCTGCCAGTGATG  
 ATGATAGGCTCATTTCCTTATACGCTGCGAGCTTAGGAAAAGGAAATAC  
 TGTTTTCAAAATTGGTCCCTCCGCAACCGGGGTCCAAAAGGGGCTAACCTT  
 TACAGAACCTCGCGTTCACTATTTTGCAGTTGAGAATAAATCTGAAATGA  
 AGGCATGGCTGTCAGCCACAATAAAGGCCACTATTCATATTGATACAAGC  
 GTCCCTGTCATTAGTTCAATGCCACACCAACGATACCTCTAAGCAAGGC  
 ACAGACGCTATTGGAAGAAGCTAGGTTACAAACCCAGTTAAGAGATGCTG  
 AAGAGGAACACCCAAAGACATCAATTTGGATGGGATGACACCCAAAATAAA  
 AGAAATTCTAATTATCCAATCGAACAAGATCAATTTGAGACCAACCGATTA  
 CCTGGAAAGTTTCAACATTTGAATAACUUTGGTGGCAGACTTTGA

YRIJ85W, 980 aa (SEQ ID NO 32)

MSLEGNTLKGKAKSFPLYIAVNQYSKRMEDELNMKPGDKFKVITDOGEYN  
 DGWVYGRNLRKKEGLYPVFTKRIAIEKPENLHKEPTQESGNSGVKYGN  
 LNDASASNIGKVSSHQENRYTSLKSTMSDIDKALBELRSGSVEQEVSKSP  
 TRVPEVSTPQLQDEQTLIQEKTRNFENTTHDSLFSSTADLNLSSSLKNI  
 SKSNISTKSLSPSSSVRQLDLKMAKSWSPPEVTDYFSLVGFQDQSTCNKF  
 KEHQVSGKILLELEHLKELEINSFGIRFQIPKEIRNIKSADSSSNKL  
 DADYSTFAFENQAAQLMPAACTVNRDEIQQIISKUNKLSSESSDKKSSSV  
 TTELQRPSSVVVNPNEKLHDPAEQLDMTEVPNLFADKDIFESPCRAPKP  
 PSYPSPVQPPQSPSPNNRYTNNNARFPQITTPPKNKNPVTVYNGLI PNG  
 STSSDNSTGKFKFPAMNGHDSNSRKCTLSATLPSINTVNTDES LPAISN  
 LSSNATSHHPNRNSVVVNNHKRTESGSSFVDLFNRISMLSPVKSSFDEFF  
 TKQPSKASRAVFDQARRKSSYGHISRDASLSEMKKHRNSSLFFSSKSO  
 SNFTSPKQTFTIDPAKMTSHSRSSQNSYSHARSQSYSHSRKHSLVTSPL  
 KTSLSPIINSKSNIALNISTPTSSMNKEAVSQFSEGGKHKHKHKSKHKH  
 KNSSSKDSSSEKSKKKLFSSSTKESFVGSKEFKRSPSELTQKSTKSILPR  
 SNAKKQQTSAFTEGIRSITAKESMQTAACSGWMSKKGTGAMGTWXRFFC  
 LMGTRLSYFTNTNDEKERGLIDITAHRVLPASDDRLISLYAASLGKGKY  
 CFKLVPQPQGSKKGLTFTEPRVHYFAVENKSEMKAWLSAIIKATIDIDTS  
 VFVISSYATPTIPLSKAQTLLEEARLQTQLRDAEEEEECRCQFOWEDTQNK  
 RNSNYPIEQDQFETSDYLESSAFEYFGGRL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGTCTTTTCGAGAGCGGAAGAAGTTGTAGGCTAAGCGC  
 AGGCTAAGCGCTAGGTCATATTTAACTATCCAAGACAATATCCACCAAG  
 CGGCTGAGCAACCAACAGAATCCTGCTTCTCCTCGACTTACCAGATAGTT  
 AAGATACTGTGCACCATGGAAATTGAAAACGAAAGTACGTACCGACTACT  
 TTATTTTTTGCAGGCCCGAAATCAAGCGATGAATGAGACATCCTTCTGTTT  
 TCTATGTTGGGACAGACAGTCGCTTATCTTAGTGAGATTCTTATTAAT

95/251

GAATTTTCTTGGCTGCTGCTGGAGATTTGCACCTGCATAGCGCAGATTCT  
GUTTCCTTCTCAATAGAGTAGCTTAATTAATTACATTCTTAGATGATGATAA  
GACGCAAACTCGACAACTCTTTCTTTATATTGATGGATTCTTCTGTCAAAA  
AGCATAACAATCAACACACTATTGTTAATTTGAAACTTACAAAAATAAA  
ATGAAAGTTTCCGATAGGCGTAAGTTTGAAAAAGCAAACCTTTGACGAGTT  
TGAGTCGGCTCTAAATAACAAAAACGACTTGGTACATTGTCCCTCAATAA  
CTTTATTTCGAAACGATCCCAACGGAAGTGGGTCAATTCTACGAAGACGAA  
AAGTCTGGCCTAATCAAAGTGTTAAAAATTCAGAACGGTGCAATGGATAG  
GAAAAGGTCTTTTGAAAAAATTGTCATTTCCGTCAATGGTGGGAAAAATG  
TAAAAAGTTCTCTGACATTGTTTGAAGACGAAACAGATTTCAGGGCGGA  
CCAATCCCTTCAAAGTATCTTATTTCCCAAGAAAATCAACTTGATGGTCTA  
CAAGTTGTTTTCAAGTGCATACTTTGAAATTCAAATAGAAAGGATTACGATA  
CCCTTTTCTTTTTTAACTCAACAGAGGATACCTATAATGAGTTGAGTTTTC  
CGTGTCTTGGAACGTTGTACCGAAATAGCGAGTCCCAAGCCGAAACGACAG  
CTCTACGATGGTACTTTCACTGACTTTGTCTTCTGGCGCACCTATTGTAA  
GGAGTCTTCAGAAAAGCACCATAAGGAAATATGGGTACAAATTTGGCACCC  
TACATGTTCTTGTTAATACACGTAGATGAGCTATGATTTTCTGCTATA  
CCAAGCAAGTTTACCTGGCGAAAAGAAAGTCCGACAAAGAGCGGCTGAAGC  
GTGATCTATGCCACGTAACCCATTGAGATAAAGTACTTTTCACAGATA  
TGTAACGATATGATGAACAAAAAGACCGATTTGGGTGATATTTCGATAT  
TATCTTCCGAGCATGTGCGCTCAATTTCCGGCGGGTCCCGGTGGTGGCG  
CTGCTGACGAAGAGGATCGATCTATTACGAATGAAGAACCCCATTTATTTCC  
TCTGTGGACGAGCATGGCTTCAAAATATGTAAGTTGGGTAGTCCCTAACAC  
TCCACGAAGACTCAGAAAAACACTAGATGCCGTGAAAGCTTTATTGGTGT  
CGTCTTGTGCTTGTACTGCAAGGGATTTFAGATATATTTGATGACACCAAC  
GGCGTTGGCAATGTGGAAATGGATCAAAATTCGTGACCACGAAGTAGCGCA  
GGAAACUACGCTGAAGGACTCTTATAGAATAACTTTTGGTAACTTTCTTTG  
ATGGTATATCAGTATGTGGAAAACTTTTAAATCCGAGTATGTCCGCGGC  
TTTTTACTTTGCATCCAGGCTCAGTTGATAACCTTTGGGGAGACTTGAA  
CAACTGCTTTTATATGCCTACAGTGGTTGATATTGCCAGCCTCATTTTGC  
GTAATGAGAGAAGTTTTGTTCCAGAGAGCCAAAGCGAGGAATTGACGAGTAT  
CTGGAAAACGATTCTTTTCTTCAAATGATACCTGTTAAATATCGTGAAAT  
TGTCCTGCCCAAGTTGAGAAGAGATACTAACAAAATGACCGCGGCTCTTA  
AAAATAAAGTCACTGTTGCAATTTGACGAGCTTACGGTGCCACTTATGTGG  
ATGGTCCATTTTGGCGTAGGATACCCCTTACCGTTATCCAGAGCTTCAGCT  
ACTCGCTTTTGGCGGTCTCTCAGCGCAACGTATAAGTCCGATGATACAA  
GACGCATCCAACTGTACACTGATTACAAACAGAACGGTTCATCGGAGCCT  
CGACTTAAGACCGCTTGACGGACTCACTTCAGATTACGTTGTTTTATTTGT  
CACTCTGCTAACCACATCCAAATATGTCGGCTTGGTAACACTATAGACG  
CTTTTAATCATGATCCTTCCATGGATGTGGTGGGATTTGAGGATCCAGAT  
CAAGTAACAAATCGAGACATTTTCGAGGATAGTTTTGTATTCCCTACAAGTT  
TCTGAATACCCCGAAGGGCTGTCTGGTTGAATACGCAACTTTTCGGCAGT  
ACATGAGGGAACTTCCCAAGAATGCACCTCACAACCTGAATTTTCCCGAG  
ATGGCTCAGGGGTTGATTGCCCTAGGACGGCACTGCGTAGGTAGCAGATT  
TGAAACAGATTTCGTAAGAGTGGGCAAGAGTGAATCATGGCCAATCATT  
CCGTTCAAACAGGGCGAAATATTTACGGTGTGGATTCTTTTCGTTAACT  
AGTGTCAGTGGGACGACCGCCACTTTATTGCAGGAACGAGCTTCCGAGCG  
CTGGATTCAATGGTTAGGCCCTGAAAGCGACTACCATTTGTTCAATCTCTA  
GTACTCGGAATGCGGAAGACGTAGTGGCAGCTCAAGCGGCGGAGTTCAAT  
CATGATCAAAAAATTTCAAGAGTAACGCGAAAAAGGCCCCGAGAGCCCCA  
GAGTACAAAAGATATCTTGGTGGCAAGGCGAGAAATCTTTTGGCAGCTCCT  
TTGAATTCAAGGACTTGCATCAGTTGCGCTTATGTCATGAAATATACATG  
GCGACACACCCCTCTGTGCCAGTACAGGCCCAACCCCTATGGTAAGAC  
GGAATTTATTTCACTCCCCCTTGATAGCACTGGCGTCTAAGGGCGAGGTGA  
AATATGTGTCGTTCTGTGTTGTACCGTACACAGTGTGGCTTGCATTAATTC  
ATGATCAGGTTGACCCGATGCCGTTGCTTGAATGTGGCCCTGTAGAAA



96/251

CTTTATTGAAGAAGGTTGCGATGGCGTTACTGATTTATACGTGGGGATCT  
ACGATGATCTTTGCTAGCACTAATTTACAGACAGGATAGCTGCCGTGGGAG  
AATATTCTTGAGTGCACCTTTAGGACCAACAACGTAAMTTGCTTACCT  
CATTGTATATGAGTTTCACAACCTTTGAAACGGAGGTCTACCGGCAGTCCG  
AATTTGGGGGCATACCTAACCTTGATTTTGACGCTTTTGAGAAAACAATC  
TTTTTGAGCGGCACACCACCTGAGGCTCTACCTGATGCTGCCCTTCCAGCC  
TATTGGGCTTACGGCACTGSCCAAGAACTCGATGGACATCAACGAGCTCA  
AACGGTCGGAAGATCTCAGCAGAGGTCTATCCAGCTATCCAACACGGATG  
TTTAATCTAATCAAGGAGAAATCCGAGGTGCCCTTAGGGCATGTTCATAA  
AATTTGGAAGAAAGTGGAAATCACAGCCCCGAAGAAGCACGAGGCTTCTTT  
TAGCCCCCTTTGAAATTGAACCAGAGTCGAAGGCCATTGTAGTTGCAAGC  
ACAACCAACCAACTCGAAGAATTGCCCTCCCTCTTCCAGAAAGTATTTAG  
GCTAGGTATGATACACGGGAAGCTGGGTGCTGCAGAAAAGGTGCTTCGCA  
CAAAGGAGTTTGTCACTGACGCTAGCATGCCGAGTTCTCATCGGAACGAAA  
TTAGTGACTGAAGGAATTGACATTAAGCAATTGATGATGGTGATCAATGCT  
TGATAATAGACTTAAATATTATGAGCTCATTCAAGGCGTAGGGAGACTAA  
GAGATGGGGGCTCTGTATTCTATTATCTAGAAAAACAGTTGGGCGGCA  
ACGAATCTTAAGGGTGAATTACCACCGATTAAAGGAAGGCTGTATTAACGA  
ACAGGTACGCGAGTTCTATCGACTTGAATCAAAGAAAGCAAAAAAGGGCC  
AGCATGTTGGATGCTGTGGCTCCAGGACAGACCTGCTGTGCTGACACAGTG  
GAAGTGATAGAAAGAATTGGACAGATTGGCTGAAAAACAGGCCACAGCTTC  
CATGTCCGATCATTGCCCTTACCCTCTAGCTTCCAGGACAGCAATAGCACTG  
ACAGGTGCAGAAAGTATTGACAGCAGTGATGAGGACAGCGACACGTCATT  
CATGGTAGTGCTAATGCCAGTACCAATGCCACTAUGCACTCCAGCACTAA  
TGCTACTACCACTGCCAGCACCAACGTCAGGACTAGTGCTACTACCACTG  
CCAGCATCAACGTCCAGGACTAGTGGGATTACCAGTGAAGTACCAACTCC  
AGCACTAATGCTACTACCACTGCCAGCACCAACGTCAGGACTAGTGCTAC  
TACCACTGCCAGCATCAACGTCAGGACTAGTGCGACTACCACTGAAAGTA  
CCAACCTCCAACACTACTCCTACTACCACCCCAAGTACCCACTCCAACACT  
AGTGCTACTACCAACCGAAAGTACCGACTCCAACACTAGTGCTACTACCAC  
TGCTAGCACCAACTCCAGCACTAATGCCACTACCACTGCTAGCACCAACT  
CCAGCACTAATGCCACTACCACTGAAAGTACCAACGCTAGTGCCAAAGGAG  
GACGCCAATAAAGATGGCAATGCTGAGGATAATAGATCCATCCAGTCAC  
CGACATTAACAAGAGTCCGTATAAGCGGAAGGGAGTCAAAATGCTTTTGC  
TAGAGAGAAAGAACTGAAAGCACAAATTTCCCAATACTCCGAGAAATATG  
AATGCTCTTACACTTTCTTGGATTTCGGTCTACAGAAATTAAACATCTTTT  
CCTCTATGGTATTGACGTATACTTCTGCCCCAGAGGGAGTATTACACAAAT  
ACUGATTATGCAAGGGCTGTCAAAAGATGTTTCGAGCTCTGTGTCTGTGG  
GCTGGCCAGAAAGTATCGTATCGGAGGATGGCTTGGGAAGCACTAGCTGT  
GGAGAGAATGCTGCCAAATGACGAGGAATACAAGAATACTTGGAGAGACA  
TCGAGCCATATCATGGGGACCCCTGTAGGATATTTGAAATATTTTAGCGTA  
AAAAGGGGAGAGATCTACTCTCAGATACAGAGAAATTATGCTTGGTACCT  
GGCCATTACTAGAAGAAAGAGAAACAATTAGTGTATTGGATTGACACAGAC  
GCAAGCAAGGGAGCCAAGTTTTCCGCATGTCTGGAAGGCAGATCAAAGAG  
TTGTATTATAAAGTATCGAGCAACTTTCGTGAATCGAAGACAGAGGTGCT  
GCAGTACTTTTTGAAGTGGGACGAGAAAAAGTGGCGGGAAGAATGGAGG  
CAAAAGACGATACGGTCTTTGTGGAAGCGCTCGAGAAAGTTGGAGTTTTT  
CAGCGTTTGGCTTCCATGACGAGCGCTGGACTGCAGGGTCCGAGTACGT  
CAAGCTGCAGTTTAGCAGGCATCATCGACAGTTGAGGAGCAGATATGAAT  
TAAGCTCTAGGAATCCACTTGCAGATCAGCTTGGCTCCGAGTTACCCCA  
TCTAAAGTGCCGATTTGGACGGCATTCCTGTCTGATGCTCATAGGGCTGT  
CTACAATAAAACATTTTGGCAGAACTGGAATATCTTTTGGAGCAGATTT  
CGSAGGTGTGGTTGTTACCACATTGGCTTGATTTGGCAAAAGCTTGAAGTT  
CTCGCTGCAGATAACACGAGGGTACCGCTGTACATGCTGATGGTAGCGGT  
TCAACAAAGAGCTCGATAGCGATGATGTTCCAGACGGTAGATTTGATATAA  
TATTACTATCTACAGATTCCAGCACAGAAGTTCCAGACTGA

97/251

YDR545W, 1796 aa (SEQ ID NO 138)  
 MKVSDRRKFEXANFDEFESALNNKNDLVHCP SITLFE SIFTEVRSFYEDE  
 KSGLIKVKVFRFTGAMDRKRSFEKIVISVMVGKNVQKFLTFVEDEPDPQGG  
 PIPSKYLI PKKINLMVYTLFQVHTLKFNRKDYDTLSLFYLMRGYYNELSF  
 RVLERCHEIASARPNDSSYKRTFTDFVSGAPIVRSLQKSTTRKYGYNLAP  
 YMFLLHLHVDLSIFSAYQASLPGEKKVDTERLKRDLCPKRP I EIKYFSQI  
 CNDMMNKDRLGDILHLHLACALNFGAGFRGGAGDEEDRSITWNEPIIF  
 SVDEHGKVKCKLRSPNTPERLRKTLDAVKALLVSSCACTARDLDIFDDTN  
 GVAMWKKWIKTLYHEVAQRRTTLKDSYRTTINPSSDNTSVCGKLFNRREYVRG  
 PYPACKAQFDNLWGE LNMCFYKPTVVDIASLILRMREVLFRFPKRGIDEY  
 LENDSFLQMI PVKYREIVLFLKLRRTNKMTAALKNKVTVAIDELTVPLMW  
 MVHEFVGVFPYRYPELQLIAFAGPQRNVYVDDTTRRIQLYTDYNKNGSSEP  
 RLKTL DGLTSDYVFYFVTVL RQM QICALGNSYDAFNHDPWMDVVGFEDPD  
 QVTNRDTSRI VLYSYMFLNTAKGCI VRYATFRQYMRSLPKNAPQKLNFRF  
 NRQGLIALGRHCVGSRFBTDLYESATSELMANHSVOTGRNIYGVDSFSILT  
 SVSGTTATLLQERASERWIKWLGLES DYHCSFSSTRNAEDVVAGEAASSD  
 HDQKISRVTKRPREPKSTNDILVAGQKLFSSSFEFRDLHQLRLCHEIYM  
 ADTPSVAVQAPPGYGKTRIFHLPLJATASKGDVKYVSFLFVPTYTVLLANC  
 MIRLSRCGLNVA PVSRNPIEEGCGVTDLYVG IYDOLASTNFTORIAAWE  
 NIVECTFRNTNNVKLGYLIVDEFHNFE TEVYRQSQFGGITNLDFDAFEKAI  
 FLSGTAPEAVADAALQRICLTCLAKKSM D INELKRSEDLSRGLSSYPTRM  
 FNLIKESSEVPLGFVHKIWKKVESQPEEALKLLLALPEIEPESKATVVAS  
 TTFEVEBELACSWRKYFRVWLIHGKLGAAEKVSRTKEFVTDGSMRVLIGTK  
 LVTFEGIDIKQLMMVINLDNRLNIIE LIQGVGRLRGGGLCYLLSRKNSWAA  
 RNREKGLPPTKRGCTTEQVREFYGLESKKKGKQHVGGCSRTDLSADTV  
 ELIERMDRLAEKQATASMSIALPSSFQESNSSDRCKYCSSDEDSDTCI  
 HGSANASTNATNSSINATTTASTNVRI SATTTASINVRTSAITTESTNS  
 STNATPEASTNVRTSATTTASINVRTSATTTSTNSNTSATTTTSTNSNT  
 SATTTTESTNSNTSATTTASINSSINATTTASTNSSINATTTTESTNASAKE  
 DANKDGNAE DNRFPVTDINKESYKIRKGSQMVLLERKKLKAQFPNTSENM  
 NVLQFLGFPRSD EIKHFLPYGIDVYFCPEGVFTQYGLCKGCKMPFELCVW  
 AGQKVSYSREMAWEALAVRMLRNDEEYKEYLEDTRPYHGDVPGYLKYPVS  
 KRGEIYSQIQRMNAYWIAITRRRFTTSVLDSTRGKQGSQVFRMSGRQIKE  
 LYYKWSNLSRESKTLV LQVFLNWDEKKCREPWEAKDOTVFVALEKVGVF  
 QRLRSMTSAGLQGPQYVKLQFSRHRQLRSRYELSLGMLHLDQLALGVTP  
 SKVPHWTFAL SMLICFPYKKTFRQKLEYLLFQISEFWULLPHWLDLANVEV  
 LAADNTRVPLYMLMVAWEKELDSELVDPGRFDLILLCRDSSREVG E

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)  
 AGAGTTGTTGCCACAACATAAGCCGCTTTGAGTGTTGAACAAATCCGTC  
 CTTGGGTCATTCAATCAATGGCTTGGCGGTATCTCAAAAGACGGCAAACT  
 AATAGCGCGCACATTGACGCAATTAATCCGGTGGTCATCGACTAGCGGCG  
 AAGAGGTCACGACCTATTTTCTCTTGCAGAAAAAACTCTGACCTTTTCC  
 GTAGCTAGACGCTATTCAGGGCGTCAGCAATGGGAGGCACAGCGGAAAAA  
 CAATAACAAATGGTAAGCGCAATTACCTTTTGAGCGTTACATTGATGAA  
 ATTGGTGACGTTAATCTAAAGATAGTCATGCTCTCAAAAGGCCCCATTAT  
 TCTCGACGCTTGAGCGTATAATAAGACTATTAAGAACTTGGTTCTTTAGATAT  
 GGTGTTCTGTTCCATTAATTAAGTTTACAGGGAUAATATCAACACATATC  
 ATAACAGGTTCTCAAAACTTTTTGTITTAATAATACTAGTAACAAGAAAA  
 ATGACACCTTCTTATCTAAATTCAAAACAGAAATGTTGCATCATATTTACA  
 ATCAAAATCAAGCCAAAGAAAAGACTCTAAAAAGAGAGATTTAGCGAATCT  
 ACCCUATCCATGCTCAAGATGTAAGGCAATTCGTTAAAGAGCATGGCAAA  
 ACTAAAATTAGCGATCTTCATTAAGAACAGGTATATGGTGGTATAGAGAG  
 TATTTCCAGGGAGCGTATGGGAAGGTTCCGTTTGGACCCAGAGACGGTA  
 TTCTGTTTCAGAGGTCTGATACCATCGCCGACATTCAAAAGGACCTGCCAAG  
 CCATACCAAGCTCACAACTACTACCAGAGGCTCTCTTTTGGTTATTTGCT

98/251

AACTGGCGAGGTTCCAACTCAAGCGCAAGTTGAAAACCTTATCAOCTCATC  
 TAATGTCAAGATCGGAACCTACCTAGTCATGTCGTTCAACCTTTGGATAAT  
 TTACCAAAAGCACTTACAUCCCAATGGCTCAATTCTATTGCTGIAACTGC  
 CTTCCAAAGCGAGTCAAAGTTTGCIAAGGCTTATGCTCAAGGAATTTCCA  
 AGCAAGATTATTGGAGTTTATACCTTTTGAAGATTCACTAGACTTGCTGGGT  
 AAATTGCCAGTTATTGTCAGCTAAAAATTATCGTAATGTATTCAAAGATGG  
 CAAAATGGGTGAAGTGGACCCAAATGCCGATTATGCTAAAAATCTGGTCA  
 ACTTGATTGCTCTTAAGGATGAAGATTTCGTGGACTTGATGAGACTTTAT  
 TTAACCATTCATTCCGGATCAACGAAGGTGGTAATGTATCTGCACATACATC  
 CCATCTTGTTGGGCTCAGCACTATCATCACCTTATCTCTCCCTTCCATCAC  
 GTTTGAACGGGTCTGCTGGCCCTTCATGGGCGTGCTAATCAAGAAGTA  
 CTAGAATGGTTATTGGCACTTAAAGAAGAGGTAAATGATGACTACTCTAA  
 AGATACCATCCAAAAATATTTATCGGATACTCTAAACTCAGCAAGACTCA  
 TTCCCGGTTATGGTCATGCTGTGCTAAGGAAAACGATCCTCGTTATATG  
 GCTCAGCGTAAGTTTGCCATGGACCATTTTCCAGATTATGAATTAATCAA  
 GTTAGTTTCAATCAATATACGAGGTAGCACCTGCCGTATTGACTGAACATC  
 GTAAACATAAAATCCATGGCCAAATGTAGATGCTCACTCTGGTGTCTTA  
 TTACAATATTATCGACTAAAAGAATCTTCTTTCTATACCGTTTTATTTGG  
 CGTTTCAAGGGCATTTGCTATTCTTGCTCAATTGATCACTGATAGGGCCA  
 TCGGTGCTTCCATTGAAAGGCCAAAGTCCCTATTCTACTGAGAAATACAAG  
 GAATTGGTCAAAAACATTGAAAGCAAACCTATAG

VCR005C, 460 aa (SEQ ID NO 72)

MTVPYLNSNRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGK  
 TKISDVLLLEQVYGGMRGIPGSVWEGSVLDFPDGLRFRGRPIAJIQKDLPK  
 AKCSSQPLPEALFWLLLTCEVPTQAQVENLSADLMRSSELP SHVVQLLDN  
 LPKDLIIPMAQFSIAVTALESSEKFAKAYAQGISKQDYWSYTFEDSLDLLG  
 KLPVIAAKIYRNVTKDGKNGEVDPKADYAKNLVNLIGSKDBDFVDLMRLY  
 LTIHSDHEGNNVSAHTSHLVGSALSSPYLSLASGLNGLAGPIHGRANQEV  
 LEWLFALKEEVNDYSKDTIEKYLWDTLNSGRVIEPGYCHAVLRKTDPRYM  
 AQRKFAMDHFPPDYELFKIVSSIYEVAPGVLTETHGKTKNPWPNVDAHSGVL  
 LQYYGLKESSFYTVLFCVSRAPGKLAQLITDRAIGASIERPKSYSTEMKYK  
 ELVKNIESKL

VOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCCCTCATACTTTTCCGTTTGTATCTCCTACTTTCTTACTTCCTTTTTT  
 TTCTTCTTTACTTTCCTTGGTTTACCATTGAACTCCATTTTACTACAGAC  
 AATAGCTAGTCATTTCGCTATCTTCCGTTTGTCACTTTTTTTCAAATTTCT  
 CATCTATATAGUGAAGTACGGAAAAGATGTCACCTTGGUGGCATCTCGGCC  
 TTCCCCCGCCAAATGGACTCATCATCTAGGATACGGCCCCCTTAATCCGC  
 AATTACTTTTCCCCATTCCGGCCGTAGCCGTTCTAAAGCCCCCGTGCCTTGC  
 CCCCATACTCCCCATAATGATCCGGGAAGTTCCGGTTTTTTTCCCTTGT  
 TTAGTGGCAATTCTGTGTTTGGCCCAAGGTTCGGAAGGTCCGATTTGACTTTAA  
 GGAACCTACCGAAGGTATCTAACGTTTCTAATAAACAAATATACACCGCCGTG  
 CGTAGATATATAAAGATAAAGATTTATCGATATGAGATAAAGATTGCTGC  
 ATGATTCTCCCTCTGATTTCTTTTCCCTGTATATATTTTCTCCCCCTCTCG  
 TATAAATCGTACAGTCAGAAGTAGTCCAGAATATAGTGCTGCAGACTATCT  
 ACAAAAGTTCAATACAATATCATAAAGTTTATACTAACATGCCCTCACTCA  
 GTTACACCATCCATAGAACAAGATTCGTTAAAAATTGCCATTTTAACTGC  
 TGCCGGTGTGTATUGGGCAGTCTGTTATCGCTGCTTTTGAAGGCTCAGTTGC  
 AATACCAAGTTAAAGGAGAGCAACCGGAGCGTTACCCACATTCATCTGGCT  
 CTTTACGATGTCAACCAAGAAGCCATCAACGGTGTACCGCCGACTTGTCT  
 TCATATAGACACCCCCCATTTCCGTGTGAGAGCCACCTCTCTGCAGGTGSCA  
 TTGAGAAGCTGTTTGCATAACGCTTCTATTGTTGTCTATCTCTGAGGTCTT  
 CCAAGAAAACCTGGCATGACTCGTGATGACTTATTTAACGTGAATGCTGG  
 TATCATTAGCCAGCTCGGTGATTTCTATTGCAGAATGTTGTGTGATCTTTCCA

99/251

AGGTCTTCGTTCTTGTTCATTTCCAAACCTGTAAATTCCTTTAGTCCCAGTG  
 ATGGT"("("PACATTC("PAGAAACCATCCTCAGTCTAGAAATTCGGCAT  
 TGAAAGAGGGATCATGGGTGTACCAAGCTCGACATTTGTTCAGAGCGTCCA  
 C"("PTCTACGIGAGATAAACATTGAGTCAGGGCTAAATCCTCGTGTAAAC  
 TUCATGCCTGACGTCCCTGTAAATTGGCGGGCATTCTGGCGAGACTATTAT  
 TCCGTTGTTTTCACAGTCAAAC"TCCTATCGAGATTAAATGAGGATCAAT  
 TGAATATTTAATACATACAGTCCCAATACGGTGGTGATGAAGTGGTCAAC  
 GCCAAGAACGGTAAAGCTAGTGTACCTTATCGATGGCCCATGCCGGTTA  
 TAACTGTGTTGTCCAAATTTGTTCTTTTATTTCCTAACATTGAGCAGA  
 TCCATGGAAACCTACTATGTGCCATTAAAAGATGCGAACAACCTCCCCAT"  
 GCTCCTGGGGCAGATCAATTATTGCCTCTGGTGGACGGTGCAGACTACTT  
 TGCCATACCATTAACTATTACTACAAAGGCTGTTTCCCTATCTGCATTATC  
 ACA"CGTTAATAGGATGAACGACATGGAACGCAACCAAATGTTGCCAATT  
 TGGCTCTCCAGTTAAGGAAAAATATCGATAAGGGCTTGGAATTGTTTGC  
 ATCCAGATCTCCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLILLFFCIYFLPFCINRTVRSSPEYSAADYYKSSIQYHKSYSNMPHS  
 VTPSIEQDSLKIALILGAAGGIQSLSLLLKAQLQYQLKESNRSVTHIILA  
 LYDVNQEAINGVTADLSHIDTFISVSSHSPAGGIENCLHNASIVVIPAGV  
 PRKPGMERDILFNVNAGLISQLGDSIAECDDLKVFYVLVISNPFVNSLVPV  
 MVSNILKNHPQSRNSGIERRIMGVTKLDIVRASTFLREINTRESGJTPRVN  
 SMPDVPVIGGHSGETIIPLEFSQSNFLSRINFDQLKYLTNRVQVGGDEVVK  
 AKNGKGSATLSMAHAGYKCVVQPVSLLLGNLEQIHGTYYVPLKDANMFPI  
 APGADQLPLPLVDGADYFAIPLTITTKGVSYVDYDIVNRNMDMERNQMLPI  
 CVSQDKINIDKGLEFVASRSASS

YBK019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTAAATTACCCAGAAATAAGGCTAAAAAACTAATCGC  
 ATTATCATCTCATGCTTGTAAATTTGATTCTGTTAATTGAAGGTTGTGG  
 GGCCAGGTTACTGCCAATTTTCTCTTCATAACCATAAAAGCTAGTATT  
 GTAGAATCTTTATTTGTTCCGASCAGTSCGGCCCGAGGCACATCTCGGTTT  
 CAGCAACCGGACCGGTGAAGACGAGGACGCACGGAGGACACTCTTCCGTC  
 GGAGGCTGTTCGCCCGCTCGGCGGCTTCTAATCGTACTTCAATATAGCA  
 ATGAGCAGTTAAGCGTATTACTGAAAAGTTCCAAAGAGAAGGTTT"CTAG  
 GCTAAGATAAATGGGGCTCTTTACATTTCCACCAACATATAACTAAGATTAC  
 ATATCGATATGTATATGTTGGTAATGCCATGTAATATGATTATTAAGCT"  
 C"TTTCGCTCCATCCAAAAAAAAGTAAGAA"TT"TTGAAATTTCAATATAA  
 ATGACAGCTCAGTTACAAAGTGAAGTACTTCTAAAATTGTTTTGGTTAC  
 AGCTGCTCCTCGATACATTGCTTCACACACTGTGGTAGAGCTAATTGAGA  
 ATCCATATGACTCTGTTGTTGCTGATAACCTGTGGAATTCAACTTATGAT  
 TCTGTAGCCAGGTTAGAGGCTCTTGACCAAGCATCAAT"CCCC"TTCTA"GA  
 GGTGATTGTTGTGACCGAAAAGGTCTCGAAAAGGTTTTTCAAAGAA"ATA  
 AAATTGA"TTCCGTAATTCACTTTGCTGGTTTTAAAGGCTGTAGGTGAATCT  
 ACACAAATCCCGCTGAGATACTATCACAAATAACATTTTCCGAAC"GT"CGT  
 TTTAT"TAGAGTTAATGCAACAATACAAAGTTTCCAAATTTGTTTTTTCAT  
 CTTC"TGCTACTGTCTATGGT"ATGCTACGAGATTCCTCAATATGATT"CT  
 ATCCCAGAAGAATGT"CTCTTAGGGCTACTAATCCGTATGGTCA"ACGAA  
 ATACGCCATTGAGAATATCTTGAATGATCTTTACAATAGCGACAAAAAAA  
 GTTGGAAAGTTTGC"ATCT"TCGTTATTTTAACCCAATTGGCCCATCCC  
 TCTGGATTAAATCGGAGAAGATCCGCTAGGTATACCAACCAATTTGTTGCC  
 ATATAT"GGCTCAAG"AGCT"GT"TGCTAGGCGGAGAGAAGTTTACATCTTCG  
 CAGACGATTATGATTCCAGAGATGGTACCCCGATCAGGSAATTATATCCAC  
 GTACTTGATCTAGCAAAAGGTCAATTTGCAGCCCTGCAATACCTAGAGGC  
 CTACAATGAAAATGAAGGTTTTGTGTCTG"AGT"GGAACTTGGGTTCCGGTA  
 AAGGT"CTACAGT"TT"TTGAAGTTTATCATGCATTTCTGCAAACTTCTGGT

100/251

ATTGATCTTCCATACAAAGTTACGGGCAGAAGAGCAGGTGATGTTTTGAA  
 CTTGACGGCTAAACCAGATAGGGCCAAACGCGAACTGAAATGGCAGACCG  
 AGTTGCAGGTTGAAGACTCCTGCAAGGATTTATGGAAATGGACTACTGAG  
 AATUCTTTTGGTTACCACTTAAGGGCTGTCGAGGCCAGATTTTCCGCTGA  
 AGTATSCCTTATCAGCCAAGATTTCTGACTATTGCTGCCGCCACCAGAT  
 TTCAAGCCACGTTTGGCAATTGGGGCGCCAGCATGCTGACCTGAAAGTG  
 AACGGACANTCAGTTGTTCTTGGCTATGAAATCAGGAAGCCTATTTGAA  
 TCCTCATAGTGCTTATATAGGGCGCCACGATCGGCAGGTATGCTAATCGTA  
 TTTTCGAAGGGTAAGTTTACTTTATGCAACAAAGACTATCAGTTAAACCGTT  
 AATAACGGCGTTAAATGCGAATCATAGTAGTATTCGGTTCTTTCCACAGAAA  
 ANGATTTTGGGACCCATCATTCAAAATCCTTCAAAGGATGTTTTTACCG  
 CCGAGTACATGCTGATAGATAATGAGAGGACACCGAATTTUAGGTGAT  
 CTATTGGTAAACCATACAGTATACTGTGCAACGTTGCCCAAAAAAGTTTGG  
 AATGGTATATATAAGGTAAATTGAATGCTGCTGGTGAAGCGACGCCAATAAAT  
 TAACAAATCATAAGTTATTTTCAAATCTGAACAAGCUATATGGAGACACTATT  
 GAGGGTACGGAGATTATGGTGCCTTCAAAAAATCTGTTGATGTCGACAA  
 AAACATGATTCTACGGGTAATATCGTCGATAGAGAAATTGCTACCTTTA  
 ACTCTACAAAGCCAACGGTCTTAGGGCCCCAAAAATCCCCAGTTTGATTGT  
 TGTTTTGTGGTGGATGAAAATGCTAAGCCAAGTCAAATCAATACTCTAAA  
 CAATGAATTGACGCTTATCTCAACCTTTTCATCCCGATTCCAATATTA  
 CATTAGAAGTTTAAGTACAGAGCCAACCTTATCAATTTTATACCGGTGAT  
 TTCTTGTCTGCTGGTTACGAAGCAAGACAAGGTTTTGCAATTGAGCCCTGG  
 TAGATACATTTGATGCTATCAATCAAGAGAAGCTGGAAAGATTGTGTAACTT  
 TGAAAAACCGTGAAACTTACGGGTCCAAGATTGTCTACAGATTTCCTCGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIVLVTCACACYIGSHTWVELIENGVDVADNTSNSTYD  
 SVARLEVLTKHHIPFYEVDLDRKGLKVFKEYKIDSVIHFAQLKAVGES  
 TQIFLRVYHNNILGTVVLLLELMQQVNVSKVFTSSATVYGDATRFPMNTF  
 LPEECPLGPTNPFYGHTKYAIENILKDLVNSDKKSWKFAILRYFNPICGHP  
 SGLIGEDPLGIPNNLLPYMAQVAVGRREKLYIFGDDYDSRDGTPIRDYIH  
 VVDLAKGHIAALQYLEAYNENEGLCRENNLGGSGKSTVFVYHAFCKASC  
 IDLPYKVTGRRAGDVNLTAKPDRAKREIKWLYPFIQVEDSCKDLWEWTE  
 NPFQYOLRGVEARFSAEDMRYDARFVTIGAGTRFQATFANLSASIVDLKV  
 NCQSVVLGYENEBGYLNPDSAYIGATIGRYANRISKGRFSLCNKDYQLTV  
 NNGVNAHISSIGSFIRKRLTGPIIQKPSKDVFTAEYMLIDNEKDTFPGD  
 LLVTIQYTVNVAQKSLEWVYEGKLTAGEATPINLTNHSYFNLNKPYGDTI  
 EGNEIMVRSKKSVDDVDKNNIPTGNIVDREIATFMSTKFTVLGPKNDQFDC  
 CFVVDENAKPSQINTLNLTLIVKAFHPDGNITLIVLSTEPYQFYVGL  
 FLSAGYEARGFAIEPGRYIDAINQENWKDCVTLKNGETYGSKIIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCTCAGCTATATTCTTCCAGCTTCGCCTGCTGCCCGTCATCGTTCTCTGT  
 CAGGTAGTTTTTCCGGATTCTGTCGGCTCATATAATACCGCAATAAACAC  
 GGAATATCTCGTTCCGCGGATTCGGTTAAACTCTCGGTCCGCGGATTATCA  
 CAGACAAGCTTCTGTGGAGAATTTTTTCCAGATTTTCCGCTTTCCCCGATG  
 TTGGTATTTCCGGAGGTCAATATATCTGAUCCGCCATTATAATGACTGTACA  
 ACGACCTTCTGGAGAAAGAAACAACCTCAATAACGATGTGGGACATTGGGC  
 GCCCACTCAAAAAATCTGCCCACTATATCCCCAGAGAAATTTCTCCAGAAG  
 AGAAGAAAAGTCAAAGTTTTTTTTCGCTTGGGGGTTGCATATAAATACAG  
 CGGCINGTTTTATCTTCAGCANGAATATCCATAATTTTACTTAATAGCTT  
 TTCAATAAATAATAGAATCAAAACAAATTTACATCTGAGTTAAACAATC  
 ATGAATTCAACTCCAGATTTAATATCTCCACAAAAGTCAAGTGAGAAATTC  
 GAATGCTGACCTGCCCTTCGAATAGCTCTCAGGTAATGAACATGCTTGAAG  
 AAAAAGGTGTTCAAGATGATTTCCAAAGCTGAGGCCGACCAAGTACTTACC  
 AACCCAAATACAGGTAAAGGTGCATATGTCACTGTGTCTATCTGTGTGTGT

101/251

TATGGTTGCCCTTCGGTGGTTCGTCTTCGGTTGGCACTGGTACCATT  
 CTGGTTTCGTGCGCCAACTGATTTCCTTGAGAACATTGGGTATGAAGCAT  
 AAAGATGGTAGTTATTATTTGTCTAAGGTTAGAACTGGTTTAATTCTCTC  
 CACTTTCAACATTGGTTGTGCCATIGGTGGTATTATTTTGGCTAAATTGG  
 CTGATATGTACCGTCCATAAAATGGGTTTCATTGTCGTCTCTTATCTAC  
 ATCATCGGTATTTATTATTCAAATTGCATCCATCAACAAATGGTACCAATA  
 TTTCATCCGTAGAAATTATTTCCGGTTTGGGTGTTGGTGGTATTGCCGTTT  
 TACCTCCTTAIGTTGATTTCTGAAGTCGCTCCTAAGCAAAATGAGAGCTACT  
 CTAGTCTCTGTACCAACTGATGATTACCTTGGGTATTTCTTGGGTTA  
 CTGTACCAACTTCGGTACTAAGAACTACTCCAACCTCTGTGCAATGGAGAG  
 TCCCATPACGTTTCGTCTTTCCTGGGCTTTCTTTATCATCGGTGCTATC  
 ACTTCGTTCAGAAATCCCCACGTTATTTGGTTGAAGCTGGTCAAATTGA  
 CGAAGCAAGAGCATCTCTTTCCAAAGTTAACAAGGTTGCCCCAGACCATC  
 CATTCTATTCAACAAGACTTCCAAAGTTATTGAACCTAGTCTTGAAGAAGCT  
 AGAGCTTCCTGGTTTCAGCATCATGGGGTGACTTCCTCACTGGTAAGCCGGC  
 CATGTTTAAGCGTACTATGATGGGTATCATGATCCAATCTCTACAACAAT  
 TGACTGCTGATAACTATTTCTTCTACTATCGTACTACCGTTTTTAACGCT  
 GTTGGTATGAGTGATTCTTTCGAAACTTCTATTGTTTTCGGTGTGCTCAA  
 CTTCTTCTCTACTTGTGTCTTTGTACACTGTGATCGTTTTGGACGTC  
 GTAACGTGTTGTATATGGTGCCATTGGTATGGTCTGCTGTTATGTAGTT  
 TACGCTTCTGTTGGTGTCCACCAGACTATGGCCAAATGGTGAAGGTAATGG  
 TTCATCCAAGGGTGTCTGGTAACTGTATGATTGTCTTTGCCTGTTTCTATA  
 TTTCCTGTTTTGCTPACCACTTGGGCTCCAATTGCTTATGTTGTTATTTCT  
 GAAACTTTTCCATTGAGAGTCAAGTCTAAGGCTATGTCTATTGCTACAGC  
 TGCTAATTGGTTGTGGGGTTCTTGATTGGTTCCTTCACTCCATTTATTA  
 CTGGTGCTATTAACCTTCTACTACGGTTACGTTTTCATGGGCTGTAIGGTT  
 TTCGCTACTTCTACCTTTTCTTCTTGTGCCAGAACTAAGCGTTTGAC  
 TTTGCAAGAAGTCAATGATATCTACGCTGAAGCTGTTCTACCATGCAAGT  
 CTGCTTTCATGGGTTTCCAACATCTCAAGAGGCTGCTAAGTACGATGCTGAT  
 GCATTGATGCATGATGACCAGCCATTCTACAAGAAAATGTTCCGGCAAGAA  
 ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLSIPOKSSSENSNADLPNSSQVMNMPEEKGVQDDFQAEADQVLT  
 NPNTGKGAYVTVSICVMVAFGGFVFCWDIGTISCFVAQTDFLRRFGXKH  
 KDGSYVLSKVRTGLIVSIFNIGCAIGGIIILAKLGDYVGRXMGILVWVLY  
 IIGIIIQIASINKWYQYFIGRIISGLGVGGI AVLSPMLISEVAPEKMRGT  
 LVSCYQLMTLGLIFLGYCTNFGTKNYNSVQWRVPLGLCFAMALFMI GCM  
 TEVPESPRYLVFAGQIDEARASTSKVNKVAPDHPFIQOELEVIEASVEEA  
 RAAGSASNGELFTGKPFAMFKETMGINIQSLQQLTGDNYPFYGGTTVFNA  
 VGMSDSPETSLVFGVVMFPSTCCSLYTVDRFGRKNULLYGAIGMVCCYVV  
 YASVGVTRLWPNGEGNGSSKGAGNCMIVFACFYIFCTFATWAPIAYVVT  
 ETEPLRVKSKAMSIAATAANWLWGFLIGFTTPTITGAINFYGVVFMGCMV  
 FAYFYVFFVFPETKGLTLEBVNDMYAEGVLPWKSASWVPTSQRGANYDAD  
 ALMHDDQPFYKMFGEK

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCGAGCTTCCTTTTCATCCGGCGCGGCTGTGTTCTACATA  
 TCACTGAAGCTCCCGGTATTTTAACTTATACAAGCAAAACATGCCGGCTA  
 GACTAGCAAGTTTTAGGCTGCTTAACATTATGGATAGCGGATAAAAGGC  
 CCAACAGGATTGTAAAGCTTAGACGCTTCTGCTTGGACAAATCCTACGTT  
 TGTGTATTAAGTAAAGCTTGGCTGGGATAGCAACATTGGCCAGAGTATA  
 GAAGACCAACAAAAAAGGTATATAAGGGCAGAGAASTUTTTGTAAATGTC  
 TGTAACTTCTCTTCUATGNGTAATCAGTATTTCTACTTACTTCTTAAATA  
 TACAGAAGTAAGACAGATAACCAACAGCCTTTCCAGATATACATATATA  
 TCTTTATTTTCAAGCTTAAACAATAATTATATTTGTTTAACTCAAAATAAAA

102/251

AAAAAAAAAA CCAAAC TCACGCAACTAATTATTCCATAATAAAATACACAC  
 ATGTCCTCCCTTCTAAATGAATGCTACAGTAGGATCTACTTCCGAAGTTGA  
 ACAAATAATCAGACAAGAATTGGCTCTTAGTGAAGAGTACCCACCATCA  
 GACCCAAATGCTCCAGCTCCCTTTTCTATGAAGATGGTCTAAAAGAAAAT  
 AAAACAGTTCATTTTCATCAAGCGGTGCATTGATCGCTTATTCGGGTGTTAA  
 AACCGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACCTCGA  
 AACACGAAATTTGGTGGGCTCGGTCAAATAAACCATGTTCTGAAAGAACA  
 TGGTCTATTCAAACCGTGAAAGAGCTGCAGATTACTTGAGAACAAGAGACCA  
 CATTTATATTTGTCGATGCATTTGCAGGATGGGATCCAAAATACAGAATCA  
 AAGTCCGCGTTGTTTGTGCCAGGCTTACCACGCTTTATTCATGACAAAT  
 ATTGCTTATTAGAACCTACAGAAGAAGAATTAGCCCATTTTGGAGAACCTGA  
 TTTTACTGTCTGGAACGCTGGTCAGTTCCAGCCCAATTTACACACCCAGG  
 ATATGTCCTTCAAAAGACTACTATAGAAATTAACCTTCADAGCAATTGAAATC  
 ATCATTTTATAGGTACCGAATACGCCGGTGAATGAAGGATATTTTAC  
 AGTTATGTTTTACTTTGATGCCTGTGCACCATAAACGTTTAACTTTGCAC  
 CTTCGCCCAACCCAGGCTATTTCAAAACGGTGACCTTACTTTATTCTTTGCC  
 CTAAGTGGTACCGGGAAAACCACTTTATCCGCAGACCCACATAGATTGTT  
 GATTCGGCGAATGATGAACAATTTGTGGTCCGACCATGGTGTCTTCAATATCG  
 AAGCTGGTCTTTACGCCAAGCTATTAATTTATCTGCCGAAAAGGAGCCT  
 GAATTTTCCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTA  
 TGACGAGAAGTCCGATGTAGTCGACTATGACGACTCTTCTATTACTGAAA  
 ATACTAGATGTGCCTACCCAAATGACTACATTCCAAAGTGCCAAAGATTCCA  
 TCTTTGCCCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGC  
 TTCGGGTGTTTTACCACCAGTATCTAAATTGACTCCTGAACAAAGTCATGT  
 ACCATTTTATCTCTGGTTACATTTCTAAATGGCTGGTACTGAGCAAGGT  
 GTCACTGAACCTGAACCAACATTTTCATCTTCTTTCCGACCAACCTTCTC  
 AGCCTTGCACCTTATAGATACGCCAACCATGTTAGCTACAAAGATGTCTC  
 AACATAAGCTTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCTTCC  
 TACGTATCTGGTGGTAAACGTTGCCCATTTGAAGTACACAAGGSCCATCT  
 GGATTCTATTCTATGATGGTTCTGTTAGCCAAATGAAACGTACGAAACTTTAC  
 CGATTTTCAATCTTCAAGTACCTACCAAGGTTAACGGTGTTCAGCTGAG  
 CTTTATGAATCTTGCATAAAACTTGGTCTCAAGGTGAATCCAAATACAGAGG  
 TGCAGTTTACCAACTTGGCCAACTTTGTTGTTTCAAAATTTCAAGACTTATC  
 AAGACACAGCCACACACAGATCTATTACCCCTCTGCTCTCAANTCCAGTAA

YKR097W, 549 aa (SEQ ID NO 264)

MNP SKMNATV GSTSEVEQKIPQELALSDEVTTIRRNAPAAVLYEDGLKEN  
 KTVI SSSGAL IAYSGVK TGRSPKDKRIVEEPTSKDEI WNGFV NKPSERT  
 WSINREAA DYLRTRDHIYVDAFAGWDPKYRIKVRVVCARAYHALFMTN  
 MLIRPTSEELAHFGSPDFTVWNAQGFANLH TQDMSSKSTIEINFKAMEM  
 IILGTEYAGFMKKGTFTVVFYLM PVHHNVITLHSSANQGIQNGDVTLFRG  
 LSGTGKTTLSADPHRL LIGDDEHCWSDHGVFNIEGGEYAKCINLSAEKBP  
 EIPDAIKFGSVLENVIYDEKSHVVDYDSSITENFRCAYPIDYIPSAKIP  
 CTADSHPKNIITLTCDA SGVLPPVSKLTPEQVMYHFI SCYT SKMAGTFQC  
 VTEPEPTFSSCFGQPFLLALHPIRYATMLACKMSQHKANAYLINTGWTGSS  
 YVSGGRKRCPLKYTRAILDS LHDGSLANETYEPLPIENLQVPTKVNQVPAE  
 LLNPAKNWSQGESXYRGAVTNLARLFVQNFKIYQDRATPDVLAAGPQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGTAAACATAAATACATTCTGTAAATCTACAAAAATCGTTAGTG  
 CTGTTTTCTTTTTGAGATTGAAAAGTACGAATCATACACATCTCTTATTC  
 TGAGAAGGGGTGCATATGACGTAAATCAATGCCGTACAAAGCGGTTTCGGGT  
 GCTGGCCTTGCCCCACCACAGTTTTTGGCGTGGTTGATTTTTAAAACCTTCG  
 CGTAGGTGAAAAACCCTCCGAAGGTTTCGAGGATGACAAATCGCCCCCTT  
 AGCTGTGGCCATACAAGCTTGGCACCGACGAAAAACGGAAAAAGGAAAAAG  
 AATGTCGTACAAAGAACTCTTACAAACCGTTGAGATTTCATTTAACAACG

103/251

CCCCCCTTCCATTATATAAGAAGGCATTAAATTTTTATGTAATAAAAAA  
 GAATTTCTGGAATATGTTTACAATTAAATTTTTCTTTTGTAGAGTAGGG  
 CTTTAATAGACTGATATATACGGTATTATAAGTGAACGAAAAAACAGCA  
 ATGGGTTTTATTTGATAAAGTGAAGCAATTTGCTAACAGCAATAATAACAA  
 CAATGATTCTGGCAATAACAATCAAGGCGATTATGTTACCAAAGCTGAGA  
 ATATGATCGGCGAACATACACTCAATCAANTCMAAAGCAAAATCGGAGAG  
 GACAGATTTGATAAGATGGAGTCCAAGCTTCGTCAACAATTTTCTAATAC  
 CTCTATAAATGACAACGACTCCAACAACAACGACTCATATGGTTCTAATA  
 ACAACGATTCATATGGTTCTAACAACAATGATTCATATGGCTCTAACAAC  
 AATGATTCATATGGCTCCAACAACAATGATTCATATGGCTCTAACAACGA  
 TGATTCTTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGTTCTAACA  
 ATGACCAATCCCTACGGCTCCAGCAACAACAATGACTCTTACGGTTCCAAC  
 AACATGACTCTTACGGTTCCAACAACAATGACTCTTACGGTTCCAACAA  
 TGACGACTCTTACGGTTCTGTCMAACAAGAATAAGAGCTCTTACGGTTCCA  
 ACAATGACGATTCTTATGGCTCTAACAATGATGATTCATATGGTTCTTCC  
 AACAAGAAGAAGAGTTCTTATGGTTCCAGCAACAACGATTGGTATGGTTC  
 TAACAACGATGATTTCATATGGTTCTAACAACAATGATTCATATGGCTCTA  
 ACAACGATGATTCTTACGGTTCTTCCAACAAGAAGAAGAGCTCTTATGGT  
 TCTAACAATGACGATTCTGACGGCTCCAGCAACAACAATGACTCTTACGG  
 TTCCAACAATGACGACTCTTACGGTTCTGTCMAACAAGAATAAGAGCTCTT  
 ACGGTTCTTCTAGCAACGATGATTCTTACGGATCTTCCAATAACGACGAC  
 TCTTACGGTTCTTCCAACAACAACAAGTTCTTATGGTTCCAACAATGA  
 CGATTCTTATGGCTCTAACAATGATGATTCATATGGTTCTTCCAACAAGA  
 AGAAGAGTTCTTATGGTTTUCAGCAACAACGATTCTGATGGTTCTAACAAC  
 GATGATTCCTTACGGTTCTTCTAACAACAAGAAGAGTTCTTATGGTTCCAA  
 CAACGATGATTCTATACGGCTCCAGCAACAACAATGACTCTTACGGTTCCA  
 ACAATGACGACTCTTACGGTTCTTCTAATAAGAAACAAGAACCTCTATGGG  
 TCTTCCAACCTACGGTTCTATCCAACAATGATGACTCTTATGGTTCTATCTAA  
 TAGAGCCCTCTCAATCAATACGGCTCTGACGACGATTACTAA

YMR173W, 430 aa (SEQ ID NO 314)

MGLFDKVKQFANSNNMNDSGNNNQGDYVTKAENMIGEDRVNQFKSKIGE  
 DRFDKMSKVRRQPFNTSINDNDSNNEDSYGSNNNDSYGSNNNDSYGSNN  
 NDSYGSNNNDSYGSNNDDSYGSSNNKKSSYGSNNNDSYGSNNNDSYGSN  
 NNDSYGSNNNDSYGSNNDDSYGSSNNKKSSYGSNNNDSYGSNNDDSYGSS  
 NKKKSSYGSNNNDSYGSNNDDSYGSNNNDSYGSNNDDSYGSSNNKKKSSY  
 SNNDSDYGSNNNDSYGSNNDDSYGSSNNKKSSYGSNNDDSYGSNNDD  
 SYGSSNNKKKSSYGSNNDDSYGSNNDDSYGSSNNKKKSSYGSNNDDSYGSNN  
 DDSYGSNNKKKSSYGSNNDDSYGSNNNDSYGSNNDDSYGSSNNRNNKNSY  
 SSNYGSSNNDDSYGSNNRGRNQYGGDDDY

YII057C, 395 bp, CDS: 501-995 (SEQ ID NO 217)

CCAACAGATTTCAASTCTGTGCGCTTAACCACTCGGCCATAGTGCCTAA  
 AACAATGTAGGTTATTTAAGCAAGTATTGTAGATACTTTTCGTAATAAAC  
 TACAATGCACCCACGACTCGCGGTGTAATGATGCGATGAATCATTTGAAC  
 GAAGTTTTGCGGCTATACGGCTGAAGGACGAGACTAAAGGGACAGCAATT  
 ATTAATGCGGGGTATAAATTTGAATAGTATTAAACGGGCACCTGCGGTTTACG  
 CATCAAAATGCTATTGTTGGGTATTCTCTCTACTTTTTGTTCTTGGCTTG  
 AACCTTTTTGCGCGGTTGGCAATCGTCCGTATATAAGCATCGGCTGTCCCA  
 ATCCTCTATTGCGCTTTTCCCTTGCACCTCCTTCTCAATCTTCGTATCT  
 TTCCGCTAAAGGTAGATCTTGATTACCTATCTGTGGAACACGATTAAAG  
 TGCAAAACGAAACAACGTACAGTATATAACAAAGTATTTTAAATAATAAGA  
 ATGACGAAAAAGGATAACAAAGCAAGCGTCCTAAGATGTCCACCAACAC  
 TACAAAAAGTGGTGAGTCTTTAAAGGTITTTGAGGATTTGCATGATTTTG  
 AAACATATTTAAAGCGCTGACACGGAAACATCAAGAGTTCCACCATGTCCAT  
 TGCCAACTCAAGTACTATCCACCCCTTTGTCTCTGCATGATGCGCATGATGA



104/251

TCCCGAAAGATCAAAGAGACTGCCAATTCGCACTCTAAGAAAGTTTGTTC  
GCCATTTACACCAGCATGTTGAGAAGCACCTGCTAAAGGACATCAAAACC  
GCTATCAACAAGCCAGAATTGAAATTCACGATAAGAAAAACAGGAATC  
CTTTGACCGGATTGTTTGGAAATTATGCCGAAGAAACGGAGTTGAACGCCA  
AGAAATTCAAGGTGTCTGTGGAAGTTGTATGTAAACACCGATGCCGCAATC  
GTAGATGTTGATTACAAGACAGAAACCCCTGCAGCCACTCATCTAA

YIL057C, 164 aa (SEQ ID NO 218)

MTKKDKKAKGPKMSTITTKSGESLKVFE DLHDFETVYLRGETEDQEFDHVH  
CQLKYYPFVLHDAHDDPEKIKETANSHSKKFVRHLHQHVEKHLKDIKT  
AINKPELKFHDKKKQESFDRIWANYGBETELNAKKFKVSVEVVKHDGAM  
VDVDYKTEPLQPLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTACGTACTTTTCGTTTTCGAATTTCCATGGTGCAAGTAT  
CTTAACCTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGTTGCTCAG  
CCGCTTCGTGGATATTCTCTTGGATACTTTAAATATGGACCTACGCTTAG  
CCTGCTTGTAGCTTACAACCTTCTTCCGCTCTCGAAAAGACCAAATAAATA  
GAAAGTTATAAATTACATTTCCTTATTAGGTATACGACCTCGCGCTTCGA  
AGTAGAGGAGCCCCCTTTTGGCGTACCTACATATGGCGCTGCAGATAGACA  
AACTTCCCCCAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATT  
CACCCAGGACGTATCAAGTTACTTCCCTGGTGCATGTCCCACTATAAAA  
AAATTCCCTTGACGCTAGATCGTTGGACTAAAATCTGCGTCACAATCGCT  
AAACAGGAATATTGCCTATTTCCGTACAAGGTIACCTTCCTAGATGCTAT  
ATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT  
ATATATACACACCACACCACACCCACACACACCACACACACCCACAC  
CCACACACACACCCACACCCACACACACCCACACACCCACACACCCACA  
CCAGAGAGAAGCCTAAGCCTAAGACTAAGACAAGCCAAAGCCTGACCAACC  
TGTCTCTCAAAATACCCCTCCATTACCCCTACCTCCCCACTCGTTACCCCTGA  
CTCATTCAACTATACCACCCCAACCACCATCCATCTCCCTGTGTACTACC  
ACCAACCGACCGCTCCACCATAACCCCTTACCCTCCAATTACCCATATCCAA  
CTCCACTACCCTTACCCTACCATCTCCCATCTACTACTCACCATACTAT  
TGTTCTACCCACCCTATTGAAACGCTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTFSSMQYSDIYLIHTTFHPHTPHRTHHTETTFPTPTPHPTHTPT  
PERSLSRLRLRQAKFDQFVSQETLHYPTSPLVTLTHSTIPPQPPSISLCCT  
TXRPSTITVTLQLPISNSTTYPTISHLLLTILLFYPPLLKR

YKK049C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

CCCTTTTCCAGTCCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCA  
CGCTGTCTATTCTAACACATTCAAGCCCTAGGCCCCCTGACCTCGCGTC  
TAGTTCCACTTTTTCATTACCTTTTCTCGGTCTTTTCTTGCTCCACAGG  
CCGTTAATGGCCTGAAACAGTTTGTGACTTTGGACTTATGATAACGATG  
TTTGTCCGGGTGCCACCGGATTCTACCGCGGCGAATCAAGTCTAGTCTGT  
TTGCATCCATCAAGGCACTGCTCATTTGTGTAAAATTGTTCTACGCTTTTG  
TCATCAATCATATCTAAACTCACAGCCGCTAGGGTAGGTGTACCTGGCAG  
TGGTAAGGTAGCCGGCTCGTCTTTGGTCTATGCGCCAACTACTGTGGAACGG  
CCCGCGCTTAGCGTTCTTGGCTTCAACCTTAGAGCTGATACCTTTTGCC  
TGGTCAAGGGCGAAAACGTCTACCTCGCTTTTCACTGCTGCTTTTGGCTTTC  
ATGACTTCGTTTCAAGCGGTCTCTTTTGGCTCTCGCTTCTAACACACTTGT  
AGCCTGCTATGCTTTTCACTTACTCGAAAAGCGTAGCTTCATGACTAGTT  
GTACCAACGCCCTTTCTTTTCTTTTCTCTTTGACACTTCGGCGTATT  
CATCGCCACTGGTACAAGCCGATGGTGTCTTTTGTCTCATTTTCTGTTTT  
GACGTTGCGATGGTTTCCCGGACCAATCGCATGGGTGCTGCTGGATGTTG  
TCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCTTCCGCTTTCTGACGAA

AAATGGCCCTTACGCATCTTTTTTCGGCGTCGTTGTGTCATCGCTGTTCA  
TATAATCGTCGTCACCTCATATCGGCGCTTTTACTGCAIGCTGTCCTTTTGA  
AGAGACTTTCATCGAAAAGTAGTGAAGAAAAAAGAAAAAAGAAAAA  
AAAAAGCAAAAAGCTTACATACGGAAAGAGAAAAAAGAAAAAGAAATT  
TTAA

YKR040C, 167 aa (SEQ ID NO 256)  
 NTSFQAVSFALGNTLVACYAFTVLEKRSLSMTSCTNALSFLFFLLTLRI  
 HRHWYKPYGAPLLIFVLTLRNFGRPIAWVVVDVFASCHVVFSPALSDP  
 NWPYVSFEFGVVVIAVHIIVVTHIGAPTACCLLKRVSLKSSFEKKKKKKK  
 KKKSLHTERRKKKKKK

YNR338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)  
TAAAGTAGTCGGTAGCTACGTTTCGTTTTCAATTTCCATGGTGACAGTAT  
CTTAACIATCTGCTTAGTCGAGGAGAACCCAGGATTCTGTTGCTTGCTCAG  
CCGCTTCCTCGATATTCTCTTGGAACTTTAAATAATGGACCTACGCTTAG  
CCTCGGCTTAGCCTACAACCTCTCCGCTCTCGAAAAGACCAATATAATA  
GAAAGTIATTAATTACATTTCCTATTAGGTATACGACCTCGCGCTTCGA  
AGTAGAGGAGCCCTTTTGGCGTACCTACATATGCGCGCTCAGACAGACA  
AATCTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCAT  
CACCCACGACGTATCAAGTTACTTCCTTGSTGCAATGTCCCACTATAAAA  
AAATTCCCTTGACGCTAGATCGTTGGACTAAAATCTGCGCTCACAATCCCT  
AAACAGGAAATATTGCCATTTTCGTACAGGTTACTTCCTACATGCTAT  
ATGTCCTACCGCCTTGCTCTAACACCATCCAGCATGCAATACAGTGACAT  
ATATATACCCACACCCACACCCACACACACACACACACACACACACAC  
ACCCACACCCACACACCCACACCCACACCCATCACAAACCTTAACCTACC  
CTATCTTCA

YNL338W, 52 aa (SEQ ID NO 338)  
MSLRPCLTPSSXQYSDIYIPTPTPTHHTHTPTTPHHPHTHTHTHHNPNT  
LF

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)  
GCUAGTATUCCCTTTCTCAAATAAGCTAAACCCCTTGCAACCACCCAGGGGTG  
CCGCCGTCTTAACCTTTCCAGCCTGGCAGCCCGTCGAGTCGCCGAATGTTG  
CGGUCGCTGCCCCGCCCGCAACACCCGCCCGGCCCTGCCCTCAGCTTAACC  
GAAACCCACACGCGCTCTGCCATCTTCCATATACCCCTGCCCTCTCTTTTCAGA  
ATGCCCGCTTCAACACGCCAACTGCAAAAAGAGCCCGCCCCCTTAGTCGGTATT  
TCCCCACTTTTGATATAACCCCCCCCCCCCCCCCCCCCCCGCATCAACTGGTAA  
TTTAAACCCAAACACCCAGGGGGTCATAATTAAAAGCCAAAAACCTTAAAG  
CGTTCTCGAAGCAAAATCTTCTGTAGATGATGTGTAGTAGCAAACCTATCTTT  
TAGAGTGTTTGTGCTTACTGCTATGTACAGTCAAAATTTACGTAGCCGCC  
CTTTTCAACCCCTGTGCAAGAGTAGCATAAACAGCAGCGCTGTGCAACGTGC  
ATGTTTCACAAATACACGACACAAATATTAATATACAAATAGTAAGGTGATGAA  
CACACACACACACACACACACACACACACACACACACATATATATATATA  
CAGGAGATCAAGTTAGTGAGGGGACGACTACTGAGTTTGAAGTCTTT  
AAAGTGTTAAAGTTATTTTTCCCTCTCCCACTCGTTGCCAACCTCTCA  
CCCACCGCTTAGCAGCATGTCTCCGTACATGACCATACCTCAGCAATACT  
TATACATAAGCAAGATACGTTTCAAGCTGTCTCAGTGCGCCCTTACTCGA  
CACCAACCAAGAGAACTTGATCTACGAAAAATGGTGGGGCCAGCCCAATAT  
GCTGGACAGGATCTTCGACGAATAGACGAAATCGACAGCGAGGTAGTAC  
TGTGTACACCGTCCCGATGGTTCTTCTACTGCAGAAGCTCAATTCCGCTTCC  
CCAGCATCCAGCGCACTTCTCTCTCTACTAATAACATCCGCCCATTAG  
CATATAGTGA

106/251

YJR115W, 169 aa (SEQ ID NO 236)

MPTNTRTILIIYNSKVMNTHTHTHTHTHTHIYIYTGQVSVRGRLLSLKFF  
 KVLKLPFPSPCLSLATSHFPLSSMSFYMTIFQQYLYISKIRSKLSQCALTR  
 EHHRELDLRKMGVGHANMLDRILDEIDEIDSEVVLCDADCSSTAEHSA  
 PASSDSSPLTNIRPISIM

YBL072C, 1103 bp, CDS: 501-1103 (SEQ ID NO 27)

CTCCTACACACCAGCATCGCTGGGAAAGCTTGAGGGCTTTCTCTTACGCAGTGTTCATGGTGTACGGG  
 ATGGAACTGGTTCATATACGTTATTTACAGGCCATCTTAAAGTTATAGGAAATTACACTTGCCTATTG  
 CTTTTTGGTACTCACAAGAAGACGTTATAAACACACCAGGACAAAACTATCTGCTATCGTCCATATGAG  
 TAATCGAATACATATTATTTTGAATGCTACAGGACCTCTCTTTGAATGGAATAGATAGTGGAAAAAGT  
 AAACCTAACCTAAAAGCGATCATATAAATTTGTGACAGGAGCAGTGCACCTAAACTGAATCCTTTCTCTACC  
 CCANNAATCAAGCCCTCTTATCAAAACGCCCACTTTTTCACAAAGAGAGATGAAAAGAAACCAAGCATAT  
 TTCAAGATAAGAAAAAATTTCCGCAACTTTTGTACGTTCTTTATTTTACTAACAGCGTCAITPAAATTT  
 TCTATTACAGTTACAAAAATGGGTATTTCTCGTGAATCTCGTCAACAAAGATCCGCTACCGGTGCCAAGC  
 GTGCTCAATTCAGAAAGAAGAGAAAGTTTCAATTAGGCCCGTCAACCAAGCAACCAAGATTCGAAACCGGT  
 AGAGAATTCACCTCTGTTAGAATAGAGGTGGTTACAAAGAAATACAGAGCTCTAAGAAATCGAAACCGGT  
 ACTTTTCTTCGGCTTTCTGAAGGATCTCCAAGAAGACCAAGATTGCTGGTGTGTTTACCATCCATCCA  
 ACAATGAATTTGGTTAGAATTAACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTC  
 GACAATCGTTCCAGGCTCACTACGGTCAAACCTTGGGTAGAAGAAAGAACGTCAGGGAAGAAAGAAATC  
 TTGCCAAGAGCAAGAACGCTCAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAATCTTCCG  
 TTGAATCTCAATTCAGCGCCGGTAGAATATACGCTTGTATCTCTCCAGAACAGGTCATCCGGTAGAT  
 GTGATGGTTACATCTTGGAAAGGTGAAGAATTACCTTTCTACCTAACAAGATTGACTGCTAAGAAATAG

YBL072C, 200 aa (SEQ ID NO 28)

MGISRDSRHKRSATGAKRAQFRKKKKFELGRQPANTKIGAKRIHSVTRTGGNKKYRALRIETGNFSAW  
 EGISKTRIACVWYHPSNNELVRITNLTKAAIVQIDATPFRQWFEAHYQTLGKKKNFKZEETVAKSKN  
 AERKWAARAASAKIESSVESQFSAGRLYACISSRPQSGRCQGYILEGEELAFYLRRLTAKK

YBL092W, 893 bp, CDS: 501-893 (SEQ ID NO 33)

TACTGGAGAAGAGTGTTCGATTCCAGCAGAAGGTAATACGCACCTTTCTCATCTATTTTCAGAAATCGTT  
 TTATCAAAATACCTTTTAAAGAAATTTAGATTTTGAATAATTAGTTTCAATCTCTTTTTTACAAGGATAATCAAC  
 AAACAGGGACAATAACATGAAGATAAAAGTATGTGACATATAGAATGCTAGAAATGAATAGCCTAGACT  
 GCATCTCTTATGAGAGCAACGTTTGATATTTGTGGCGATTGGACCAACATAGTACATGCCAAAAATGAGA  
 TGAAATGTCCAATTTEAACCTGAATTAACATACACGCGCAAGCTGTATTTGTTTACTGCTACACCTAGAG  
 TTAGCCGATCAAAGAGACAGTGGCAGATATATGGGAAATTTTCTCCGGAAGATTCCATCCGAGAGTCT  
 CATAAACAGTCAATTTCCCAACATACAAATCTCTCGGAGCTGTATACCTAACAACTTTTAAATTTTCAATTTT  
 TTTTCTTTTTTGATTAGATGGCTCTCTTACCCTCACCCAAAGATTCTCAAGAAACCAACCAAGAAAGTTCA  
 AGCGTCATCACTCTGACCGTTACCACAGAGTTGCTGAAAACCTGAGAAAGCAAAAGGGTATTGACCTGTG  
 TTGTTAGAAGAAGATTCAGAGGTAACTCTCTCAACCAAGATCGGTTACGGTTCTAACCAAGAAAGACCA  
 AGTTTCTGTCAACATCTGGTCCAAAGACTTTCTTAGTCGCTAACGTTAAGGATTTGGAAACCTTCACCA  
 TGCACACCAAGACTTACGCGGCTGAAATTTGCTCACAACTCTCCCTAAGAACAGAGTTGTCATTTTGG  
 CTAGAGCTAAGGCTTIGGGTATCAAGGTCACCAACCCAAAGGCTCGTTTGGCTTTGGAAGCTTAA

YBL092W, 130 aa (SEQ ID NO 34)

MASLEHFKIVKHKTKKFKRHHSRYHRAENWRKQKGIDSVVPRRRFRGNISQPKIGYGSNKKTKFLSPS  
 GHKTFILVANKDIERITMHTKTYAAETAHNTSAKNRVVITARAALGIKVTNPXGRLALEA

YBR009C, 812 bp, CDS: 501-812 (SEQ ID NO 37)

GAAAAATCCCCCGGCATTTTCGTTATCTTCCACGCTAAAAGTCAAGGAGAGATATTACGCCAGGATCC  
 CAAAGSTGCAGAGCAAGGAATGTGAGAAATTTGTGAGAACATTAATGTATGGGACAATCCGAAAAATGTG  
 AGAACGAGAGCAAAAAATCTTTTGTATCTCCCCCGCAATTTGGAACCCCGTTCCTGAAAACCTCCCA  
 TCTTTCACATAGTAAACTGTTCGAGAGCGCTTCTCCCATTAATGTTAGTGGTAAAAACCGAAGTTCTTT

107/251

ACTTTAGCAAATGCCCGGAATACGGTGGTAAATTGGCCACCCCCCTTCCCGAATTCATTGGGTAAAGAC  
CAATTTGATGGATPAATTGGTTGTGGAAAAGGTCTAATTCTTTTCCTATAAAATACCGAGATATTTCTT  
CTATATGATGGTTTCCCTCCCATTTATTCTACTCTATAGTACTAAAGCAACAAACAAAAACAAGCAACAA  
ATATAATATAGTAAAATATGTCCGCTAGAGGTAAAGGTGGTAAAGGTCTAGGTAAAGGTGCTGCCAAGC  
GTCACAGAAAGATTCTAAGAGATAACATCCAAGGTAATTAAUTAAAGCCAGCTATCAGAGAGATTAGCTAGAA  
GAGGTGGTGTCAAGCGTATTTCTGGTTTGATCTACGAAGAAGTCAGAGCTGTCTTGAAATCCCTCTGGG  
AATCCGCTCATCAGAGACTCTGTACCTACACCGAACACGCCAAGAGAAAGACTGTTACTTTCTTTGGATG  
TTGTTTATCTTTCAAGAGACAAGGTAGAACCCTATACGGTTTCGGTGGTTAA

YBR009C, 193 aa (SEQ ID NO 38)

MSGRGKGGKGLGGGAKRHRKILRUMIQGITKPAIRRLARRGGVKRISGLIYEEVRAVVKSFLESVIRD  
SVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W, 1501 bp, exon1: 501-507, intron1: 508-920, exon2: 921-1501

(SEQ ID NO 59)

TGGCTTCTTCTTTGCCCTGTTTTGCCAGCTGGTTGATACGGGCACGTAACCTGATTTAATTCTTGGTCCC  
TTTCTAGTGATAAATCTTCGAGAGAGGGGCATCTCTGGTTGTAAAAAGTAGTCCCAACAGTAAGTCGTAA  
AAAACTAGATCTAATGGAAGGCTTTGAAGGAACGCTAGCCAGCTTTTCTGTATCATTCCTAGCCTAAAT  
TGACAGCATCTTGACCTTCTAGTATGGAACTTTCAATTTCCAGAAAGCGGTCTTCCCCCTTCGGAUGAT  
TTAATCCGTACATTTACACATCTGTACATTTCTCAATTTCCGCAAAACAAAGGTTACTTGAAAAATCAT  
AAAGTTGGCGGCTTCAGGTGGACGGCTTCACCTCATGTAGUTTAACATTCAATCCCATTAACCATTTATG  
CATAAATTTCTAGAGCTTTACTTTAATAAAATTTGTTCAATTTGCATAGACAAGAAAGAACCAACAGACA  
ACTAAGACTAACCAACAATCCCAACTACGTATTAGACTATATCGAAGAGGAGGGAATTTCTTCACTCTG  
ACTCGTTGATTTTGAANGAGGTTCCGGTCTCTATAAAATATTGAGAATATGAANTCCMTAATACTATA  
CCTTTCATTGAGTAGCAACGACAACAGCCTCAATTACTATCCATATTTATGAATATCTTTATTTACACTGAA  
CTCCCGACACTTCAGTTAAACAGGGATACATTAGAATCAAGGTGATCTAATAAGCAACATCTCTCTCG  
TAACAATGGGACAGTATTTTATTTTCCAAAGGCGGATACCTAATPATGGCTTTTAAATCATATCTCTACA  
ATATTTATGAGCACCTACCTGGGCGCTTGCAGACTTTTGTTCGGGAAACCTTTTGACTAACCAAGAAATC  
CAATTTTACTTTTTTTTTTTTAGGAGCTCCAAAGACTTACTCTAAGACTTACTCTACACCAAGAGACC  
TTACGAATCTTCTCCTTTCCAGCCAGAAATTGAAGTTTGGCCGGTGAATTCGGTTTGAGAAACAAGAGAGA  
AATTTACAGAATTTCTTTCCAATTGTCTAAATTCGTCGTCTCTGCCAGAGACTTGTGTAAGTACAGAGACA  
AAAGCACCCAAAGAGATTGTTGGAAGGTAATGCCCTGATCAGAAGCTTCCTTAGAGTTGGTGTCTTCTC  
CGAAGACAAGAAGAAGTTGGATTATGTTTTGGCTTTCAAGCTTGAAGATTTCTTTGGAAGAGAGATTGCA  
AACTCAATCTCTACAAGTTGGGTTTGGCCAAAGTCTGTCCACCACGCCAGAGTTTAAATCACTCAAGACA  
CATTGCTGTGGTAAGCAAAATCGTCAACATCCCATCTTTCAATGTTAGATTTGGAUTTTGAAAAGCACAT  
TGACTTGGCTCCAACCTCTCCATTCCGTGGTGTCTAGACCAGCTAGACTTGCTAGAGAAACCGCTGCTAG  
AAAGCCTCAAGCTTCCGGTGAAGCTGCTGAAGAAGCCGAAGACGAAGAATAA

YBR189W, 195 aa (SEQ ID NO 60)

MPRAFTYSTYSTPKRPYESSRLDAELKLAGEFGLKNKRETVRISFQLSKIRRAARDLLTRUQKDPKR  
LPEQNAITRRRLVRVGVLSDDKKKLDYVLAALKVEDFLERRLQTVYKLGAKSVHHARVLTQKHIAVCK  
QIVNIPSFMVRLDSEKHIDFAPTEPFGARFCRVARRNAARKAAASGEAAEEAEDEE

YBR191W, 1371 bp, exon1: 501-511, intron1: 512-899, exon2: 900-1371

(SEQ ID NO 61)

AATCCTTATTTGTACGAAATGAAGCCGTTAATATTTAAAGCCTAATTTCTCCATGCCATCTTGCATTCAC  
TTTGGTATATATCTCTTGACCTCAATATATCTCGTAAATATAAATCGCAATATTATACCTGTGTAGTCTG  
ACAGTTTTTACACCTGTACATCTTCCACATCACCACACCCCTTTTCTTACTGAGGSCAAGCATGAGTTTCAA  
JATCGCCCTTTTTCUAGUGUGUTAGAACATGCTUAGAACCAGGAAAAGCAACCGCTGCCAAACCTCCCTTT  
GATGTGTTGGCCCCACCGCTACTAGTGGCGGTGCTGGAAAGCCAGCCAGCGGTGGCGGCCACAAATACGAG  
AGCTGGAAACCTAAACCGCTCTCTCGGCCCTCTGTGAATTTTATCACCATGGAGTGTCAATGTCTGCTAA  
AGATAATATAGAAAGTAGTGTGAATTTACAGGCATTACCGATTGAACTTTGGAATTAAGAGAACCAAGAC  
AAAAATAACTAGCAACAATGGGTAAATCGTAATGTCATTTAATCTTATGAACTTACAGCCACGAACGAATC  
ATGGTATCTCAAAACGAACATAATCGTACAGAAATAAAAGATTTAAAGACGCTGTCTAGTGTGAATATA  
GCAAACATATCATTTAGAGUAAAATATTGGGCAGATAAGATGATGCTACACTGATTCTGAGAAAATACG  
TGACATGATAGGCTTTTAAACGGGCTGTAAGTCATTAAGTTTACAGTCTGTGGCTTTGAAATTAAGTTCAC

108/251

AFTAGAACTGTAGTAATTACAAGCCCTTTTCCAAACATTCCGTTATGTGCTGGGACGUATCTCAGAAA  
CTCCCAAAACAAATACAATACTAACATGATTTCTTATAAACTCTTAATTTTGATTTATTTCCCTTATAATAC  
AGACACGGTTACAGATCTCGTACTCGTTACATGTTCCAAACGTGACTTCAGAAAGCATGGTGCCGTCCAT  
CTTTCCTACTTGAAGGCTTACAAGCTTCCTGACATTGCTGACATCAAAAGCCCATGGTTCTATCCAA  
AAGGCTATGCCACACAAGTTTACCAAGCTAAGACCCGCTCTGTCTACAACGTTACTAAGTCTTCTGTT  
GGTGTATCATCAACAAGATGGTCCGTAACAGATATCTAGAAAAAAGATTAAACTTAAGAGTTGAACAC  
ATCAAGCACTCCAAGTGTAGACAAGAATTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGTGAA  
GCTAAGGCTCAAGGTGTTGCTGTTCAATTGAACAGACAACAGCTCAACCAAGAGAATCCCGTATCGTT  
TCTACTGAAGCTAACGTTCTCAACCTTGGCCCCAGTTCCATACGAACTTTTCATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYRSRTRVMFQRFKRGAVHLSTYLKVKVGVGDIVDIXKNGSIQKGNPHKIFYQKKTGVVYNVTK  
SSVGVIINKVMGNRYLEKRLNLRVEHIKHSKCRQEFLEVRKANAAKPAEAKAQGVAVQLKRQPAQPRES  
RIVSTEGNVQTLATVPYETFT

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTTGTTTTCCTGCTCCCTCCAATGCTTTATCACTCTCTCACACTGTCACAAT  
CGTGTGTGCTTTCATCCTTAGAAAGGATACCACATTGATAAACAACATATATAAAGTTTAACTATTACCT  
TGATCACTTTACACGTCAAGGTCAAAAACAGTTTCATAGTTACCACTTGAAGTATGGCTCCATCATCTA  
TAAACATGAAGTTTCATGCACAAGTGAGCTGTCTACAGATAACGAGCAGCCGCAACGGCGTTTCCAGAT  
TGCGATGCTTGTCTTCTTCTTCTACTACTGCTTACTACCCCCCTTGGCCCTCCTGATTCAAGTGATGT  
GGGAATTTGCTCTTGAAAGGAGTAAATATATAAATAAATCAAAAGTTTATATATATATAAAAGGGACT  
TTAGCATATAAATAAAGAACCTTCGTGCAGTACTTATACGAGCATTTCGATAATTTATACAAATAGACAAAA  
CCTCAGAACGCAAAAAATCCTATCTCAAGAACTATCAAGCACGTCAACACCTTATTCAGCAAAACG  
AGATCTTCGTGCTATCCAAAACGTACTGTCCATACTGCCATGCGGCCCTAAACACGCTTTTGTAAAGT  
TAAAGGTTCCCAAGTTCAAAAGTTCTGCTTTTTCGAATTTGAATGACATGAAGGAAGGUGCAGACATTTCAGG  
CTGCGTTATATGAGATTAATGGCCAAAGAACCGTGCCAAACATCTATATTAATGGTAAACATATTGGAG  
GCAACGACCACTTGCAGGAATTGAGGGAGACTCGTGAATTGGAGGAATTGTTAGAACCATTCTTGGCAA  
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSQETIKHVKDLIAENELFVASKTYCPYCHAALNTLFKCLKVPRSEVLVLQLNDMKEGADIQAALYBI  
NGQRTVFNHIXNGKHIGGNDDLOELRETGELEELLEPILAN

YDL004W, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATBAACATAGATATAATAGTTTAAATGGTCAACGTATGCGATGCACAACCTAAAAGGTACCAATTC  
ATTAAATATATATAATATTACTTCTTACTATTACACGAAGACAAGTGTGAAATGCCTAGGAGATTGAT  
GATTGACAAGCTCTGGCTTGCATAAATACTTATACACAACCTTCAAATAATATAGAAAAGAAACAA  
GACTATAAGCTAAAAATGTAGACAACCTCATTTAAATATTATTCCTAGGACTTGGTAATAATAGCTAAT  
TTGTATATTATTCACCTTCGGTCACCGCTGTAAATCACCTTTTAAAGAAAATAGATGCCCAGCCAAATCAA  
GCCATTTATGGAGTCTCTAGGAAGGGGCGCTCCCATCATTTGTAAAGTTTCATGTTAAATTAGATGGAG  
GATAACAAATAAAGCTATCCTACACACACCTGCTAAAGAGGCTCAATCAATTTGTGAAGGTATAACTGTA  
GCCGTGAGGATAGGAAAATGTTACGTTCAATTATTGGAAGAGTGCATCAAGATCATTTGAATTTCTGTCG  
CTAAGCGTTTCATATGCAGAAGCTGTGTCGGCATCATCAGGTTTGAAGTTACAATTTGCTCTACCACAG  
AACTTTTATATAGTGGCTCCGAAGTTACTCAAGTGAACCTGCCTGCTAAGTCAGGACCTACTGGTGTAT  
TGGCCAAACCATGTTCCCAACGTTGAACAACTACTACCAGGTGTGCTTGAAGTTATGGGAAGGCTCTAAGT  
CTAAAAAATCTTTATATCAGGTGGATTTTGAACAGTTCAACCCAGACTGCGAGTTATGTGCAACTGCAA  
TTGAAGCTTTTCCATTGGAATCCTTTTCACAAGAAAATATAAAAAATTTGTTGGCAGAAGCTAAGAAAG  
ACGTTAGTTTCATCTGATGCCAGGGAAAGCCGCAGAAGCTGCAATTCAACTAGAACTTTTAGAAAACCTAC  
AATCCCTATTGAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRLNFVAKRSYAEAAAASGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP  
TVSQLLPGVVEVMKGSNSKKFFTSGGHATVQPSQICVPAIRAPLESFSQNNIKNLAEAKKNVSSSD  
AREAAEPAIQVEVLENLQSVLK

109/251

YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263  
(SEQ ID NO 85)

ACTATATTTTCTTTTCCCGAACCCTCTCCCTTTCTGGGCCCTTTTTCATTATTACACAATATTTTTCATAC  
CTTTACCTCCGTACACCAATCTTTATTTTACCCCCATACCTTTGTATTCTGAAATTGAGAAATGATTT  
GTGGTGCTTTTITTTTGGACAACTGCTTCTGGTGGACAGTTTGAACGGCTAGGCGACAGTTTTGCCAA  
CCGAAGCAACTGGGACAGCCAGAAAGCTTTCTCTCGATGGTGGATCATTCCTTGGCAGGCGGAGGAT  
GGGAAAGCTCCGTTCAAGTTTGGCGCTTTCTTTCTGGCATTTCCTTCTCCCAACTGGCGAGGCAGAC  
ATACTTGGACTTTACATCATGCTCGCATAGGCCGGTTGAATCTCATAGCTTGAAGGATAGTATTGAATT  
ATATTGAAGATTTTATAACTAGTGATAATTTCAATTCAGTTTAAAGAAAGAATTAATAAGCAAAACAG  
ACTCAATCAAAAGCAAAAATGGCCCGTTTAAANAAGTTGTCACTCGTGAATACACCATTAACCTTGCACA  
AAACATATATGAGAAAGAAATAAAATATAATGCCCAAGGCTTTGTCTCTGAATGGTTAATTAAGAAGAT  
ATTTCTATAGTCAAGGAATACAATATCAAGAATTTGTACCACAGAAACCTATCAACAAGATCATTTGAT  
CAAGATATATTTTATATATCGGAATTTGAAGACCATAATCAATATTATAACATCCAAGAGGGGAAAGAT  
ACACTTCGGCTGGACCTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGGAAATCCTACATTT  
TAAGTCGACAAATATCCATATCCCAAGTTTGAATATAATCAATCAGAACAAATTCGCTCTCCAAATATA  
CAAAACCATTCATCAAGATTACACTAATATTAAATGAACAATCGTTACTAACAACAAATTTACCATTT  
TATTTTAAATAGTTGCACGGTGTCTCTCTCAAGGAAGAGAGCTCCAACAGCTGTCCAAGGAATTAAGAAG  
TTCCGCCAAGTTACACATGGGTACTGATGATGTCCGTCTAGCTCCAGAATTGAACCAAGCTATCTGGAAG  
AGAGGTGTCAAGGCTGTTGAATACAGATTAAGATTGAGAATTTCCAGAAAGAGAAACGAAGAGAGAC  
GCCAAGAACCCATTGTTCTCTTACGTTGAACCTGTCTTAGTTGCTTCTGCCAAGGCTCTACAACTGTT  
GTTCCTCGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGIKDVVTFREYTNLHKRLHGVSEFKRAPRAVKEIKKFAKLHMGTDDVRLAPRLNQAIWKRCVKOVEY  
RLRLRISKRNEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495  
(SEQ ID NO 89)

TGACGGTCTGTTTACAGGAATGGAAGATGCTTTATGCCCGCGGCATTAGAAATGATCAGAGAGCGAGTGGC  
GTACTTTTAAATGATAGACCTTTCTTCACTTTGGACGGATGACTCAGACGTTCAGGAATTGAGCGAGC  
AATTAGAAATTTGTTAGTATAGTCTATCTTAAACACTAAACTACCTCCTATAATCATGTAGTGTACTTT  
AAACATTTTITATCTTCATAGCAATAATATAAGCCTTTTACCACCCATAAAACCTAAAGTAGACCCAA  
ACATTTTAAAAAATTTTACGTTATAATTTTTCTTTGTCTTTTCTGAGCGCGCAAAAGTAGCGCT  
GAAATTTTGATACGAATGAGATTTCCACTTCTGTACAGATGGAAATTTATGTTGGCCGACATATATCAC  
AGTCTGTGATTGAATTAACAATTTCTTTCTCATTAATATTTATCTTAAACGGTTAAUCCACTAAATCATC  
AACAACAATCAGTCAAAATGGGTCTGATGCACAGTGGCGTATGTTTATTAACACCATAGCGGAGATATTA  
ATGCCAAACTTGCATTTGAATAGTTTCGCTAAATCAGATGACACTCTAATGTGGAMTCAAAAAGTGGATTT  
CTAATATATTTGTCTCTGTCCGATCACAATTCATTTACAAGTTCCCGTCTGTACACAGGTACAGTTTA  
TACTGGAGAGTAGTTTCTACTTCGCTGTACATTAGCTGGGTGATTCCAAATTTCTTTTACAAATATGTTGC  
ATTAGTTTAAACAGGTTATACTATCTGCCCTTTCTTCACTATAATTTACGCCGGAAAAATTACTGATGCTTA  
GCCGCCCTTTATGAATTAGTTTTCACAAAGCTCATAAATACACGTTAACCTATCGGAGGAGAACCAG  
ATTGAAGATTCACCCGGAATAGCTTACTTTAATGGAATTGTATGGTCTGAACGAGGAAATATGTCTATG  
ATACACTTTTCTTCAAGCCATATCAATCTTCATGTTACTAACAATCGATAAATTTTTTGAATATCCAA  
TTCCACTTAAATATTACTTTAAACAGGGTAAAGGTATTTCTTCTCTGCTATTTCCATATCTAGAAATGC  
TCCAGCTTTGGTTCAAGTTGTCTCTGAATCTGTCAATTTGAACAAATGTCAAGTACCGGAGAAAGGTTT  
GACTCCATCTCAAAATTCGTGTCTGTGTGAGAGATGCTCACCGTGTACCCAAGCTCCTGTTATCACTGG  
TAACAAGATCATGAGAACTTTGAAGTCCAAATCGTTTCGCTCCAGAAATCCAGAAAGATTTGTACTACTT  
GATTAAGAAGGCTGTCTCTGTGTAGAAAGTACTTGGAAAGAAACAGAAAGGACAAAGACGCTAAGTTTCA  
ATTTGATTTTGAATCGAAATTTAGAAATTCACAGATTTGGCCAGATACTACAGAACTGCTGCTGTCTTACCAC  
AAACTGGAAAGTACGAATCCGCCACTGCCCTCGGCTTTGGTCAACTAC

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAGKGISSSAIPYSRNAPAWFKLSSESVIRQTVKYARKGLTPSQIGVLLRDAHGVTQARVITGN  
K(MRILKSNGLAPEIPEDLYVL)KKAVSVRKHLHNNRKDKDAKFRLLILIESRIHRLARYRRCVAVIPEX  
WKYLSATASALVN

110/251

YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

TTGTTACGACCAATCCGTAATTCAGCGGTGGGTATTCATATGACCAGAGATAATAATACAGCGAATACT  
 ATTGAANTCGTCCCTTTTGTGTTAGGAAGAACGGACAAATCGGTGCTCTGCTCGAAATGATTAGTAGT  
 GTGTACCCGGATCAGCAAAATGACACACACGAANTACGAGCAAAAATCGGTGCGAAAGGGGCAAAATGT  
 TATTATAAGTCCCTCCAGTAGTCTTTTTTTTTTCAAAATATTCATCATCAAAGGTTACGAAATCTTTTGA  
 CCTATCTTAAACATTGCTTCTTTTTTATCAAAATTCGAATTACTTAACCTATTTTTTTCAAAAAAAATTGCCCT  
 CTCCCGGTTTTTAATCATTATTTTTTTTCGATTTGATTAAGCGGGAAAAGCAAACAACCGAAGAACTTCGA  
 CAGAAGGTTAATACTCTTACAAATTCAAAACGAAGTAAAAAGAAAAATTATCAAATCAACAAAAAGTAC  
 CCGTTACAACAAAAAAATGTCCCAAACTCGTGAAGATTCTGTTTACCTAGCTAAATTAGCTGAACAAG  
 CCGAACGTTATGAAGAAATGCTCCAAAACATGAAGGCGGTTGCTTCATCAGGTCAGAGTTATCTGTCTG  
 AAGAACCGGAATCTATTGTGCTTACAAAGAACGTCATCGGTGCTCGCCGTGCTTCATGGAGAAATAG  
 TTTCTCTCGATCGAACAAGAAAGAAATCAAAGGAGAAATCTGAACATCAAGTTGAATTAATCCGTTCTT  
 ACCGTTCTAAAAATTGAAACTGAATTGACCAAAATCTCTGACGACATTTTATCTCTCTTAGATTCTCAAT  
 TAATCCCTTCTGCTACTACTGGTGAGTCTAAAGTATTTTACTATAAGATGAAGCGTGACTACCACCGTT  
 ATTTAGCTGAATTTTCCAGCGGAGATGCAACAGAAAAGGCAACCAACTCTCTTTTGAGGCTTATAAAA  
 CCGCTTCCGAAATCGGCACAACTGAATTGCCCTCCAACCTCACCAATTTCGTTTAGGCTCTAGCTTTGAATT  
 TCTCGTCTTCTATTTAGGAAATTCAAAACCTCTCTGATAAGGCTTGCCACTTGGCCAAACAGGCTTTG  
 ATGATGCTTATGCTGAGTAGACTTTATCTGAGAATCATACAAGGATAGCACTTTGATCATGCAAT  
 TATTAGGGACAACCTTGACCTTATGGACCTCTGATATTTCTGAATCTGGTCAACAAGATCAACAACAC  
 AACAACAACAGCAACACCAACAGCAACAACAGCAACAACAAGCTCCAGCTGAACAAACTCAAGGTGAAC  
 CAACCAATAA

YDR099W, 273 aa (SEQ ID NO 94)

MSQTREDSVYLAKLAEQAEERYEEMVENMKAVASSGQELSV EERNLLSVAYKNVIGARRAEWRIVSSIEQ  
 KEESKEKSEHQVELIRSYRSKIETELTKISDDILSVLDSHLIPSAITGESKVFYFKMGDYHRYLAEFS  
 SGDAREKATNSSLEAYKTASRIATTTTLPPTHPIRLGLALNFSVFYIEIQNSPDKACHLAKQAFDDAIAE  
 LDTLSEESYKIDSTLIMQLLRNLTPLWTFSDISESGQEDQQQQQQQQQQQQQQQQQAPAEQTQGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

GGAGTTTTCCTATTTTCGAATTCATCCCTGGGTTTGAGCTGCAGGACACGCTGCAGTGGGGGAAGCCCTTT  
 TAAATCCGCGAGTCCGGTCCGTGCTCACTTTTAGACCGCTCTTCCATCCCGCTTCGGATGGTITTCAGT  
 GAGAAAGGGGCTACGGTATGGTCTGTTAGTCCCTTCAGGGGACCAGTGACAGAGGGTGAATCAACGGCC  
 CCTTCACAGAAACCGCGCAGGAATTTTCTGCTGTTTGTATTTTTTTTTTTCTTGTACTTATCTCACTT  
 TTCTTTTTCTAACTATTTTTTTTCCAATTTTCTGCTACACTTCCACAACATATAGGATGGTTTAET  
 CATCTCTCGAAGTATATAAACCGTTGCTGGATCGTGGTTGTTCTTCATCGACTTCTCTCTGCTAGACTC  
 TCTTTTTTTAAATTTTTTCATAGAATAAAAAACCAAGGATAACAAACATCTTCTTTGTTTGGCTTCAAA  
 ATAACTACAAATTAATAATGCAATTCTCTACCGTTCGCTCTATCGCTGCTACTGCGGCTGTTGCCTCCG  
 CCGCTTCTAACATTACCACTGCTACTGTCACAGAAGAATCTACCACTTTGGTCACTATCACTTCTTGTG  
 AGGACCACGTTTGTCTGAACAGTTTCCCCAGCTTTGGTTTCCACTGCTACCGTCAACGTAATGACG  
 TTATCACTTAA

YDR134C, 66 aa (SEQ ID NO 98)

MQFSTVASIAAIAAVASASNITPATVTEESTTLVTTTSCIDHVCSETVSPALVSTATVTVNDVIT

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

CTGGGGTTGCTTAACAAGTGACCAAGGGAAAAAGTGAACATTTTAAGAAGAACAAATAAAAAGCAAGAG  
 ATGGAATGGTAATGCTTGGCTCTCGAGAAGAGTACGATAAACGAGACTTCTTTAAACACCATATGAC  
 ATACTCAATTCAGCTTTTCCCTATCAGCCGCTCGAGCAGTTATATAGGTGTGTTTCCCCGACTAATTTGG  
 CCGACGCCCAACACTGGCTAGGCGGCAACGCCCTGGAACACCGGCTTAAAAAGTTCTGGAAGGTTCCGGAAT  
 TGAGAAGTGTCTAGGGGCGAATAACAGGGGCGGCTTTCGGGCAAGGCGCACGCTCTGTGAAGTTACTT  
 ATATAAGACTTGTCTGTCATCGTTTCTTTGATCCCGGCAGGAAGTATCTTTTATTCTCATACATACGGTC  
 AACAGCTATAATTATACATAACATAGGGACAGCTTCAGGCAATTGTCCATATCCACACAAATTAAGAT  
 CATACCAAGCCGAAGCAATGAGTTTTTATCAACCTCCCTATCTCTTTATGACGTTTGAACGCAATAT  
 CCAACCAAACTGGCCAGAGAGGGGAGCAAGGATATCTTCCCAACCAAAAGGCCACAGACATACCATC  
 CCCATTATGGACAAGTGACGTTTGGCGGCAATCACTCTCGTTCATCATCCATTGTATAGCAGATACAAATG

111/251

GTGTTCCCTAATACCTATTACTACCAGTTCCCTCGACAAAGCCATTACTATAGTCCTGAATACCGGTTATG  
 ATGACGAGGATGGTGAAGAAGAGGACCAAGACGAAGATATGGTGGGTGACAGCGGCACTACAAAGACAGG  
 AAGATGGTGGCGAGGACAGCAACTCGAGAAGATATCCATCATATTACCATTCTAATACTGCCAGGAATA  
 ATAGGACCAACCAACAGGCPAACAGTTTAAACGACTTATTAACCCCGTTAATAGGTGTTCCACCATATG  
 AAGGCACCTGAACCAGAAATTGAAGCAAAATACCGAACAGGAGCGCGAAAAGGCAGAAGAAAAGGATAAGA  
 AGGATAAGTCTGAAGCAUCCAAAGAGGAAGCTGGCGAANCCAACAAAGAAAAACCTTTGAATCAGCTCG  
 AGGAATCCTCGAGACCACCATTAGCCAAAAAATCTTCATCGTTGCTCACCTACAAGCGCCTTCCCCAA  
 TACCTGACCCGCTACAAGTATCCAAGCCTGAAACGAGAATCGACTTACCATTTTCACCCAGAAGTGAATG  
 TCTATGATACCGAGGACACTTACGTAGTTGTTCTTTCGCTTACCAGGTGCTAACCTCAGGGCTTTCCACA  
 TTGATTACCATCUATCTTCTCATGAGATGCTTCATCAACGCTAAAGATTGAAGACAGAGTGGGCATTGAGG  
 AAAAATTCTTGAAGATCACGGAACTAAAATATGGTTCGGTTTGAAGAGAACCGTTAAATTTCCCCGTGCTGC  
 CACGCATTAAAGGACGAAGAAATTAAAGCTACTTACAAACAACGGTCTACTACAAATTAAGGTCCCTAAAA  
 TTGTCAATGACACTCAAAAGCCCAAGCCAAAAAGAGGATCGCCATTGAGGAAATACCCGACGAAGAAT  
 TGGAGTTTGAAGAAATCCCAACCCCTACGGTAGAAAAATGA

YDR171W, 375 aa (SEQ ID NO 104)

MSFYQPSLSLYDVLNALSNTGQRGQQGYRQRPQRPRQRYHPHYGOVHVGGHHPRHPLYSRYNGVPNTY  
 YYQFPQGAYYYSPHYGDDDELGEEDQDEDMVGDSTTRQEDGGEDNSRRYPSTYHCNTARMNRFWQQ  
 ANSLNDLLLTALIGVPPYEGTEPELEANTEQEKEKKEKDKDKSZAPKEZAGEINRKRKFLNQLBESSRP  
 PLAKKSSSFALHQAQSPJPPLQVSKPETRMDLPSPEVNVYDTEDTYVVLALPGANSRAFHIDYHPS  
 SHEMLIKGKIEDRVGIDEKFLKITELKYGAFFERTVKFPVLPRLKDEELKATYANGLLQLKVPKIVNDETR  
 KPKPKKRIAIEELPDEELEBFEEPNPTVEN

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TGGTTATCCCTTTTGAACIGCATCTGGCATCGTTAACAGTAAGGCUATCTGGMACATCAAGCAAGCAC  
 TCCACTTTTACGTACACAACCATAGTTGGTTAACTAAGAAAAGACAGTACATATTTCCCTCCCGAGTCAC  
 TTATTTTCTTTCTTCTCTGAAAAATTAATTAGATTAATTTCAATTAATATCAATTTCCGCTTATCTGAC  
 TTCTTTTCAATTTTCTCTATATTTTCGCGTTTACTAGGAAGAAAAAGGAAAAAAATTTTCCCTCTC  
 CATCTGTCCCAAATCGGGTAGCGATGAGCTGCTTATAGAATTTTCTATTTAAACATGTTTGATAAGCCCA  
 ATTTCCGCTTAGATTTTGTTCCTCTTCGCTAGTTTGTCTTTCCTTATTTTATATTACCGTTCGCTGTTTATTATA  
 AGCTGGAGTAATACGATGTAGTGCCTTGTAAATCTTCTTATTTTATATTACCGTTCGCTGTTTATTATA  
 TCCATTTACGTTTCCCATATGTCCGCAAAACGATAAACAATACATCTCTGTACACAAACGTACATCAACTAT  
 GTCAAGTATCCGCTGAGAGATTAAGAATTTTCAAGCCGGACTTAATCATTCCTATTGCTGCTGGTGGT  
 TCATTCCTGCTTAGGATCCTACGTACGTTCTTAAAGAGCCCGGCTGCTCAACCAACAGAAATTTTGTCTA  
 TTAATTTTGTCTTTGTACGAAGATTTGAACAGTGTAGGCTCAGAAATTGAGGAAGTTGGTGTTAAGGTTA  
 GCAGAACACAATGGATTGATTACGAGCAATGTAAATTAGATCTAGTCCGCAACAACCTTTATCTGTTG  
 ACCAAGTCGATGACACCCGTACCACTTCAATTACCTTTTGAAGTGAATTTGAAAAGGATGCGAGCTGAAC  
 AGGCAAGGCTTAAAGGTATCGATACTGAAAAGTCTCCAGAGATGAAAACAAACTTGGGGATTTTTGTCTC  
 TACACGATAAGCAAAAACCAAGAAAGCAAGATTTTCTGCTGCCCCAAATGTTGAATGACAAGAACCTTATT  
 TTGCAGCTAAAACTGTTCCAGACAAGTGGTATGCAATATCCATGGGAATCTACTGACATGTTTTCCATA  
 CTAGAATGGCTATTGAACAGGCCAATGACATCTTTATTCTGAGCAGGAACACAAGCAATGA

YDR399W, 221 aa (SEQ ID NO 130)

MSANDKQYLSYNNVHQLCCVSAERIKNPKPDGLIA:GGGGFIFARILRTFLKEPGVPTLRIPAFILSLY  
 EDLMSVGSEVEEVGVKVSRTQWIDYEQCKLDLVGKQVLIIVDEVDDTRTTLHYALSELEKDAAEQAKAKG  
 IDEKSPFMKTNFGIFVLHDKQKPKKADLPALMLNCKMRYFAAKTVFDKWAYYPWESTDVLVHTRMAIE  
 QGNDLFLPEQEHKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCCTGTGGATGTTTGGGTGTGTATTTTGCTTTTCAACATACAGATATTTTGTTTAAGCAAGTGAA  
 ATTAACAATATCATAAAACAGGTACTTCATAGACCATAAACCNATAACCCAGATTATCCTCTTAGATAGC  
 AATGCTAATGTAAACAGAGATCCGTTTGGGTGACTTTATACTAATAAGATATGTCTACTTCCCTTTGTG  
 CTCGAGCAGCCTGGCAGTCCCTCTAGCCGCTTTTTCCTTTTCCGAAGGTTTCCCTCTAAGCCCCCTG  
 GCTCTAGGCCGAGAAAATGTTAATGCTCCTTCTACAGAAAATGCTTGTGCTCACCAAGCAGGAGGAG  
 CCGACGACCGCTTCCGCTAATCTTCTCAATGTTGTAATCTTTTGGCGGTACATTACTAGTATGAATA  
 GGAATAAAAACAGTACCTAATTAATTTTACTTACTTCCCGTTTAAAGCAACCCCAAGTGCCTCAATAGAAGC



112/251

ATAAATCAATAGTCAATATGCUCTCCAAAGTTTGATCCAAATGAAGTTAAGTACTTGTACTTGAGAGCTG  
TCGGTGGTGAAGTCGGTGGCTTCGCGCGCCTTGGCTCCAAAGATCGGTCCATTCGGGTTTATCCCCAAAGA  
ACGTTGGTGAAGATATCGCCAAGGCCACCAAGGAATTCAAAGGTATCAAAGTTACTGTCCAATTGAAAA  
TCCAAAACAGACAAGCTCCTCCTCTCTGTTCTTCCATCTGCTTCCTCTTTTGGTCTATTACTGCTTTTGAAGG  
AAACCAACAGACACAGAAAGGAAGGATAAGAACGTCAAGCATAGCGGTAAACATCCAAATTGGATGAAATTA  
TTGAAATTGCCAGACAAATGAGAGACAAATCCTTCCGTAGAACTTTGGCTTCGGTTACTTAAGGAAATTT  
TGGGTACTGCTCAATCTGTCTGGTTGTCTGTGATTTCAGAACCCTCATGACATCATTGAAGGTATTA  
ACGCTGGTGAATTTGAAATTCACAAAACTAA

YDR418W, 155 aa (SEQ ID NO 132)

MPPKFDPNKVLYLRAVGGVEVGASAAAPKIGPLGLSPKKVGEDIAKATKEFZGIKVTVQLKIQNRQA  
AA5VVPSSASSLVITALKEPDRDRKDKNVKHSQNIQLDEIIETARQMRDKSFGRTLASVTKELLGTAQS  
VGCRVDFKPNFIDIIELGILNAGEIELPEN

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)

TCTCCCTCTCCTGCCATATAACCCCACTGGTATTTTCCAATGCCCTTATTTGTTGGAAACCTGATCTTTAT  
ACCATTCCTGCACCTTTCACAGGGTCATTGCCGTGGATTAATACAAAACCTGAAATTTGGACACCTGCTTGT  
CACATGATGTAAAATCTCCATATCTGTAATAGCTTCTAAATTTGCCCTCCAAATCGAAATAGCAACTCGTCA  
GTTCAATCAAATCCCTCTCGGCAACTCATGCTTGTCTGGATATTTTGTACTCATCTTTTCCCTGTTCTTCC  
TCAAGCTECTCTCTTTTACCTAATAGAACCATCGCCTCCCTCTTATTTATCTTAATACCACATCCAA  
TAGCAGAACTATTACTAAGATCCGATATTTTCGGCCCCCTTCGCAAGGGGCCCCGCCGCACTTTTCTCAT  
GAATTTTTCATATAAAAAGTCCAGGACGCCAAGAAAGGTGCCCTCTTGATTTAAGGACACTTCAAACCTA  
CTGTTATATATTGTTTCATGGAGACCAATTTTTCCTTTGAGTCTGAATTTAATTGTTATTATCATTAATCA  
CGTTGTTTGGCACAAGAATTATTGCTAAAAGATTTTATCTACTCCAAAAATGGTATCCCAAGGAAACAG  
TTCTCTCACGTAAAGGATCTGATTTGGCCAAAAGGAAGTCTTTGTTCCAGCAAGACATACATGCCCTTACT  
GTAAAGCTACTTTGCTTACCTCTTTTCAAAGAATTGAACGTTCCCAATCCAAAGGCCCTTGTGTGGCAAT  
TAGATGAANTGAGCAATGGCTCAGAGATTCAGACGCTTTAGAAGAATCTCTCGGCCAAAAAACTGTAC  
CTAACGTATACATCANTGCCAAGCACATTTGGTGGTAACAGCGATTTGGAAACTTTGAAGAAAAATGGCA  
AGTTAGCTGAATATTGAAGCCGGTATTTCAATAG

YDR513W, 143 aa (SEQ ID NO 134)

METNFSFDSNLIVIIITTFATRIIAKRFLSTPKMVSQETVAIVKDLIGQKEVFVAAKTYCPYCKATLS  
TLFQELNVPKSKALVLELDENMNGSEIQDALEELSCQKTVPNVYINGKHIGNSDLETLEKNGKLAETI  
KPVFQ

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTTCACTAGCGAATTATACAACTCACCAGCCACACAGCTCACTCATCTACTTCGCAATCAAAACAAA  
ATATTTTATTTTAGTTTCACTTTATTAAGTCATTATCAGTATCGTATTAAAAAATTAAAGATCATTGAAA  
AAATGGCTTGCTAAACCGATTATATTTTGTCTTTTAAAGTAGATTATTATTAGAAAATTAAATAGAGAAAT  
ATGTGTTAAATTTATTGAAGAGAGAAAATTTATTTTCCCTTATTAATTAAGTCCCTTTACTTTTGTGAA  
AACTGTCAGTTTTTTGAAGAGTTATTTGTTTGTATACCAATTGCTATCATGTACCCGTAGAAATTTTATT  
CAAGATGTTTTCCGTAACGGTTACCTTTCTGTCAATTTATCCAGGTTTACTCGCCCAATAAAAAATTCCTT  
ATACTATCATTAAATTAATCATTATTATTACTAAAGTTTTGTTTACCAATTTGTCTGCTCAAGAAAATA  
AATTAATAACAAAATAAAATGTCGGAATATUAGCCAGTTTATTTGCTTTAAATCCAATGCGTTTCTTCAC  
CATTTGGATGGTTCTAAATCAACCAACGAAAATGTATCTGCTTCCACTTTCTACTGCCCCAAACCAATGGTTG  
GCCAATTEATTTTTGATAAATTCATCAAGACTGAAGAGGATCCAATTTATCAAACAGGATACCCCCTTUGA  
ACCTTCATTTTTGATTTTTGCTCTTCCACAAACGGCAACTGCACCTTGATGCCAAGACCGTTTTCGCCAATTC  
CGGAGCTAGATGACGCTGTAGTGGAAATCTTTCTTTTGGTCAAGCACCTGANTTCAACTCCAATGTTTGAGT  
ATGAAAACCTAGAAGACAACTCTAAAGAATTCGACATCCCTTGTTTGACAATGACATTCAGTTTACCACTG  
ACGATGTTTCATTTCCCTGATAAGGCAATTGAATCCACTGAAGAAATTTCTCTCTGCTTAUUAATCCANTCTGG  
AAGTCTCGACAACCTTCATTCTTACCCACTCCTGTTCTGGAAGATGCTAAACTGACTCAAAACAGAAAGG  
TTAAGAACAACCAATTCAGTCTTAAGAAGTCACATCATGTTGGAAAGGATGACGAATCGAGACTGGATC  
ATCTAGGTGTTGTTCTTACAACCGCAACAGCGTTCGATTCCTACTTTCTCCAATTTGTGCTGGAATCCA  
GTGATCTCTGCTGCTCTAAAACGTCCTAGAAAACACTGAAGCCGTCAGGCGTTCTCTGTCGAGAAAGTTGC  
AAAGAATGAACAACCTTGAAGACAAGGTTGAAGAAATGCTTTTCAAAAAATTAATTAATTTGGAAAATCAGG  
TTCCACATTAAGAATTAAGTTGGCGAACGCTGA

113/251

YELC09C, 281 aa (SEQ ID NO 140)

MSSEYQPSLPAALNPMGFSPLDGSKSTNENVSASTSCAKPMVGQLIFDKFIKTEECPIIKQCTPSNLDPDF  
ALPQTATAPCAKTVLPPLPLDDAVVESFPSSSTDSPMF EYENLEDNSKEWTS LFDNDIFVTTDDVSLA  
DKAIBSTFEVSLVPSNLKVSSTTSFLPTPVLEDAKLTQTRKVKKFNSVVKKSHHV GKDDERLDHLGVVA  
YNRKQRSIPLSPIVPESSDPAALKRARNTTEAARRSRARKLQRMKQLEDKNVEELISKNYHLENEVARLKK  
LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGCGCTATTCACTAAGGATTCTTAAGSTTTTUTTAATAGTTTTCTACGTCCGCCATGCGATTGPTTGGT  
TAGAAGACTGCTTTCTAAATATGCTTCGGTGTATTTAAGCTAGACCCATACACCCGCTCTATGGGATTA  
TTTACTTTGTGTGAATTTTAAGATTGTGTGATAATGGAACCTGGACGCAACATTTGATGGAAAACGCATGT  
CATCATTAACGACCTAACCTAGGTATCTGTCTTGCCTTAGTATTGCACGCAGCTTCCCAGGACGCCATAG  
CTATTTTTTTCATCTATTCCCCCTCTGTAGTAACGTAAGAGTTTTCAAGTTTTTAATTCACACTTTCTCTT  
CCCTTGTTTCCAAFTTCCCTTCTTACTGCTTGATACCTTTTCAATCCCAAAGAAACCGTGTCTTTTATA  
TATTGTCGATTGAAAGTTACCTACATCAACTTTCCGTCTTCCATTCCGACTATAACAAACAACCAATAA  
GCTCAACTAATTAAGTAATGTCTGCTCCAGAAGCTCAACAACAAAGAGAGGTGGTTTTCGGTGGCCGTA  
ACAGAGGCCCTTCCAAACAGAAAGAGCAACCAAGAAACACTGAAGAAAGGGATGGGTTCCAGTTACCAAAAC  
TAGGTAGATTAGTCAAGGCTCGTAAGATTACCAACCATTGAAGAAATCTTCTTGCACTCTTTGCCAGTCA  
AGGAATTTCCAAATCATTCACACTTTGTTGCCAGGTTTGCAAGACGAAGTCATGAACATCAAGCCAGTTC  
AAAAAGCAAACCCAGACCCCGTCAAAAGAACAGATTTAAGGCTGTGTGCTGTTGTTGGTGACTCTAACGGTC  
ACGTTGGTTTTCCGGTATCAAGACCGCTTAAGGAAGTTTGCTGGTGCCAACAGAGCTGGTATCATTAATGCCA  
AGTTGTCGGTTATCCCAATCAGAAGAGGTTTACTGGGGTACCAACCTTGGGTCAACCACATTTCTTTGGCCA  
CCAGAGACCACTGGTAAGTGTGGTTCCGTCAGTGTAGATTGATCCAGCCCCAAGACCTTCTGCTATCG  
TCGCTTCTCCAGCTGTCAAAAAGTTGTTGCCAATTGGCTGGCTGTTGAAGATGTCTACACCCCAATCTAACG  
GTAAGACTAGAACTTTGGAAACACCTTGAAGGCTGCTTTGCTTGTATTGGTAACACATACGGTTTTCT  
TGACTCCAAACTTTGTGGGCCGAACAACCAATTGCCAGTTTCTCCATTGGACATCTACTCCGATGAAGCTT  
CTGCTCAAAAGAGAGATTCCTAA

YGT123W, 254 aa (SEQ ID NO 164)

MSAPEAQQQKRGFGGHNRRGNRRCPNTEEEKGWVPVTKGRIVKAGKCTTYISETFLHSLPVKFFQTI  
DTLLPGLQDEVMMNIKPVOKQTRAGQRTFRKAVVVVGDSDNGHVGLGIKTAKEVAGAIRAGIIIAKLSVIP  
IRRGYWGNTNLGQPHSLATKTTGKCGSVTVRLIPAPRGSGIVASPAVKKLLQLAGVEDVYTQSMGKTXTL  
ENTLKAAFVATGNTYGFITPNTWARQPLPVSPLDIYSDEASAQKKRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

ATCATCCAGACTTTTACGGGTGGCAACCGGAACCAACGTATTTAGAGATTGTTTTTTGGTCAAGCCGAGGA  
ACCCCTGTGTGGCAAAGTTGCCAGGTATATCATGGGTGGCGAGGTCAACATTCCAAAGCATTCAAAACCTT  
GGCGGCGTGAGAGTCAGTGAAGAAAGTCTTGTTGAGCCCGGTAAGAATGACATACTCGGCTTCAAGATC  
GCTCCAAGATCAGCATAACTTGAGTGCCAGTGAATATTAACTAATCATCAAAGTATATGCTGAATTCCTT  
TATACTCTTAGTAAAGGAATGCTCCCTACAGCTGCTCTCTTTTCTTACTAAGCGCGTTCAGTTTCCAACC  
AGCCGAAAGAGGGATATCAATATATAAGAAAGCCATTCGGGGGATGAAAAGCTGACAAAGAGAATAACGA  
GGACCAGTTTTTATTTGTTGCTCAGCAAGAAATTATACAGGCACACATACACGAGAGTCTACGATATCTT  
TAAATAACACATCAATAATGGTCACCTCAATTAATAATCCGCTTCTGAATACGACAGTGCTTTAGCATCTG  
GGCACAAGTTTACTCGTTGTTCACTTTTTTGCCACATSGTGTGGGCCATGTAAATGATTGCACCAATGA  
TTGAAAAGTTTGCAAGAAATATTTGACGCTGCTTTTTTAAGAGTTGGAATGTGAATGAAGTCTCAGATG  
TTGCTCAAAAAGCTCAAGTTTCTTCCATGCTTACCTTAATCTTCTACAAGGGCGGTAAAGGAGGTAAUCA  
GAGTCGTGCGTGCCAAACCGAGCTGCTATCAAGCAAGCTATTGCTTCCAACGTATAG

YGR209C, 104 aa (SEQ ID NO 188)

KVTQLKSASEYDSALASGDKLVVVNPFATWCGPCCKMTAPMTKFPABQVSDAAPYKLDVDFVSDVAQKAF  
VSSMPTLIFYKGGKEVTRVVGANPAATKQAIAASNV

YHR039C B, 1007 bp, exon1: 501-563, intron1: 564-665, exon2: 666-1007 (SEQ ID NO 197)

GTACATGCACCACTCGCTTCAACTGCGTCAGATAGTTGTAGTCCCTCTGGACATAAGCATTTTCGTTGCT  
GCTTGTGCTGCTCCGCTGTTTTCAACGCCCTCACTCGATATATACTCCTTAGGATCATGTGTTTGACCTG

114/251

ACCAATTGTCCCTTGTCTTGTGCTTCTTGGGAACACTCCAAAAGCAAGTTTGCACUCAAACATCTTTGGAC  
 ACTTGTATTTGAACTCTTTTATTCCGCATACACCACACAACACCGCCATCTTGCATATTTCCACACCCC  
 TTTCCCTATTAACCTGGACTCCTATTCCAGCTCATCTCATCGAATATGAACTTTTGACATCCACTATTATTA  
 CCGCGAATTTTTTTTTTTTTTCAATTTGCTTACCCTGCCCTTGGGTATCAAAAATTCATCTCTAAAAAGGGA  
 GCGTGATAGATAAAGCAATCACACCTTAACAATAACATTTTCTTTTCTGCAATCTCCAAAGTGTGC  
 AAGGTATACAAAGCAGAAATGGTATGTGCCATTACATTACGTGTCAACACTTCTGTCTCTAACAAAGCGTT  
 CTTACTAACATGAAAACTTTTTTAAABCTGTGCTCTCTTGTGTGGACTGGTACCTCGTGACAAAGGTAT  
 TGCTTTTTCATTTGTTGCTCAGAACTATGTAATATTCTCTTTAGTCCCCAAAAAACGGAAATTGCCACCC  
 TACTACAAGCTGAAAAGGAACCCACGAAATAGTATCAAAAGCCTAGAAAAGTACAGACAAGATAAGTTGA  
 AGCAAGCCAAAGACTGATGTCAGCCAAAGGAAATCGACTCATACAAAATTCAAAAAGACAAGGAATTTGAAGG  
 AGTTTGAACAAAGGAATGCGGTGGTGTGTTGTTGAATTGGAAAAAGAAAGCAGAGGCTGGTGTCCAAAGGTG  
 AATTAGCTGAGATTAAGAAATTTGCAGAGAAGAAAAAGGATCACGTTGTCAAAATTTTGATCGAGACTTG  
 TCATCAAGCCCTTCTGCTGAAGTCCATATCAATGCCTTGTAA

YHR039C-B, 114 aa (SEQ ID NO 198)

MSQKNGIATLLQAEKEAHEIVSKARKYRQDKLKQAKTDAAKEIDSYKLQDKELKEFEQKNAGGVGRLE  
 KKAAGVQGELEAEIKKIAEKKEDDVVKILIEYVIKPSAEVHINAL

YHR053C, 686 bp, CDS: 501-686 (SEQ ID NO 199)

AACTTCAACGATTTCTATGATGCATTTTATAATTAAGTAAAGCCGATCCCATTACCGACATTTGGCGCGCTA  
 TACGTGCATATGTTCAATGTATGTATCTGTATTTTAAACACTTTTGTATTATTTTTTCCCTCATATATGCGC  
 ATAGGTTTTATACCGATCATTAAATTATTACTTCCACCACCTTTATTTACGGCTGATATCTTAGCCTTGT  
 TACTAGTTTACAAAAAGACATTTTTTCCCTGTCACTGCTCAAGAGATTCTTTTGCTGGCATTTCTTCTA  
 GAAGCAAAAAGAGCGATCGCTCTTTTCCGCTGAACCGTTCCAGCAAAAAGAGACTACCAACCCAAATATGG  
 ATTTGTGAGAAATCATATAAAGAGAGAGCAATAACTCCTTGTCTTTGTATCAATTTGCATTATATACATCTTC  
 TTGTTAGTGCATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAAACTGTACAAATCAATCA  
 ATCAATCATCATATAAATGTTTACGGGAATTAATTAACCTCCAAAATGAAGGTGATGAGTGCCATATGCC  
 AATGTGGTAGCTGCAAAAATAATGAACAATGCCMAAATCATCTAGCTGCCCAACCGGGGTGTAAACAGCG  
 ACGACAAATGCCCTGCGGTAACAAGTCTGAAGTAACCAAGAACTCATGTGCTCTCGGGAAATGA

YHR053C, 61 aa (SEQ ID NO 200)

MFSELINFQNEGHECQCQCSCSKNNEQCQKSCSCPTCCNSDDKCPGKNSSEBTKKSCCSGK

YHR055C, 686 bp, CDS: 501-686 (SEQ ID NO 201)

AACTTCAACGATTTCTATGATGCATTTTATAATTAAGTAAAGCCGATCCCATTACCGACATTTGGCGCGCTA  
 TACGTGCATATGTTCAATGTATGTATCTGTATTTTAAACACTTTTGTATTATTTTTTCCCTCATATATGCGC  
 ATAGGTTTTATACCGATCATTAAATTATTACTTCCACCACCTTTATTTACGGCTGATATCTTAGCCTTGT  
 TACTAGTTTACAAAAAGACATTTTTTCCCTGTCACTGCTCAAGAGATTCTTTTGCTGGCATTTCTTCTA  
 GAAGCAAAAAGAGCGATCGCTCTTTTCCGCTGAACCGTTCCAGCAAAAAGAGACTACCAACCCAAATATGG  
 ATTTGTGAGAAATCATATAAAGAGAGAGCAATAACTCCTTGTCTTTGTATCAATTTGCATTATATACATCTTC  
 TTGTTAGTGCATATCATATAGAAGTCATCGAAATAGATATTAAGAAAAACAAACTGTACAAATCAATCA  
 ATCAATCATCATATAAATGTTTACGGGAATTAATTAACCTCCAAAATGAAGGTGATGAGTGCCATATGCC  
 AATGTGGTAGCTGCAAAAATAATGAACAATGCCMAAATCATCTAGCTGCCCAACCGGGGTGTAAACAGCG  
 ACGACAAATGCCCTGCGGTAACAAGTCTGAAGTAACCAAGAACTCATGTGCTCTCGGGAAATGA

YHR055C, 61 aa (SEQ ID NO 202)

MFSELINFQNEGHECQCQCSCSKNNRQCQKSCSCPTCCNSDDKCPGKNSSEBTKKSCCSGK

YHR056C, 2999 bp, CDS: 501-2999 (SEQ ID NO 203)

ATGCTNTAGTTAAAGGTAAATTAACATAGAGAACGTGGGAACACTTCCGCACTGTGACCACCGGAACGTAU  
 CTCTGGTTAGCCCAACCATTAGTCCCACTTACATCCGATCAAAATGCAACAGCAAGTATTAATTGGCGA  
 AATCATATCATTTTTGAATATAACCTTGGCGTCCCTACTAAGGATCGTTATACATCCCTAGCTCGGTASTG  
 TGATNTTTTGCAGGAATGATGCAAGAGAGGAAGAACAGAGACAGACTTGTGTCTTTTAATGTATCTTTA  
 GCAATTTATGAGACGAGCATTTTGTGCTGTCTGTGTAAGTGTGCGTAGCTTTGCGGTCTTGTCTTTTAAAT  
 CATGATGGACATGCAAGTGAGAAAAGTGAGGAAGCCGCTTCTTGCACCCCAATGCAGGAAGAGAAAAGAT  
 CCGGTGCGACAGGGCCAAAACCGATATGTCCCAATTTGCGTCAAGTATTAACAAGCCGGACTGTTTTTATC

115/251

CAGATGGAACCTGGTAAGATCGTGGCTGTCGCCCTCTGCGTCCCGGATGTCCACGACCGGCAATGCCCAAG  
 GTTCCAAACCATTCTTAGTCAGGGGAAACGGTGTAAATCAGAAAAACGTAATGATTCAAACCGCAGTATCCGA  
 TTATGCAAACGTCGATAGAGGCATTCAACCTCTCGTTCAACCCCTCTGTGGTACTGCGGATGCAATGGGA  
 CCAAGGCCGCTAGCTACCGAGAATAATAACCAATAATAACTGCTCCTCGTCAGAAATAGTAGTACCG  
 TTAGTAGTAATGTTCATGGAAACACTATTGTGAGAGCGGATAGTCCAGATGTGCCCTCCATGGATCAGA  
 TTAGAGAATATAACACACGAATTACAACCTGGTTTAAACGCTCAAGTCTTGACTATACAGATAAACCCTACT  
 CTCTTAAATGTTGGTATCAATCAAGACTCGGCCGTTTTCGATCTAATGACTTCTCCGTTTACTCAAGAGG  
 AAGTATTAATCAAGGAGATAGACTTTTTTAAAAACAATTTGCTTGATTACAAAGCTTGCAACTGAAAA  
 GTTTGAAAGAAAAATUGAATTTAAATGCCGACAATACCAACGCAACAAAAATTAACAAAACAGGTGAGA  
 ATTCTAAGAAAGGCAACGTTGACGGTAAAGAGCCGGATTGATCATCAGACTTCGAGGACTTCTCAGT  
 CCTCACAATAATACTTTACAGCGCTCACAATAACAGATGTGCAAGTTTAGTCCAAAGTGAAACCGGTTGA  
 AGGATAUUUUCAAUTAUCCTTTCACTAAAAACCTCAATCAATTTTAGAGATCATTAATCTTTCAAGTCTCT  
 ATAATATTTTTGCACGATATCTGCCATATTAATCAGTTCAAATTAAGTCTCTCTAACCAATAAAAAATCACC  
 AACAATATATGGAAGTTTGCAAAGTTAACTTCCCAACCAAAACCAATTAATTTAGACACCTAAACTCTG  
 AATCCCTTAACAATCTCAATATTGAAGAATTTTTGCCAATCTTTGACAAAACCTCTTACTAGAATTTG  
 TTCATAACTCTTTTCCAATGCTCATACCTCTCTCTCAATCTCAACGGTCGATCTTCTCTTATCTCAAC  
 TGACCAAACTAGGCGAATTAACCTGTGCTTCTACTGTTGTTAAACGATTCATGACCTTCAATCAATAAGC  
 AGGCTATTAATAACCACTGTTTCGGCATTAATGAATAAATTTGAGGTGATTTCGAAGCCAAATCACATTCGA  
 TAAACCTGGAATATTATGACCAAGAGACAATCAAAATTTATGCCATCACAAAATTTTATGAATCTCTCT  
 ACATGCATGATGATCAATAATCAAGTTTAGACGAAGATTGAGCTGTCTGTTAAGCTTCCAGATAAAAC  
 ATTTCAAGTTATTTCACTTTTGAAGAAAACTGATTAATCAAGACATTCGCTCTTAGGTGAGCTTCTCAT  
 TCAATGATACCGCTGCTGAAACCTATCTCGGATACCTGCTCTCAATGATAAGAACGACATTTCTTTTAA  
 TTGCTAACGATTTAAAACTACTGGAACCGCAAGCAAAATTGATAAATATTCTGCAAGGTGTTCTCTCT  
 ACTTGCCAGTAAATTTAACCAAAATTGAAAGTCTGTTAGAAACCTTGACTATGGGCGTAGTAATACAG  
 TAGACTTATATTTTCATGACAACGAAGTCAGAAAAGAAATGGAAAGACACTTTAAATTTTATCAATACCA  
 TTGTTTATACAAATTTTTCTCTTTTGTTCAAAACGAATCTCTTTGTCTCATGGCAGTTCAACATTTCTT  
 CTAAACAATAAGACCTCGAATCTGAAAGATGTGCAAAGGATCTGATGAAAATTAATTTCTAATATGCA  
 ACATTTTCTACTCAATAACATTTAATTTTATCTTCCCATAAAGTCGATAAAGTCATTTTCAAGCGGCA  
 ATAATCGCTTTCAATCTAATGGTAAAGAACTTTTATTCGCAAACTCACTTTTATGAAATCTTACAGAATT  
 TTATAGCAATCACATTTGCTATTTTCCAACCTGTGAAGTAATAATATATGACGAATTTTACAAAAATC  
 TTTCAAACTGAGGACATTAATGTTCAATTTCTTATTCATTCATGACAAGATTTTCGAAATTTTAAAAAAA  
 TAGAAATTAATCGTATCTCTTTTACGAGATGAATGAAATAGCAACGGAAGTTTCAAACTCATTAAGGTT  
 TCAACAAGGTTTTGAATCTGATTAATATATGCTGAGATTTAGCAAGAAAAACAAAAATTTTGGCGAAG  
 ACTCTGATAACCAATAATGTTACAGATTTATAGTCAGTCGGCGAAGAAACAAAAATGTTCTCTTCAAAATTC  
 CCGTTAGTGAACGAAACAGAACTTATTTAAATTTAAGGAGATTTAGATTTTAAATGGAAGAGAGAAAG  
 TTGTCAAAGGAGTATAATTATTGACAAGGATTTGGAATCTGATAATCTGGGTATTACTACGGCAACT  
 TCAACGATTTCTATGATGCATTTCTAATATTAG

YHR355C, 832 aa (SEQ ID NO 204)

MVAVPSAAGMSTHGNGQGSNHPSQGNQVWQKNVMIQTQYPIMQTSTIEAPNFSNPSPVDTAMQWIKAAAY  
 QNNNTNNNTAARQNSSSTVSSNVHGNITIVRSCSPDVPMSDGIREYNTRILQLVNAQSPLYTDNTPYSFNVGI  
 NQDSAVFDLMTS  
 FFTQEEVLIKEIDFLKNKLLDLQSLQLKSLKEKSNLNADNNTANKINKTGENSEKKKGKVDGKRAGFDHQ  
 SRTSQSSQKYFTALTITDVQSLVQVKPLKDTPNYLFTRKNFIIFRDHYLPKFYNILHDIICHINQFKVSP  
 NNKNHQQYMEVCKVNPFPKAIITETLNSESLNNLNIEEFLPIFDKTLLEFVINSPNGDTCPSPSTVD  
 LPLSQLTKLGELTVLLLLLNDMTLFNKKQAINNEVVSALMNNLRILRSQITLINLEYVDQETLKFLAATK  
 FYESLYMHDDHKSSLDLCLLSFQIKDFKLPHFLKKMYYSRHSLLCQSSFMVPAENLSPIPASIDP  
 NDIPLIANDLKLLETQAKLINILQGVFPYLPVNLTKIESLLETITMGVSNSTVDLYPHDNEVRKEWKTIL  
 NFINTIVYTNZFFLVQNESSLSMAVQHGSSNNKTSNSERCADLMKIIISNMILFYSTTFNFIPIPKSIK  
 SFSSGNRRFHSNGKEFLFANHPIEILQNFIAITWALPQRCEVILYDEFYKNLSNEEINVQLLLIHDKII  
 RILKKITETIVSFRDEMNSNGSPKSTKGFNKVLNLIKYMIRFSKKKQNFARNSNNNVTDYSQSAKNKN  
 VLLKFPVSELNRIYLFKFEKSDFLMEREVVR311TEKDLESNLCITANFNDFYDAFYN

YJ1138C, 1688 bp, CDS: 501-1688 (SEQ ID NO 223)

CTGTTGAATCATGGTAAAAGAGAAAATCAAAGCACGTTGACCTGGATATAACCTCAGTAGATCCAAAT  
 GCTTCCACAGAACGTAAGTGCAGAGAAACATGATATTGAGAAACCGACATCTAAGCCGCAATCTGCTTTT

116/251

AAATTTGATTGGGAGTCTACGGATTATTTAGACCCGGTCCAAAGAGCATTCCCAAAGCCTGATACCTGA  
 TGCCATCCCTCTACCTCTTAGCTATCAATCAATCAALTAAACTACTACATAGTATACATTAGCTGTACA  
 GTCCCTCACATCAGACGAATACAAAAGGCCGGGTGAAAGCGTGGATTTTGGCTACCTTTTTCTTTTTTTC  
 GAAATTTTTTTTATTTTTTTTCAGCATCATATATPAAAGAAATCTCATCTCAACGAGAAGGAAACAGCA  
 GATCCCAATACACATAGTAGGAAAAAAAAGGTTGGCTAAACAAAGGACTGGTGTGTACAAGAAACTAA  
 TAAATAGTAATTGCAATATCTCTGAAGGTATTACTGATATGAAGAATCCCAAATTCAAACCAACTATG  
 ACAAGGTGGTCTACAAGTCCGATGATATGGAATTGGACGAAAACCTGTAAAGAGGTGTTTCCGGTTACG  
 GTTTTCGAAGAACCATCTGCCATTCAACAACGTGCCATCATGCCATTATTATGAAGGTACCGATGTCTTGG  
 CTCAAGCTCAATCTGGTACTGGTAAGACCGGTACTTCTCCATTGCTGCTTTGCAAGAATTGACACCT  
 CTGTCAAGGCTCCTCAAGCTTTGATCTTGGCTCCAACTAGACAAATTCGCTTTGCAAAATCCAAAAGGTTG  
 TCATGCCCTTTGGCTTTCCACATGGACATCAAGGTCCACGCTTGTATCGGTGGTACTTCCCTTGTGTGAAG  
 ACGCTGAAGGTTTGAGAGATGCTCAAACTCGTCTGGTACTCCAGGTGGTGTGTTTGAACAACATCCAAA  
 GACGTAGATTTCAGAACTGACAAGATCAAGATGTTTCATCTTAGATGAAGCTGATGAAATGTTGTCTTCTG  
 GTTTCAAGGAACAAATCTACCAAAATTTACCTTACTTCCACCAACCACTCAAGTTGTTCTATTGTCCG  
 CCACCATGCCAAATGACGTCTTGGAAAGTACCACCAAAATTTATGAGAAACCCAGTTAGAAATTTTGGTTA  
 AGAAGGATGAATTGACTTTGGAAGGTATCAAACTATCTACGTTAATCTTCAAGAACAAATTCAAAT  
 ACCAGTGTGTTGACCGATTTATACGACCTATCTCCGTTACTCAAGCTGTCTCTTCTGTAAACACCGAA  
 CAAAGGTCAAGAAATGACCACTAAGTTAAGAAACGACAAATTTACCGTTTCTGCCATTCTTATTCGATT  
 TACCACAACGAAGAAAGAGACACCATCATGAAGGAATTCAGAAGTGGTTCTTCCAGAATTTTGATCTCCA  
 CTGATTTGTTGGCTAGAGGTATCGATCTCCAACTAGTTTCTTTEGTTATTAACTACGACTTACCAGCTA  
 ACRAAGAAAACTATATTACAGAAATCGGTAGACCTGGTGGTTTCCGTAGAAAGGGGTGTTGCCAATCAACT  
 TTGTTACTAACGAAGACGTTGGCGCTATCAGAGAACTAGAAAAGTTCTAUTCACACTCAAAATGAAGAAT  
 TGCCATCCGACATTGCTACCTTGTGAAGCTAA

YJL138C, 395 aa (SEQ ID NO 224)

MSEGLTDIEESQIQTNVYDKVYVKFDDMELDENILRGVPGVGFRRPSAIQQRAIMPTEEGHDVLAQAQSG  
 TGKTTGTFISIAALQRIDTSVGAPOCALMLAPFRELALQIQKVMALAPNMDIKVHACIGGTSFVEDAEGLR  
 DAQIVVGTGPRVFDNIQRRFRFTDKIKMFLDEADEMLSSGFKEQIYQIFTLLEPFTQVVLLSATMPNE  
 VLEVTTKFMRFVRILVKKDEFTLEGIKQFYVNVVEEEYKYECCLDLYDSISVTQAVIFCNTRRKVEEL  
 TTKLRNDKFTVSAIVSOLPQQRDTIMKEFRSGSSRLISTDLLARGIDVQQVSLVINYDI.PANKENYI  
 HRIGRGGRFGRKQVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

YKL060C, 1580 bp, CDS: 501-1580 (SEQ ID NO 239)

TGGGTCATTACGCAAAATAATGATAGGAATGGGATTCTTCTACTTTTCCTTTTTCATTCTACCAACCGT  
 CGGGAAACGTGGCATCCTCTCTTTTGGGGCTCAATTGGAGTACGGCTGCCGTGAGCATCCTCTCTTTCC  
 ATATCTTAACAACGAGCAAGTAACCAATCGAAAAGCATGAGCTTAGCGTTGCTCCAAAAAAGTATTGGA  
 TGGTTAAATACCAATTGCTCTCTCTCTCTCTGACTTTGACTCCTCAAAAAAAAATCTACAATCAACAG  
 ATCGCTTCAATTACGCCCTCACAAAAACTTTTTCCTTCTCTCTCGCCACGTTAAATTTTATCCCTCA  
 TCTTGTCTAACGGATTTCTGCACTTGATTTATTATAAAAAGACAAAGACATAATACTTCTCTATCAAT  
 TCAGTTATTGTTCTTCTTCTGCTTATTCTCTGTTCTTCTTTTCTTTTCTCATATATAACCATACCA  
 AGTAATACATATTCAAAATGGGTGTGTAACAAATCTTAAAGAGAAAGACCGGTGTCATCGTTGGTGAAG  
 ATGTCCCAAACTTATTCACTTAAGCTTAAGGAACACAAGTTCGCTATTCCAGCTATTAAAGTACCTCTT  
 CTCTACTGCGGTCTGCTGCTTTAGAAGCTGCTACAGACAGCAAGTCCCAATCATTTTGCAAAACCTCTA  
 ACGGTGKGTGCTTACTTGGCTGGTAAGGCTATCTCTAACGAAGGTCAAAATGCTTCCATCAAGGGTC  
 CTATTGCGGTGCGCACTACATCAGATCCATTGCTCCAGCTTACGGTATCCUAGTTGTCTTACATCTG  
 ACCACTGTGCCAAGAAGTTGTTGCCATGGTTCCATCCTATGTTGSAAGCTGATGAAGCTTACTTCAAGG  
 AACACGGTGAACCAATTATCTCTCTCCACATGCTGGATTGCTCTGAAGAAACCGATGAAGAAACACTCT  
 CTACTTGTGTCAAGTACTTCAAGAGAATGGCCCTATGGAACTGTTAGAAATGGAAATCGGTATTA  
 CCGGTGGTGAAGAAGATGGTGTAAACAAACAAACCTGACAAAGCAAGACTTGTACACCAAGCCACAAAC  
 AAGTTTACAAAGCTTACAAAGCTTTGCAACCAATCTCTCCAACTTCTCCAACTGCTGCTGCTTTCCGGTA  
 ACTGTCACGGTTTGTACGCTGGTGACATCGCTTTGAGACCAGAAATCTTGGCTGAACACCAAAAGTACA  
 CCAGAGAACAAAGTTGCTTGCAGCAAGAAAGCCATTGTTCTTGGTCTTCCACGGTGGTTCGGGTCTA  
 CTGTCCAAAGAAATCCACACTGGTATTGACAAAGGTGTTGTCAAGGTCAACTTGGACACTGACTGCAAT  
 ACGCTTACTTGTACTTGGTATCAGACACTACCTCTTGAACAAGAAGGACTACATAATGTCCCGAGTCGGTA  
 ACCCAGAGAGGTCCAGAAAAGCCAAACAAGAGTCTTCCGACCCAAAGAGTCTGGCTTAGAGAAGGTGAAA  
 AGACCAATGGGTGCTAAGATCACCAAGTCTTTGGAAACCTTCCCTACCACTAACACTTTATPAA

YKL060C, 359 aa (SEQ ID NO 240)

YKL097W-A, 779 bp, CDS: 501-779 (GEO ID NO 245)

YKL097W-A, 92 aa (SBO ID NC 246)

YKL150W, 1409 bp, CDS: 501-1409 (SEQ ID NO 249)

YKL150W. 302 aa (SEQ ID NO 250)

MFSRLSRSHSKALPIALGTVAIAAATAFYFANRNQHSFVFNESNKVFKGDDKWTDLPISKTRRSHDTR  
RFTPKI.PTEDSEMGIMIASALFAKFVTPKGSNNVVRFYTPVSDLSQKQHFQLVWXYIEGGKMTSHLFGK  
PKDTSVFKGFIMKWKWQPNQFKITLLGACTGINFLYQLAHHIVENPNDKFKVNNLLYGNKTPQDILLRK  
ELDALKKKYPOKFNVTYVDDKQDDQDFDGEISFISKFIQEHVFGPKRSTHLFVCGPPPFNNAYSCEK  
KSPKDGELIGLNNLGYSKDOVKF

118/251

YKL156W, 1099 bp, exon1: 501-503, intron1: 504-853, exon2: 854-1099  
(SEQ ID NO 251)

CGAAGGTTTCGATCAAAGTTTGGCTCAATCACTGGACACTATTACTTCCGAAACCCCACTCCCGTTAAAC  
AGAGACCGTGATGTGTCGTCACAAGTATTTCAAGGAAAAATGCTTACTATTAAAGAAAAATCTCTTTTCTA  
GCCATTTTGGCTTTTATATAGTCAAGTATCTATATGTGACAAATACTTCTTCTAAGC"/"GGGCTTCTG  
ATAGGCTTAGCTTGCAGTGGTTGCACAACATACATAAATCAACAAAAAAAGTACGGCT"/"AAAAATTTTGGTA  
TTCATTTATTTCAACCCGTGCACACTGGAAATAAATCTGTACATAACAGCATATTTTGTTTTGAAGAAA  
ATTTCTGTGTTCTCCGATGTCGGACCAATTTTACGATCGGCTAAATTTTCGTAAGATATCAGTAACCTTG  
GTATCTGTGTATAAGCGGAGTCTAATTTTCGATAACCAAGCAACTTCATCGTAACACCTTCCAAACAAACCA  
AAGATAGATATCCCAAAATGGTATCTTACTATCCCAATAAATTCAGCGCAACTTGCACCAAGTGAATAGAAC  
AATACATATAGATAAGTTCGCAAAAGAAAAGAAACACATGTGCTGGAAAAATTTTTCACCAAGAGAGGCCAAG  
AACTATGAAGAAAGACTTTTGAATATTTCAAGCGGTTGCTACATATAGTGGATAAGATTCAGGATCGA  
CGTATGAGCTTACAGTTCATTGTACCGGAATATCAAAATTTCTGATGATGGCGAACTTCATTCCAGCAAC  
TCAAGCTTATGTTATTTTCTATTCTGCACCGAGATGAGGAGAAAAAGGAAGT"/"TACTAACAGTTTACA  
TTTATTTCTTTATTTCTGCTACAACAGGTTTACGTTCAAGATTTATTGCAACCAACTGCACCTTCTGAAGC  
AAGAAAGCACAAATTAAGACATTAAGTCCAAAGGTCACAGATCGTACTTCTAGACGTTAAGTCCCGCAGG  
TTGTTTGAACATCACTACAGT"/"TTCTCACACGCCCAAACTTGCAGTTACCTGCGAATCCTGCTCAACCAAT  
TTTGTCCACCCCAACTGGTGGTAAGGCAAGCTTTCTGAGGCTACATCTTTTCAAGAAAGTAA

YKL156W, 82 aa (SEQ ID NO 252)

MVLVQDLLHPTAASEARKHKLKTLVQCPRSYFLDVKCPGCLNLT"/"VFSHAQTAVTCESSUSTILCTPTGG  
KAKLSEGTSPFRK

YLR029C, 1115 bp, CDS: 501-1115 (SEQ ID NO 265)

TGCACACTTACTTAATATGFT"/"TGGCGCCCTTCATAAGAGUGTGTTTCTAAAAATTTATTCGCCCAAGAACT  
GAGATGGACTCGCACCCCTACATGACGTTTAAATATTTTACTGTTPAGGTTTCAAGACATGCACCAGG"/"GUG  
ACATGTGTTCGGATTATCATGACAATGTCTCTATCCGAGATGCATTTGTAGTATCAATTTGATGCGTATCT  
ATGACATGACTTACATAGCNTACATCGTCAACATGATATTTATATCT"/"TTTTTGTATAATGTACCGGAT  
TTAAAGCTGTCGAATATATTTTCTGAAATTTCTTGGAGCTGACGCCAAATTTTCAAGGTGCTAAAACT  
TTTCAAGATCTCTCACCTTTGCTTGGTAACAAAGAAATCATGCGCATTTCCAT"/"TTACCACCGGTACAT"/  
AACTGCTATCTCTCACGTTTCTTTCCCTATCTTTAAGTAATTTCTTTTACAATCTTAAGAAAAACCGATC  
AAACAAATRAATCAGCAATGGGTGCCCTACAAATAT"/"TGGAAAGAAATTCGCAAAAGAAAGAGCAATCTGATG  
TTTTTGAAGTTCTTTCGAAAGAGTCAGAGTCTGGCAATACAGACAAAAAGAAATGTCATTTCACAGAGCCGCTA  
GACCAACTAGAACAGACAAGGCTAGAAAGATTCGGTTACAAAGCTAAGCAAGGTTTCTGTTATCTACCGCTG  
TCAGAGTTTAGACGTGGTAACAGAAAGAGACCTGTTCCAAAGGCTGCTACTTACGGTAAGCCCAACTAACCC  
AAGGTGTGCAATGAATGAATACCAAAGATCCTTGAGAGCTACCGCTGAAGAAAGAGTTGGTCTCTCGTG  
CCGCTAACTTGAGAGTCTTGAACCTCTACTGGCTTAACCAAGATTTCTACTTACAACTACTTCAAGT"/"TA  
TCTTGGTTCGACCCCTCAACACAAGGCTATCAGAAGAGATGCTCGTTACAACTGGATCTGTGACCCAGTTC  
ACAAGCACCGTGAAGCTAGAGGTTTGAATGCGCACTGGTAAGAAATCCAGAGGTATCAACAAGGGTCACA  
AATTCACAACAACCAAGGCTGGTAGAAGAAAGACCTGGAAGACACAAACCACTTTTCTCCTTGTGGAGAC/  
ACAGAAATATA

YLR029C, 204 aa (SEQ ID NO 266)

MGAYKYLEELQRKKQSDVLRFLQRVRVWEYRQKNVTHRAARPTRPDKARRLGYKAKQGGVITYRVRVRHG  
NRKRPFVKGACTYKPTNCGVNELKYQRLRATAEERVGRRAANLRVLNSYWNQDSTYKYFEVLLVDPC  
HKAIRRDARYNWICDPVILKIREARGLTATGKKSRGLNKGHKFNNTKAGRRKTTWKRQNTLSLWRVRK

YLR038C, 752 bp, CDS: 501-752 (SEQ ID NO 267)

GGAAAGCRAAGCTCTAAATGATAACTCTACAAAAAAGTCAGAGAAATCTGTGACTAATTTTATTGAAGCA  
TGAAGAAATTAATGCTTAAAGTCTTAGAGCTTTTGGTGACAAGTCTGCAAAACGTCACAGACCCCAATPAA  
AGCTACCGA"/"TGGTGGGACATGTGTTTCCAAATTANTACGCTTACTCAAGCAATTAGACAGAGAAACAA  
CACACAAATTTGGTCAAAAAGCACTCGAGAGATTCAAAATAAATCTATATGACACCAATGTATTTCTTTACCA  
TATAGCTTCACAACATTTGACCAATCAATTTTCAGAAATGCGTCCGCGCGTAGTTT"/"TGGCGGATATCCCCA  
TCCCTTCAGGACCTTTAAAAGGTGATGAAGATGCACCAGATACAAAATTTCCATPAAAAATGATTAGCA  
GAGATATACAAATATTTTAGTAAGAATACATAAAGTATCT"/"TGGCTTTTCACAAAATAGGAACAGGCACATA  
AATACAGTATAAATAGACATGCTGTATCAAGAAACTCTCCCACTACATACAGTTGGTTTCCATGCTAGAT

119/251

TTCCCCAACAAAACCAACCAAGCATTGTTGGCAATCTTACGTGGATTATCACAAGTGTGTTAATATCJA  
AGGGCGAAGATTTTGTCTCCGTGCAAGGTCCTTTTGGAAACACCTATAACGCCTTATGTCCCTAGACTCCA  
TCGAAAAATGGGATGATCAAAGAGAAAAAGGTATTTTCGCACGTGATATCAACTCAGACTAA

YLR038C, 83 aa (SEQ ID NO 268)

MADQHN SPLHTVGF DARFPOC NQTKHCWQSYVDYHKCVNMKGEDFAPCKVFWKTYNALCPLDWIEKWDD  
QRPKGIFAGEINS

YLR312C, 1697 bp, CDS: 501-1697 (SEQ ID NO 285)

CATCAANTTAGGCCAACTTGAATAGTCAGCTAGGTCATATATTAAAATCAATTAGCCCTATGACTACA  
TTAGGTTTTATTGTTAGGTCTTTACGGCTGCATATTTGCTTTTCGCCGTTCCGGCGGGGTCCTGCCAGCAT  
CTCTCCGCGGTCTTTGTATGGGTGGAGTTGACAGTTAAACCTCCCGACCCCTACCCCGGTGTGCCCCCGG  
TCCATCTATCCATTTTTCGGTAACCCCTTTCCGCGACAGCTGCTTATCAAGGTAACCTGGATCGAGCCAT  
AAAAATTGATCTACACAGATGAGATGGGGCATTTGGGATATATTATTAGTCGGAGTATCATATAGTTAT  
TCAGTTTATCCAGCTTACTGGCCAAAACGTTTTCCTTCATTGGAATAATCGTTTACGGAGCTACTGTTTC  
CGGTATAAAGTAACAAGCACAGTAGCAGAGTAATACCGCACTGACGATAATAGAGACTAGTAAAAACAGTC  
GAGTTGTCCGACCTAAAATGTCAGAGAAGACGACATTCCTCGAATTTAGTTAGATTACGTAGATTACGTA  
AAGGGAGAGAAGGGGAAGAACAGTCAATCGAAGTCAGAAAATATCTTTGGATAGTTTGCATGAAAGCTCCT  
TTCCAGGACAGGACGACGAGGACATTCGATGCAGATGTCCTATCGAACACTAGCAGTGAAGAGTCTGCAU  
AGATCAANTCGTACTTTACGATTTTATGACATCTAATGAATTTAGTAATGCTGGAGTTAATATTGATCAA  
CTGGAGTTCCCACTATTTCAAGAGTCATTTGATACTTTGTCCGGCTCAAAATGTTGGCGGAACCGTATTGC  
CAAGTATGCAGCGGTCGAAATGAAGGATAGTACGATAAGGAATTCAGCAACTATCGGATCATATCA  
TAGATAAAAGTGAGGGTAAATCTGCTAAATGAAGATGTGGCATGTTATCACTCTAATCTCATTGCTTT  
CCATGACCTTTTTCATACCTCGCCCTCGAATATTCCCTGACTGGTGATGTGTGCCAGCTTTTAAATCAC  
AACAGTCATTACGTAATAATGAAAGGAAGCTGTTGTACGGCAATATCGATTTTGTGATAAAAATCCTT  
ACGATTTCAACAGTGACTCTTTAAGTCAGTGGGCTCCTTCAGGAAAATACTAUGTTCGACCTTCGACAATC  
ATATTGCATACCCATTAAAGGATGATGACCTAATCGCTGGAGACGATACAAACAGACTTAGTTATTT  
TATGGTATACAACAAAAGCTCGAATGAAAGACGGTTGGCACAPAGAGAAATTAACAAATAAACCCAGCAA  
GAATAAAGTTACACCTATTTCTCAAGAATTCCTTTAATCCGCTCAAGAAAGTTAAGGGTATTGCATA  
AAGAACAGAAACCCCGCTGGAAAAGGCTCTTTGTCTACTTCAATAATAAAATACAGGCAATTTTCTCCAC  
ATATTAATAAAGGTATTTCCATCATCTTCCCAAAAAGACAAACAAATGTTGGTCCGGATCCAGATTGCAGT  
TGCCTAAGCTTCGTTTCAAGTCAATGAAACCATTCGAGTTTTTCAGTTTAAGGTTCCGAAAGATACCA  
ACTGGTTTGTAAAGCAGCTCAAAACGGTTCGGATTGAAATTACACCATTCGAGGATGTATAAAGCGATGT  
CAGAATGCAGGAAAAAAATTATTTTAAAGTCCAAACACTAG

YLR312C, 398 aa (SEQ ID NO 286)

MSEEDDHWNLVRLRLRKCRECEEQSSKSEISLDSLHSSSFAGEDDEDFDADVLNNTSSEPSAQMNRIY  
DFRTSNFESNAGVNLDTGVPTISESFDTLGSGNVGCTVLPSMEGSKLKDSTIRNSSTLSPHIIDKSEG  
KSARKLKMWHVIMLSLLSMTFSYJALEYSLTGDLVLAGFKSQSLRNNEKIJYGNIDFVEKKSYDSSSD  
SLSQWAPSGKYVDFDNHIAYPELKDDFMGWRRYKTDLVILWYTTKARMKDGWHKRLNKLINGRIKLHL  
FLKNSFKSAQESLRVLIKEQKRWKRJLFVLJHNKYRQFSPHIXRYFDHSCQKAKQCWSGSKLQLRKLRF  
KSMKPFPRVFQFKVRKDTNWFVXQLKRFGLKLQHSRMKAMSECRKKNYFKCKH

YLR414C, 1292 bp, CDS: 501-1292 (SEQ ID NO 293)

TAGTCAGCCACACATTGACGTACACTGTGAACAGCCTATTTCCTTCCATGTATCTCAGTSCCCAGCTTA  
TGAGAACTCTCACACCCCTCCCACTTGAACCTCAGAGCCCTCTCCACTCCCCCTCTTTCAACATCGCC  
AGATAGCCCGCCCTTGAATGGTCCGCGACAAACCGCCCTGGCCCTGGCCAGGCAAAAAAGGACGCAGCAG  
CCTCGAGCGTTATTTCCAAATCGGGCCCTACTATCAOCCAAAGCCAGCTCGGTATTTTTAGCGCTTCTCG  
CAGGAAAATTGGCTCACAGTATATATACGCGAGAATGTTGCTCTTCCATGTCTCAGTACTCAATGAGT  
GTCCAGTGGTGTTCATTCTGACACCACTTCTTTTGAAGTGAAGCAAAAAGAACTAGATCAAGATCATA  
CAACCGCTGCGCAGTAGTGAAACTTGATTAAAGCAATAGAGAACTAATAGAAAAAACAAACACATCAT  
CGAACGACGCTATAAGCATGAGGAATTTTTTCAAGTTATTTTTCAGCTATATTTTCGCTAAGAACAC  
TTATATTAGCCATTGTTCATGCCACGATCAACGAAAAATACAGTCCCATAAATAAAATTTACTGTG  
CAGAATTGGATCTGTCCAGATGAAGGTATCCAGCGTCTCCTTCTTTGAGTTCTCTCAAGCTATCTT  
CCTTGGGCTTCCCTCATATATAAAATATAGCGCTTTCGTCGTACTGTAACAOTGCCTCCTCGCATAACA  
TCCAATCATGTTCTTCGCCCTCACGGTATCCAGAATTTTAACTATCTGTCATTAGTGTATGACAATATCA



120/251

ACAACAATGAGGCTCTGGAGCTTATGGATTCCGTGGCCAGTGTGTGTTTTGCCCCAAAAACTAAAAAGTAA  
 AAATGACATACTACAACAATCTGGTCAAGTGTATGTTCAATTACCAATTCCTATTGGTATTGTCTTGATCCT  
 TTGTGAATCTAGTGTTCACGTATTGGCGCTGGATCATCCACATAAGGCCCGCTAACGTGGTCTTGGTGGCCT  
 TTTTTTCATTTTTTGGCCTTTGGCGCCCTATTAGTCAGTATAGGTTGGTGTGTTGGGCACCTTACTCATACA  
 TCAAATACATCCTAANGCATAACTATAGTGAFTACGGTATTTCAATGAGCATTGGTAAAGAACTACCAGG  
 GTTTGATGTGGGGGGCTGTGTTGGAGCATTACTGAATTTCAATTCATATGTTGTAGCGTGAGATCGAGGC  
 CCACCGTCTATCTATGCGAACGCTCCARTTGAGGAAAAACCATTGATTTGA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFFTFFFAAIFSLGALILAIIVACAGSTKNYSPINKIYCAELDLSOMKVSTVLPSSLSSATLSSLGLPS  
 YINIGLWSYCTVDSSHNIQSCSSPHGIQNFNLSSIVYDNIMNNEALELMDSVASVVLPEKLKSKMTYVY  
 NLVKCMFITILIGIVLTFVNLVFNVLRWIIHIRFLTWFCAFFSFFAFALLVSIGSCLGTYSYIKYILK  
 INYSDYGISMSIGRNYQGLMWGAVVGALLNFIKCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCCGTTGAAGCAACCGCACCATGACTAAATGGTGCCTGGACATCTCCATGGCTGTGACTTGTGTGCTAT  
 CTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAAATTCCTAGAACAGGGGCTACAG  
 TCTCCGATAATAGAATANTAAGCGCATTTTTGCTAGCGCGCCCGCGCGCGCTTTTCCCAATAGCGAGGC  
 ECAGTTTTATCGCGGAGCTCTACTTCTTCTTATTTGGGTAAAGCCCCTTCTGTTTTCGGCCAGTGGCTG  
 CTGCAGGCTGCGCCGAGAACATAGTGATAAGGGATGTAACTTTGATGAGAGAAATTAGCAAGCGGAAA  
 AAAACTATGGCTAGCTGGGAGTTGTTTTCAATCATATAAAAGGAGAGAAATGTTGTGCTCAUTATGTAC  
 AGTTTTCTGGGACGCTTAACTTTTATTGACAGGAGCTATCAATCATACAGATATTGTCAAAAAAAA  
 AAGACTAATAATAAAAAATGAAGTTCATCAAGTTGTTGTTTCCGCCGTCCCTTCACTGGTTTTAGTAA  
 GTGCTGCTAACAGTTCTAACAGCTCAAGCTCAAGAAATGCTGCCCAACCAAATGCGCGTTTAAACCAACC  
 CTAAGGTTCCACGCCCCCGCTGGTCTTGGCTCTAGCTCGTGCTTTGCCCTTTTTGATTTAA

YMR251W-A, 39 aa (SEQ ID NO 318)

MKLSQVVVSAVAFTGLVSAANSSNSSSSKNAAQPIAGLNNKXVAGAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTGACACCGAGCCATAGCCGTGATTGTGCGTCACATTTGGGCGGATAATGAACGCTAAATGACCCAACT  
 CCCATCCGTACGAGCCCTTAGCCCTGCCAATAGTTTCACGCGCTTAATGCCAAGTGTCTCGGAACCGGA  
 CAACTGTGGTCTTTTGGCACCGGGAAAGTGTACTACACCCAGACTTTGCGATTTCTATGCCAGGACGT  
 TCTGGGAGCTTTCGCTCTCAAGCTTTTTCGGGCGGGAATTCAGACCAGACCAGAACAAAACAACCTGAC  
 AAGAAGGCGTTTAATTTAATATGTTGTTCACTCCGCCCTGGGCTGTGTATTTCGGCTAGATACATACG  
 TCTTTGTGCGTATGTACTTATATCATATATACTATATTAGGATGAGCCGGTCAAGAGATTTTTTTTTT  
 TTTCTGCTTAATTTATTTCTTTCTCTACCTTTTTTTCCTACATCTTGTTCAAAAGAGTAGCAAAAACAACA  
 ATCAATACAATAAAATAATGTCCGGTAGAGGTAAAGGTGGTAAAGGTCTAGGAAAGGTGGTGGCCAAAC  
 GTCAAGAGAAAGATTCTAACAGATAACATTCAGGTATCACTAAGCCAGCTATCAGAGATTAGCTAGAA  
 GAGGTGGTGTCAAGCGTATTTCTGGTTGATCTACGAAGAGTCAAGAGCCGTCTTGAATCTCTCTTGG  
 AATCCGTCATCAGGAGCTCTGTTACTTACACTGAACACGCCAAGAGAAAGACTGTTACTTCTTTGGATG  
 TTGTTTATGCTTTGAAGAGACAAGGTAGAACCTTATATGGTFTCGGTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRKGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKKISGLIYEEVRAVLKSPLESVIRD  
 SVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

GGAGGCTCTGCTTCAAGAGCGCGGTGTGCGCTAGTATTGCCCCGACGGTCCGCGTGCCTATCCCTAGAT  
 TCCCTCGTCCCCCGACCCAAATAGTTAAACGTGTGGTTTTATGGGTCCACCAGGGCTTTATCCTGTTTTA  
 TATCGATGGCGATTTGTGCTCCAGTGTATTTTTGTATATCCAATTAAAGGTTTCTTACCTAATTTTAT  
 TTTATCACTTTAGTTAATGCTGGTTTGTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCTTCTCTT  
 GTTTCTTCTGTGTGTCCCCCATCGCCGATGGGCTTATATGGGCTATATATATAGAGCGAGTTTTTACGT  
 CCAAGATCATCTCAGTTTGCCTGATAGGCTTTCTACTTTATTTACTTTCTGTTTTTAACTTCTATTATACTT  
 TAGTTTTCTTTGATCGGTTTTTTTTCTCTGTATACTTAAAGTTCAANTCAAAGAACATACAAACTAC  
 GTTTATATCAANTAAATATGTCTGAATTCAAAACAAAGCTGAAACTGCCGCCAAGATGTCCAAACAA

121/251

AGTTGGAAGAAACCAAGAATCTTTGCAAAACAAGGGCCCAAGAAGCTAAAGGAACAAGCTCAAGCTTCTA  
 TCCACAACCTAAAAATGAAGCTACTCCAGAAGCTGAACAGGTGAPAGAAGGAAGAACAACAAATTCCTG  
 ATGGTGTCTGAACAAAAGAACCGGAAGCTGCCAACAAAGTTGAAGAACTAAGAAGCAAGCTTCCGCCG  
 CCGTCAGTGAGAAGAACGAAACCAAGAAGGAAGGCGGTTTCTTGAAGAAATTGAACCGTAAAATTGCTT  
 CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSFIQNKAEAAQDVQQKLEETKESLQNKQDEVKEQAEASIDNLKNEATPEAEQVKKEEQNIADGVEQK  
 KTEAANKVEETKKQASAAVSEKKETKKEGFLKGLNRKIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCGTCAGATATGGTGATTATTTTCCCTGTGCATGTACTTCAAAGATCATACAGCA  
 TACTAAGCGCTTCCACGGGACACCTTCTGTGCGAAAATATCAGAAATTTTCTTGATTAAACGCAGCATA  
 TTGAGTATATGAAATTAACGGGACACTGTGTGAAAAATTTGTAGTTGTACTTTTTTGTATCCCCCTTG  
 GTAGACATATGGACGAATTACTACTAAGATTGGCTTCCATAAGGCCCAAATCCAGATATCACCTACCGT  
 ATGTCCCTTTTCCCTACTTGCAATGACAAAATAATTTGTTATTTATCTTGGAACTATATAAGATTACATCTG  
 ATTCCTTTTCTATCTTTTTCGAGAATAATTATTAACCCGCGGGGAAGCAAGTAAGGGGAGAAATTTTGAG  
 GTGTATAAAGAGAGTGGAGGCTTAATCAATCAAAGAATTCTTCTCGTTTATTTTCAGGGTTTGTGAC  
 TAAGAAACGATATTAAGATGTGGAAGGCCGTGATGAATGCTTGGAAATGGAACCGAGAGTCAAAGTAAGA  
 ATGTTTCAAATATCAATCTTACAGTTTTGAAACATGAAAAGAATCGTTGGAAAGCATGATCCTAATG  
 TGGTTTTGGTAGATGTTAGAGAACCATCTGAGTACTCGATTGTTTATATTCCTGCTTCCATCAATGTGC  
 CATATAGATCGCACCCCTGACGCATTTGCCTTAGATCCTTTAGAATTTGAGAAACAGATTGGCATCCCAA  
 AACCTGACAGTGCCAAAGGAGCTAATATTTTATTGTGCTTCTGGCAAACGCGCCGCCAGAAAGCTCAAAAAG  
 TCCCTCCTCAGATGGATATTCAAACACCTCACTATATCCTGGCTCTATGAATGATTGGGTTTCTCATG  
 CGGCTGATAAACCTGACTTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNAWNGTESQSKIVSNIQSYSPEDMKRIVGXIDPNVVLVDVREPSEYSIVVILPASINVFPYRSHF  
 DAFALDPLEFEKQIGIPKFDSEKELIPYCASGKRGGZAKVASSHIGYSNTSLYPQSMMLDWVSHGGDKLD  
 L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAAATACGAACAAAATAAAAAATATGCCGACCAATTCTGTAGTAGTACTGTAATATATTGAA  
 TATTAAAGCGTTTTTCTGCTCTTAGCGTATTCCTTTATACAGTCCGTGGAACAAAGCCACGGGCGGCTGTA  
 ACAATGACCATGGAATCATTCACTCGCCCTAAAAGCGCATTCACGGAAGCTTTTATAGTGATCTTGGTC  
 ACATGATATACGCGTGACTTTTTTTTTTACTTTTTCTCCCTGTCTTCCGCAAAAGTGGCTCAAAATTCCTT  
 CGGATTTTGGCATTATAGCGCGAATGGTGCAGCCCAACCAACCAACACCACTTCTCCACCCAAAAGA  
 TGCAAAAGCGGGGAGCCACTTAGTTTTCTTCAAGTTTGGTTGAAACAGCCTTTAATATTTTATAGAA  
 AGGTAAACATATCTGCTCAGTGAATAGTATCTTAAAGTCAGGCATACATTGGAACACTTCCAAATACAA  
 AATAAGAACGCGCAACGATGTGCTCATCAGTGCATACGATCCATATGTGCCTCCACAGGAGAGTAACT  
 CAGCGCCAAACCCAAATTCCCAAAACAAGACTGCTGCTTTGAGACAAGAGATTGATGACACGGTGGGAA  
 TAATGAGAGATAATATCAACAAGGTGTGCTGAACGTGGTGAAGGGCTAACATCCATTGAGGACAAAAGCTG  
 ATAACCTTGGCTATCTCCGCACAAGGATTCAGAGAGGGCCCAACAGGGTCAGAAACCAATGTGCTGG  
 AACATCTAAAAATGAGAACTGCTTTATTCCTTACCTTCTTATTATTATTACTAGTGGTAATTATCGTTCC  
 TCGTCTCCATTTTCACTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSVVPYDPYVPPEESNSCANPNSQNKTAALRQEIDDTVGIMRDMINKVAERGERLTSIEDKADMLAIS  
 AOGFKRGANRVRKQXWWDLEKMRMCLFLVVIILLVVIIVPIVVMFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTGCTCTTCTCTCTTTTCGCATATTCTAFTTTATCATCGACTTCCCTAATTCGCACTCGTACC  
 AAAAAAGTTAAGCAGTAAGGCGAAGAACGTGGCGCGCTGGAGTCTGTGAATGTTTGGGTCCCTTGATGATCG  
 ACTACGGTAGTAAGTATGTACTAGTTCCAACTTCAATATGTTTACCTGATCCAAGGAAGAGCGGTTAT  
 GAATTAATCTCTTGGCATGAGCGGACGGGTAAAGGGACACCGCCCTTCTCTCGATGGGAATCAGCGTAA

122/251

TGGTATATGATGGATTATTTGTGGAATCATTTAGTAACGGCAGATGTTGAAAAAAAAGCAGAAAAATTTT  
 GAATTTTTTTTCGTTGACATTGGAAGATTTTCGTAGTGGAACAGCTGCAATTGCTTGTAAAGTAGTAACC  
 CCTCCTTTGTGCACAAGAGAGCGAATATTCTTTCTAGGGAGGTTTAAAGATAGAACATCTCACACCAGAC  
 GCGACTCATAMTTCATATGCCCAATTGACCAAGAAAAATTAGCTTAGCTACAAAAGTTGTCTGCTAACA  
 ACAAGTTTCGTCCTACTAGAAGAAAGCTTAACAGAAAGGACAGGCTCTTTCTGCCGGTGCCAAACAGGATG  
 ACACCAAGTTGCAAAGTCAATTAGCTAAGTTGCACGCTGTCCACCATTGACAAUGTCGCCGAGGCCAACT  
 TTTTCAAGGACGACCGTAAGGTCTATGCACCTTCAACAAGGTCGGTGTCCAAGTTGCTGCTCAACACAACA  
 CTCTGTATTCTACCGTCTACCCACAGGAAACAACTTGCAGGATTTGTTCCCAGGTATTATCTCTCAAT  
 TGGGCCCTGAAGCCATCCAAGCCTTGTCTCAATTGCGCTGCCCAAATCCAAAAGCACCAGGCCAAGGCTC  
 CAGCTGATGCTGAAAAAGAGGATGAAGCTATTCCAGAGTTAGTTGAAGGTCAAACCTTTTGATCGCTGACG  
 TCGAATAA

YFL037C, 157 aa (SEQ ID NO 378)

MFIDQEKI AKLQKLSANMKVGGTRRKLNNKACSSACANKDDTKLQSQLAKLHAVTIDNVAEANPFKEKG  
 KVMHFNKVGVQVAAQHNTSVTFYGLPQEKNLQDIFPGTIISQLGPEATQATSQLAAQMEKHRAKAPADAEL  
 KEFAIPELVEGGTFDADVE

YFL079W, 1404 bp, exon1: 501-511, intron1: 512-932, exon2: 933-1404  
 (SEQ ID NO 381)

AAATAGGACGAAGAAGCTTTTTATATACGAGCAATTTCTTAATTAGTAGGAAGCGGAAATAATAATAIAA  
 GAAAGTAAACGCAAAAGATAGGCTGACTGCCTTCATTCCGACTAGGAGGTGAGGCGACATATTTGTCAAC  
 ATTCAAGTTACCGAGATGGTAGAGAGGTGGATGGCTCGCGTGAGCTTGATTGTACACTGCCAGCAACGAT  
 GCTTTTTCTACCCATTTTATGAAGTTTAAACATCCGTACCTTTCCACCTCCAAACATTTTTTGTAACTTC  
 CTCTTTTGAAAAATCAACAGTAATAACCTGTGCACTATAGCCCGCTTGAGCCCGCAATATCCGTGAGT  
 GAGGTAAGATCCATCCATACCTTAGCAAAATATGGTAGTGAGGAGGCCAACTGTATTGCGTTAAAGGCCAA  
 AAGGATTGGTATATACGAATGATTGGTAATTTGAAAAGTAGGTTTCGAATCAAAGAAAAGCTGAGACAGTC  
 AAGGACACTAAACAAAAATGGGTAAATCGTATGTCCATATAACTTCAAAATGAAAATATAGCAGTTCAA  
 ACATATCAATTAAATCATTATACATCTCCAATAAACATGTATGCRAGAGGAAAGCGTAAATATCTTCGA  
 TTTGCACAATACCTTTGCTACTGAACTAAAAATGAAAATGAAGTTGAATTCTCAAAGGAATGTCAATGCAA  
 GTTCGTTAAATTAAATATGGTTTTTASTGGAAATTATACAGTTTGTGATAGATACACACGAGGAGTAGCA  
 GCAAAGCAAGTGCAACAGCAATGATATGTTAGCAGGAAATAATATTATAAATTTGGATATTGTGTGTTTT  
 TTTGATATATGTTTGTGCGAAGCTAATACAGAATGACTACTAACTGGAATTTAAAGCACAATCATGCTC  
 TTAGATGATTGATCTATTAAAAAAATATAAAACAGACATGGTTACAGATCTCGTACACGTTACATGTTC  
 CAACGTGACTTCAGAAAGCATGGTGCCGTTTACATGTCCACCTACTTGAAGATCTACAAGGTTGGTGAC  
 ATTGTCCGACATCAAAGCCAAATGGTTCTATCCAAAAGGGTATGCCACACAAGTTCTACCAAGGTAAGACC  
 GGTGTGCTCTACAACGTTACCAAGTCTTCTCTTTGGTGTATCATCAACAAGATGGTGGGTAACAGATAC  
 TTGGAAGAGAGATTGAACCTTACAGATTGAACACATCAAGCACTCTAAATGTAGACAAGAATTTTTGGAA  
 AGACTTAAGGCCAATGCTGCTAAGCCTCTCTGAAGCCAAAGCCCCAAGCTCTTGCTGTCCAAATTCAGAGA  
 CAACCAGCTCAACCAAGAGAAATCCCGTATTGTCTCTACTGAAGGTAACGTTCTTCAAACTTTAGCTCCA  
 GTTCCATACGAAACCTTTCATTTAA

YFL079W, 161 aa (SEQ ID NO 382)

MGKSHGYRSRTRYMFQRDFRKHGAVHMSTYLKIKYKVGDIVDIKANGSIQKGMPhKPYQCKTGVVYNVTK  
 SSVGVIIINKIVGNRYLEKRLNLRVSEHIKHSKCRQEFFLERVKANAAKRAEAKFAQCVAVQLKRQPAQPRR  
 SRIVSVKGNVPTPLAFVPEYTFI

YBL109W 836bp CDS: 501-836 (SEQ ID NO 35)

CATCGCTTGATTCCCGCCCTGCAAAAAATAAAGTAGTGGGTACGTAATTTCCGTTTTCATTTTCATTTGGTG  
 CACACTATCTTAACTATCTGCTTAGTCCAGGAGAACCAAGATCTGTTCTGCTCAGCCGCTTCGTGG  
 ATATTCCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTCTCGAAAAGACCAATATAACAAAAATTT  
 ATAAATTACATTTCCCTTATTAGGTATACGACCTCGGCTTCGAAGTAGAGGAGCCCTTTTGGCGTACC  
 TACATATGGCGCTCACACAGACAAACTTCCCCCAAAATGTATTACCCCGCGAATAAGAAAACAGAC  
 CCAATTCACCCACGACGTATCAAGTTACTTCCCTTGGTGCAATGTCCCACATATAAAAAAATTCCTTTGACGC  
 TAGATCGTTGGACTAAAAATCTGCGTTCACAATCGCCCTAACAGGAAATATTGCCATTTTCGGTACAAGCT  
 TACTTCCATAGATGCTATATGTCCCTACCGCCTTGTCTAACACCATCCAGCATGCAATACAGTGACATAT  
 ATATATACCCCTAACACTACCCCTAACCCCTAACCTATTTCAACCCCTTCCAAACCTGCTCTCAACCTTACCCCT  
 CACATTAACCTTACCTCTCCACTTGTTAACCTTGTCCTCATTTCAACCATACCACTCCCAACCAACCATTCATC

123/251

CCCTCTACTTACTACCACCAATCAACCGTCCACCATAAUCGTTACCCCTCCAATTAGCCATATTCAACTTC  
ACTACCACTTACCCTGCCATTACTCTACCATCCACCATCTGCTACTCACCATACTGTTGCTCTACCCCTC  
CATATTGA

YBL109W 111aa (SEQ ID NO 36)

MSLRPCLTPSSMQYSDIYLYPNTTLTLPVFNPSNLSNLPSHYPTSPVPTSHSETPLPPTTHPSTYYH  
QSTVHHNRYFPISHIQLHYHLPCHYSTIHHLLLTILLFYFPY

YHR094C 2213bp CDS: 501..2213 (SEQ ID NO 205)

GCATTTAOTCAAAAGTTTTTCCGAAGTGACCCAGTGCTCTTTTTTTTTTCCCGTGAAGGACTGACAAAT  
ATGCGCACAAAGATCCAATACGTAATGGAATTCGGAAAACTAGGAAGAAATGCTGCGAGGGCATTCGCCG  
TGCCGATCTTTTGTCTTTTCCAGATATATGAGAAAAAGAAATATTCATCAAGTGCTGATAGAGAAATACUAC  
TCATATGACGTGGGCAGAAAGACAGCAAAACGTAAACATGAGCTGCTGCGACATTTGATGGCTTTTATCCG  
ACAAGCCAGGAAACTCCACCATTATCTAATGTAGCAAAATATTTCTTAACACCCGAGGTTGCGGTCTCCC  
CCTCACGTTTTTAAATCATTTGAATTAGTATATTGAAATTATATATAAGGUAACAATGTCGCCATAATC  
AATTCUATCTGGGGTCTCAAGTTCTTTCCCCACCTTAAANTCTATAAAGATATCAATAATCGTCAALTAAG  
TTGATATACGTAAATCATGAATTCAACTCCCGATCTAATATCTCCTCAGAAATCCAATTCATCCAACT  
CATATGAATTTGGAATCTGGTCTGTTCAAAGGCCATCAATACTCCAGAAAGGTAAAAATGAAAGTTTTTCAG  
ACAACCTTAAGTGAAGTCAAGTGCAACCCGCGCTTGCCCTCCAAACACCGGAAAGGTGTCTACGTAA  
CGGTTTTCTATCTGTTGTGTTATGGTTGCTTTCGGTGGTTTCATATTTGGATGGGATACTGGTACCATT  
CTGGTTTTGTGTTGCTCAAACTGATTTTTCTAAGAAGATTGGTAAGAAGCAACACGAGGTAAGTCAATTACT  
TGTCCAAAGGTGAGAACTGGTTAATTGTCTCTATTTTTTAACATTGGTTGTGCCATTGGTGGTATCGTCT  
TACCCAAAGCTAGGTGATATGATGGTCTGATAGATCGGTTTGATTGTCTGTTGTAGTAATCTACACTATCG  
GTATCATTTATTCAAATAGCTTCGATCAACAAGTGGTACCAATATTTTCAATTGGTAGAATTATCTCTGGTT  
TAGGTGTGGGTGGTATCACAGTTTTATCTCCCATGCTAATATCTGAGGTCCGCCCCAGTGAAATGAGAG  
GCACCTTGGTTTCATGTTACCAACTCATGATTACTTTAGCTATTTTTCTTAAGTTACTCTACCAATTTTTG  
GTACCAAGAATTACTCAAACTCTGTCCAAATGGAGAGTTCCATTAGGTTTGTGTTTTCCGCTGGGCTTAT  
TTATGATTGGTGGTATGATGTTGTTCCCTGAATCTCCACGTTATTTCGGTTGAAGCTGGCAGAAATCGACG  
AAGCCAGGGCTTCTTTAGCTAAAGTTAACAATGCCCACCTGACCATCCATACATTCAATATGAGTTGG  
AAACTATGGAAGCCAGTGTGGAAGAAATGAGAGGCGCTGGTACATGCAATTTGGGGCBAATTTATTCACATG  
GTAAACCAGCCATGTTTCAACGTACTATGATGGGTATCATGATTCATCTCTACAACAATTAACGGTTC  
ATAACTATTTCTTCTACTACGCTACCATTGTTTTCCAGGCTGTGCGTTTAAAGTCACTCTTTTGAAGCTT  
CTATTGTCTTTGGTGTGCTCAACTCTTCTCCACTTGTGTTCTCTGATACACCGTTGACCGTTTCTGGCC  
GTCCTAAGATGTTTGATGTGGGGTGTCTGTGGGTATGGTCTCTCTGTTATCTTGTCTATGCCCTCTGTTGGT  
TTACCAGATTATGGCCAAACCGTCAAGATCAACCATTCTCAAAGGGTGTCTGTTAACTGTATGATTTGTTT  
TCGCATGTTTCTACATTTTTCTGTTTCGCTACTACCTGGCCCCCAATTGCTTACCTTGTATTTTCAGAAT  
GTTTCCCATTAAAGAGTCAAAATCCAAGTGTATCTCTATTGCCAGTGTCTCTAAGTATGATCTGGGGTTTCT  
TGATTAGTTTCTTCAACCCATTTTATCACTGGTGGCATCAACTTCTACTACGGTTACGTTTTCAATGGGCT  
GTATGGTTTTTCGCTTACTTTTACGTTCTTTTCTCTGTTTCCAGAAACTAAAGGTTTATCAATTAGAAGAA  
TTAATGATATGTACGCCGAAGTGTCTCTACCATGGAATCAGCTTCCCTCGGTTCCACTATCCAAGAGAG  
GCGCTGACTACAACGCTGATGACCTAATGCATGATGACCAACCATTTTACAAGAGTTTGTTTAGCAGGA  
AATAA

YHR094C 570aa (SEQ ID NO 206)

MNSTPDLISPOKSNSSNSVELESGRSKAMNTPGKXNESFHDNLSSESQVQPAVAPPNTGKGVVTVSTCC  
VMVAFGGFIFGWDIGTISQFVAQTDFLRRFGMKHHDGSHYLSKVRIGLEVSLFNIGCAIGGIVLAKLGD  
MYGRRIGLIVVVVIYTTGTTIQIASYNKWKYQYFIGRIISGLGVGGITVLSFPLISEVAPSEMRGTLVSC  
YQVMITLGIPLGYCTNFGTKNYSNSVQWRVPLGLCFAWALFMIGGMMFVPESPRYLVEAGRIDEARASL  
AKVNKCFPDHPYIQYELETIEASVEEMRAAGTASWGLFTGKPAKFQRTIMMGIMIQSLOQLTGDNYFFY  
YGTIVFQAVGLSDSFETSIIVFGVWNFFSTCCSLYTVDRFGRRNCLMAGAVGMVCCYVYASVGVVWVWF  
NGQDQPSKSGAGNCMVFACFYLPCTACTWAPIAYVVISCEFLRVKSKCMSIASAANWTWGLTSFFT  
PFIITGA1NFYGYVFMQCMVFAYFYVFFVFPETKGLSLEEVKDMYAEGVLPWKSASWVPVSKRGADYNA  
DDLMDQDPFYKSLFSRK

YBL099W 2138bp CDS: 501..2138 public: 1..2138 (SEQ ID NO 693)

CCCCGGTGATGCAGTTCCCGCCGGCCCTGGCCAATCAGATCCCTTTAAAPATGGGCCCCGGTGCGCTTCT  
ACCCCTTCAUGGCTTTTACGGCTTTTTCGAATCTTGATTTATTTGTAATTTATTAACATTTGGTCATATC  
AATTCACATCAGACTTCATTTTTCAATTCACCTTCTGAATAAGAGCCCTTCCCTTCATACAGTAGA  
GATATTATACATCATAGCTCTTTCAATTGGCTTATTAGATTGCTCTCATCTTTCCCATTTGACGTGTG  
TACTTCTCTCTCTTTTTCGTTTAACTGATTTCTCATATATTCCAAACAGGCATATATACTCGACG  
CAAGAAAGAAAAGAAAAGAAAACCCCTCATAAAAACATAATCGACAACTTTTTTCTCATCCCAACC

124/251

A:TAGTATAACAGATTGATCGTTCAAGCTCTCATAACTATCGCAAGAACAGTAACAAAATAAATAAAJAA  
 AACACGCACATATAATAATGTTGGCTCGTACTGCTGCTATTCCCTTCTCTATCGAGAAGCTCTAATTAACCT  
 CTACCAAGGCCGCAAGACCTGCCGCTGCTGCTTTGGCTTCCACCAGAAGATTGGCTTCCACCAGGGCAC  
 AACCCACAGAAATTTCCCTCATCTTAGAGGAAAGAAATTAAGGGTGTGTCCGACGAGGCCAATTTGAACG  
 AAACCTGGTAGAGTTCTTGCAGTCGGTGATGGTATTGCTCGTGTTTTGGTTTGAACAAATTCAGGCTG  
 AAGAATTGGTCGAGTTCTCCTCTGGTGTAAAGGTATGGCTTTGAACCTGGAGCCTGGTCAAGTCGGTA  
 TCGTTCTTTTTCGGTTCCGATAGACTGGTTAAAGAAGGTGAATTGGTCAAGAGAACC GGTAATATTGTTG  
 ACGTCCCAGTCGGTCCAGGCCCTTTGGGTAGAGTTGTGCGACGCTTTAGGTAACCCCTATTGATGGTAAAG  
 GTCCCTATTGACGCTGCCGGTCTGTTCAAGAGCTCAAGTCAAAGCACCAGGTATTTTGCCAAGAAGATCTG  
 TCCATGAACCAGTCAAACCGGTTTGAAGCGGTTGACGCTTTGGTCCCTATUGGTAGAGGTCAAAGAG  
 AGTTGATTATTGGTGTATCGTCAAACAGGTAAAGACTGCTGTGCGCTTAGACACCATCTTGAATCAAAGA  
 GATGGAATAACGGTAGTGACGAATCCAAGAACTTTACTGTGTTTACGTTGCCGTTGGACAAAAAGAT  
 CTACCGTTGCTCAATTGGTCCAAACTTTGGAAACAATGACGCCATGAAGTACTCTATTATTGTTGCGAC  
 CTACTGCATCTGAAGCCGCTCCTCTACAATACTTTGGCTCCATTTACTGCCGCATCCATTGGTGAATGGT  
 TCAGAGATAATGGAAAGCACGCTTTGATCGTCTATGACGATTTGTCCAAGCAAGCCGTGGCATACCGTC  
 AATTATCTTTGTGTGTTGAGACGTCCTCTGGTCTGTAAGCCCTACCCCTGGTGTATGTTTACTTTCGCTC  
 CAAGATTGCTTAGAAGAGCCCGCTAAGCTTTCTGAAGGAAGGCTCTGGTCTTTTAACTGCTTTGCGCTG  
 TTATTGAAACCCAAAGGTGCTGATGCTCTCGCTTATATTCCAACCAATGCTTACTTCCATTACCGATGGTC  
 AAATATTCTTGGAAAGCTGAATTATTCTACAAGGGTATCAGACCTGCCATTAAAGTTGGTTTGTCCGTTT  
 CTCGTGTGGTTCCGCTGCTCAAGTTAAGGCTTTGAAGCAAGTCGCTGGTTCCTTGAAATTGTTTGTGG  
 CTCAATACAGAGAAGTCGCTGCTTTTCTCAATTGCGTTCCGAATTAGATGCTCTCCACCAAGCAAACTT  
 TGGTTAGAGGTCAAAGATTGACTCAATTGTTGAAGCAAAACCAATATTCTCCTTTGGCTACAGAAGAAC  
 AGGTTCCATTGAATTTATGCCGGTGTAAATGGTCAATTTGGATGGTATTGAACATCAAGAATTGGTGAAT  
 TTCAGTCTCTCTTTTGTCTTATCTAAATCCAATCACAATGACCTTTTGACCGAAATTAGAGAAAAGG  
 GTGAATTGTCTAAAGAATTGTTGGCATCTCTAAAGAGTGTCTACTGAATCATTTGTTGCCACTTTTAA

YBL099W 545aa public: 1..545 (SEQ ID NO 594)

MLARTAAIRSI,SRTLINSTRKAARPAALASTRR,ASTKAQPTVESSILEERIKGVSEANLNETGRVL  
 AVGDGIARVFGLNNIQABELVEFSSGVKGMALNLEFGQVGVILVFGSDRLVKEGELVKRTGNIVDVVPVGF  
 GLLGRVVDALGNPIDGKGF,UAAGRSRAQVKAPG,LPKRSVHEPVQGT,KAVDALVP,IGRGQRELIIGD  
 RQTGKTAVALDITILNQKRWNNGSDESKKLYCVVYAVGVQKRSTVAQLVQ,LEQHDAMKYS,VAATASEA  
 APT,QYT,APPTAASIGEW,FRDNGKHALIVYDOLSKQAVAYRQLSLLLRPPGREAYPGDVFFYLIPRLLER  
 AKLSEKEGSGSLTALPVIETGGDVSAYIPTNVISITDGQIFLEAELFYKGRPAINVLVSRVGSAA  
 AQVKALKQVAGSLKLFLAQYREVAFAQFGSDLDASTKQTLVRGERLTQLLKQNYSP,PLATEEQVPLIV  
 AGVNGHLDGIELSRIGEFESSFLSYLKSNNHLLTEIREKGELSKELLASLKSATESFVATF

YDR504C 884bp CDS: 501..884 public: 1..884 (SEQ ID NO 695)

TAAAAGCCTTGCAATATTGCTCAGAGTAAATTACAAGCGTTAAATGATAATTCAAATCTCAAANTACAA  
 ATGACAGCTCTTCCCAATACTTTACGAATGCTGCAACTTATTCAAAGCCTAAATTTGAATATCAAGATT  
 TAAACGCAGAAATTTCCAAATTTAATAGAAAGGAATTAACGTTTTFACTAUGTTTGTGAGGAGAGAAATGATT  
 TTAGAGACTTGATPAAAGAGCTGTTCAAATATTACAAGACAAGAATTTGGTTGTGTGCCATCCCGAATA  
 ATCTGTCTATTCAATCTAAGTATTATGATAACAAACAAAAGAGCTGAAATTATATCAAAACATAGTAA  
 AAAATTACAATGCTGAAGATTTAATGAAGTCAATGAGTTTTCGCAGAACAGGGGGAATPACAGAGTTA  
 ATTTTGCACCTCCGTTGAACGAAATTGAACTCGACAACCTTCAGATTGCTGTGTATGAAGAATTAGTTC  
 ACGAATTATTTTCAATTAATGATCTGTTATTTCCCTGTTGTAACTATAAATTTTCTAAAAGCAAAAGACAA  
 CCATTTGCCATTATTTTGTAAACATTTTTCATTGTTTTTTGTTTTTTGTTTTTTGTTTTTTGTTTTTTA  
 TTTTGTCTACTTTTTTTATGTTATTTTGTTTTTATCGTTTCTGTGTTGCTTGTGTTTACCTATTTTCCCTGCCA  
 ATTCAATTTGGTACTATCTTTCTATTATCAATATTTTCTTTCCCTTATGTTTTTTCTCTATATGAAAACT  
 TCACAGGGAGAAATACAGAGAAATGTTCAATATTCTGTTTACTTTGATAAAAATTAATTTATACGCTCTC  
 CCAATCATGGTTTTCATGGTCACTGGTAAGGAAAAATTCGAAAACTACGGGACTAA

YDR504C 127aa public: 1..127 (SEQ ID NO 696)

MLCYFLVVTINFLKEKTTICHYFVNIFSLFLSLFVFEVVFIFVYFFVVLFYRFCSLFTYFFANSIWWY  
 I,SIINIFFPLCFPI,YENFTGRNRRK,SLP,CM,TK,ITYTSPNSGFMV,TKKKKPKLRD

125/251

YEL032W 3416bp CDS: 501..3416 public: 1..3416 (SBQ ID NO 697)  
 TATCTACCGGCTGCAAGCAGUUGGTGGGTGGUAAATUUGGGGCTTUUUUUUTCAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAGGAACCTCTCAGAACGGGGAGCTTGAAGAGCAAGCCAAAGGGAAATATTAGTCTTTGACCTA  
 TGTGGGAAACGAAATTTTCAATGAGTTATGGCAACTTGGCCGAGTGGTTAAGCGGAAAGATTAGAAATC  
 TTTTGGGCTTTGCCCGCCGAGGTTGAGTCTCTCACTTCTCGTTATTCTCTCTTTTTCATTTTCC  
 CTGTTCTGTCAGATCCAGCCCGGTAGAAGAAACAATTACTTTTCTTAAATGGGTAAAACTCGTGTTTTA  
 GGAAAAAAAAAGAAAAATTTGGTCAAACTCCAAAGATAGGTTCTTAATCTTCTTTCAAGTTGAAAGGGC  
 CTACGCTCTTTTCCCTGAGCATTTCATCCCTACTGCTCGTATTGAACTCCACTATAAGCGCACCAAAA  
 AGATACAAACCTCAATPATGGAACGCTCAACGGGATTTGATGGAGACGCTACTACTTTTTTCGCTCCAG  
 ACCCTCTGTTTGGTGACAGAGTGGCGAGATTTCAGAGATTTTTAGATACTTCCACCTCATACAGAGACT  
 CTGTAAAGTCCATACAGTTTACAAACAGCAATTAACGGGCGCAACTACAACGATGATCAAGATCAGCCAG  
 ACCAACGAGATTGCTAGGTGATGACGACCGTTATGATCTTTGAAAAGGAAAAGAAAGCAGCATCGTCCA  
 CCTCATTTGAATATACTCCCTCACAGGATTATCATCTCGCTTGATGACTTGAGAGATTTCGACAGGTCTG  
 TCTGGTCCGGCATTTTATGCGAACCCAGCATACTTCATCCCGCTTGCCGAAAAGGGCGTTACTGACCTAG  
 CAGATTCCATGGACGATGTTCACATCCCAATGCTCTGCACTATCGTCTCGCCATCCTTGAAGCTTT  
 CCTTCAAGGCTCATTTGGTGACACGCAATGCTCTCTGCTACTCTAACGGCACAACATTTAAACAAAC  
 TGGTCTCTGTTGAGCGTATCGTAACCTAAGACTTCTTGGTCAGGCCAAAGCTTATCAGATCTGTCCACT  
 ACCGGGCAAGACTCGTAGATTCCATTACAGAGATTATACAGATGCTACTACAACCTCACCACCCCA  
 TCCCAACCGCTGCCATCTATCCAAACGGAGCACACTCAAGCTTAACAAACTAACCCGGAATGGGTATA  
 GTACGTTCAAGACCATCAGCGTATCACTCTGCAAGAAATGCCCAAAATGGCCCCCGCTGGCCAACTTC  
 CCAGCTCCATTGACGTCATTCTCGATGACGACCTTGTGGACAAGACCAAGCCAGGTGACAGAGTTAAGG  
 TTGTCGGGGTATTCAAGTCGCTTGGTGCTGCTGCCATCAACCACTCCAACCTTAATACATTGATCGGGT  
 TCAAAACTCTGATCCTAGGTAATACGGTGTATCTCTCCACGCCAGATCCACGGGTGTGCTCGGAGAC  
 AAAATGTTGACAGATTTGATATAAGAAATATCAATAAACTATCCAAAAAAAGGACATTTTCGATATCT  
 TGTCTCAATCTTTAGCCCTTCTATTTATGGACATGACCATATAAGAAAGCCNTTTTATTGATCTCTCA  
 TGGGAGCTGTGGAGAAAAATTTAGAAAAATGCTTCCGATTTAAGAGGTGACATCAATATCTTAATGGTGG  
 GTGATCCATCCACTGCCAAGTCCCAATTTGCTTAAGGTTTGTGTGGAATACAGCATCAUTGGCAATTGCTA  
 CTACTGGTAGAGGTTCTTCCGGTGTGCGTTTGACCGCAGCGGTCACTACTGATAGGGAAACAGGTGAAA  
 GAAGACTAGAGGCTGGTCCCATGGTTCTTGGTGAACCGCGGGGTTGTATGTATTGATCAATTTGATAAGA  
 TGACAGATGTGGATAGAGTCCCATTCATGACTAATGGAACAACAACCGGTGACGATTGCCAAAGCAC  
 GTATTACACAAACATTAATGCTCGTTGTAGTGTATTGCTGCCGCAAAATCCCGTTTTTGGGCAGTACG  
 ATGTCATATAGAGATCCACACCAAAACATTGCTTACGGGATCCGCTGTTGTCTCGTTTTCTATTTACTAT  
 TTGTGTGACAGACGATATCAATGAAATCAGAGATAGATCCATTAAGTGAAGCATGCTTAAGAACAACA  
 CATATTTGCCCTCCAGCTTATTTAGAGGGTGAACTCTGAGAGAGCGTTTGAATTTATCATTTAGCCGTTG  
 GGGAGGATGACAGATATAAATCCCTGAAGAGCATTTCAACTTCCGGGCTGGTGTAGAAAATGAAGGAGAA  
 ATGATGAAGACCATGTCTTCCGAAAAGTTCAACCCCTTATTACAAGCAGGTGCTAAGTTAGCAAAAAACA  
 AAGGTAACCTATAACGGTACACAAATTCGAAAGCTACTCACCATCCCATTCTTAAGAAAGTACGTTCAAT  
 ATGCCAAGGAAAGGGTTATTCCACAGTTAACACAGAAGCCATCAATGTTATTGTAAGAAAATTACTG  
 ATTTAAGAAACGATGATATTAACAAAAATCGCCUATTACTGCCAAGAACTTTGGAGACTTTGATCAGAT  
 TAGCCACAGCTCACGCCAAAGTCAGGTTATCCAAACAGTCAACCAAGTCCATCCCTAAAGTGGCTGCCA  
 ATCTACCTAACCTTTTGCCTATTGGGTGAGGATATCGGCAATGATATCGATGAAGAGGAAAGTGAATACG  
 AAGAGGCTTTGTCCGAGAGGTTCTCCACAGAAATCACCGAAAAAAGACAAAGAGTCAGACAACCCAGCAA  
 GCAACTCTGGATCCCCAATCAAACTTACTCCAAGAGGTCAACCGGCATCTTCCGTTAATGCCACGCCAT  
 CGTCAGCACCCAGAAATATTACGTTTCAAGATGACGAACAGAACGCTGGTGAAGACCATTAACCATATA  
 TGTACCCGCTTCTGCGGATGAGGAAGCTGAATTACAAAGAGGCTTCAACTGGGGTTGAGAGTGTCTC  
 CAAGACGTAGAGAAATCTTCAAGCACTTGAGGAAGGTTCTGTTGCGGACCTCTTACCGAGCTCCGTACTC  
 CAGATTACTTAACGTATCTTCTGCAAGGTCAAGATGAAGCAACAACAGTCACTTATTCTTTTGTACA  
 ATGTCGAGCCCTCTTACCTTTCTACTGGTAGATTGTCTTTAATCTCAGGTATTATTGCGCGCTGATGAC  
 AAACAGAAATATTTGAAGAAGAATCCCTATCTGTGGCTCTTTTGTGGAAGAAATCAACCAAGAACTAC  
 CGGAGGAGGAAAAATCTCTCGCTCAACAAATATTTAGCAGCTTTGAACATCATGTCGACAGAAAAAAT  
 TAATGGTTGCTGACGATAAAGTTTGGAGAGTCTGA

YEL032W 971aa public: 1..971 (SEQ ID NO 698)

MEGCTCFDGDATTFAPDAVFCDVRVFQEFLLDTTTSYRDSVRSIQVYNSNNAANYNDQDDADEROLL  
 GDDDGDDLEKEKKAASSTSLNILPHIRIILSLDLREFDRSFWSGLLVBPAYFLPFAKALTDLDASMD  
 VPHPNASAVSSRHPWKLSPKCSFGAIALSFRLLTAQHNLKLVSVGGIVTKTSLVRFKLIRSVHYAAKTG

126/251

RFHYRDYTDATTTLTTRITPAIYPTEDTGNKLTTEYGVSTPLJLQRLTVQEMFEMAPAGOLPRSIDV  
 ILDDDLVDKTKPGDRVNVVGVFKSLGAGGMNQSNSTLIGFKTLILGNTVYPLHARSTGVAARQMLTDF  
 DERNINKLSKKKDIFDIILSQSLADSIYGHDKKATLIMTMGGVEKNENGSHLRGDINILMVGDPSTA  
 KSQLLRFVLNTPASLAIATTGRGSSGVGLTAAVTTDRETGERRLEAGAMVLADRGVVCIDEDFKMTDNDR  
 VAIHEVMEOQTVIIAKAGIHTTENARCSVIAAANPVFGQYDVNRDPHQNIALFDSLLSRFDLLFVVTDQ  
 INEIRDRSISEHVLRTHRYLPPGYLEGEPPVRELRNLSLAVGEDADINPEEHSNSGAGVENEDEDDEHDV  
 FEKFNPLLQAGAKLAKNKGNYNGTEIPKLVTIPFLRKVYQYAKERVIPQLTQEAINVIVKMYTDLRND  
 NTXKSPITARTLETILRLATAHAKVRLSKTVNKVDAKVWNLRLFPALLGEDIGEDIDEESEYPPAISK  
 RSPQKSPKKRQVRVQPASNSCSPKSTPRRSTASSVNATPSSARRILRPQDDEQNAGEDENDIMSLPA  
 DEPARTQRRLQIQLRVSPRRREHLHAFEEGSSGPLTEVGTPELPMVSSAGQDDEQQQSVLSFQNVPEPT  
 ISTGRLSLSIGIARLMQTEIFEESYPVASLPERINEELPEEEKFSAQEYLAGLKTMSDRMNLNVADD  
 KVWRV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)  
 CTTTCAGTTGGGCATCTTTTFTTTTTCACAATFAGCCCCCCTTTTTCACAAATTGGCATTGTTTGTA  
 CGATCTTTTAGCTAGAACTGGAGACCTGAAACGTGGTGATTCTTATATTAAAGGAATACCGATCTTTT  
 CCGTTTCAACACCCCAATCTGTGAGAATCTTTACTCTTTCGCAATTCGGAAATTTAGATACATTCACATCC  
 ATACTTGGACACATATATATATACATATAATCATTGACACACCCCATCCGCATTGAGTAAACTGTCTT  
 TGAAGTGTCTAAAGAACTTAGAACTATAGTGTGTGTCCTCAAGAACTTAAAAATTCAACACTTTGTGAGAAT  
 TATAAAACAGAGTAAGCAAAAGAAAGAAATAGAGAAACAATACTCCGCTACCGATTCTCTCTTTTTCCTT  
 ATAAAAAAATTCGAGAATAATTACTTTTATTCTTATUUCTUCAUUCTTTTTCAGGTATTCTTTTACCGATT  
 TGCATATCAATCATATAATGAGCACCGCATTCACCGATTACTGCACTGTTTGTGATCGCTCTCATTCCAA  
 CATCTCCACACAAAACGAACATTAAATACCAGGAAGATCCAAAGGGACAATGAAACCAAGAGCAGTTTAC  
 AATCAATAAGTTACATTGCTCCGAAGATTGTAAAGCTGAAGGATTCGAACCCCTTTAAATGAGAAATTAT  
 TATUUCUACTGCAAAAAATCAAAAACCTTCTCATTCGCCATAATCTCACTCCACCGCTTTTCATATTCTA  
 AAAATTTAAGTGCATCAAACTCTTCGAGCCGACTACCTCACTATCTTCATCTCCGAUATCTTCAACTA  
 TCCCTTTTGACGAGTTGGAGAAGCTAGAGTCCCTATTAAATTTCAACATTGCTGCTACCTCAGGATGGTA  
 TAGTCAATCTTAAGCAGGAGTCTAATCTTCTCGTCTTGACGAAATATGATGAAAATGAACATTATTTGA  
 ACTTAGCCGACTCTCTTAGACTCGATTCTAGTAAACAAATTCGATTCAAAACCCACATTTGGGTACGAAA  
 ACAACTTCCACGATCAAAACGATCTAATTGATGATUATTGATCTCAGATCAGATCATTGAGAAATAACT  
 ACAACCTATGGTTTAGACCATCTCCAGTTAA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)  
 MSTAFNDYCTVCDRLPTSPQKTNINTRKIQRDNETKSSLSQSNKLYCSEDCXKLKPSNPLNEKLLSHLHK  
 KSKTSHSHNLTPLSYSKILPASNLPEPTTSLSSSPSTSTIPFDELEKLESJLISPLLLPQDGIIVNPKQ  
 ESNPSRVDEYDENEHYLNLADSLRLDSSYQLHSAHLGYEMNLPRNDLIDHILTSDQTIENNYNLWFR  
 LSSS

YHR136C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)  
 AGAGTATAACGACTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAAACCGCTGCGCGCCGTTT  
 AAGCAAGCTCGCCCATGACTTTTGGGAGAACGACTGTGTCTATTGACGAAGACATATTGGAAGATTGCTC  
 TGACGAAGAACAATCATGATTGCAATCTCTTAAATCGTTTACACATAUATACCTTCTACCTCTGTACTGTTA  
 CATATGCAATGACTTTACGATCTAATATAAATCCTTTTGTATGTTACCCCGCCTGTGGGCTCGTTCTCTCT  
 TTTCGTTTCTTACGATTTTTTTCGCCGGAACAAGAAAAAACAGAAACAAAACAAATCAGCGATCGTATACAT  
 GGGTCTTTGACTTCTGCTTGTCTTCTTACAAACAACAAACGCAAAACCGTTTCAATTGAGTGCTCTGTGACTG  
 GTTTTCAATGCGGATGCCATAGTAGAGAAAGACACATACAAAAATTTCCGCCATTGCTTGGCCCTTTTC  
 CTGCTCTCTCTTCCCATGCTCCATGCCCATAGCAAGTACCCTCTAGCAGTTAACAACCTCACCATA  
 TAAACGGAAACGCAATTTTAAAGTACPAAGCAACAAACAACCTCCACCACCGAGCTGTGAGCTCGCCCG  
 CAAGATCTTUGATGACCGCCACGACCGCGCCCAACTCCAACAGCAACTCTCCAGAGATGACTCTACTTA  
 TTGTGCGGCTACATTACAAGATCGGCAAAAAATAGGGGAAGGTTCTTTTGTGTGCTATTTGAAGGTA  
 CTAAATATCATCAATGGCGTACCGCTCGCGATCAAAATTCGAGCCCGAGAAAAACGGAGCCCTTCAATTAA  
 GAGATGAATAAAAAACATATAAAATTTGAAATGGCACTCCCAATATCCCCIACCCCTACTACTTCGGCC  
 AAGAAGGTTEGCACAATATCTTGGTCATTGATCTTTTGGGTCCCTCTTTGGAAGATTATTTGATTGGT  
 GTGCAAGAAAAATTTCTGTCAAAAACGGTTGTGCAAGTTGCTGTUCAATGATTACTTTGATTGAAGACT  
 TGCACGCACATGACTTGATATACGTTGATATCAAACAGACAATTTCTTGATTGGAAGGCCCGGCCAAC  
 CTGACGCAAAACAACATCCATTTGATCGACTTCGCTATGCCCCAAACAGTATCGTGATCGGAAACATAAC

AGCACATCCCATATAGAGAGAAAAAATCACTCAGCGGCACTGCCAGATATATGTCCATTAACTACTCACC  
TTGGAAAGAGAGCAGTCCAGAAGAGATGATATGGAGGCCTTGGGTCAAGTPTTTCTTTTATTTCTTGAGAG  
GCCACTTACCCTGGCAGGGTTTAAAGCTCCAAACAATAAGCAAAAATACGAAAAGATTGGTGAAGAAG  
AAAGATCTACTAACGTTTACGATCTAGCTCAAGGCTTACCTGTGCAATTTGGCAGGTATCTAGAAATCG  
TCAGAAGTCTTTCTTTGAAGAGTGTCCCGATTATGAAGGCTATAGAAAACTATTACTATCTGTACTGC  
ATGATTTAGGTGAAACCGCGGACGGCCAATATGATTGGATGAAACTGAACGATGGCCGTGGTTGGGATC  
TAAACATAAACAAGAAGCCAAATCTCCACGGATACGGCCATCCAAATCCACCAAAACGAAAAATCGAGAA  
AACATAGAAAACAAACAGCTCCAAATGCAACAGCTCCAAATGCAACAGCTCCAAACACAGCAACAGCAAC  
AGCAATATGCTCAAAAAAATGAGGCAGATATGGCAATTTCTCAATATAAACCAAAGTTAGACCCCTACTT  
CTTATGAAGCTTACCAGCATCAAAACCCAGCAGAAATACCTGCAAGAAACAACAAAGAGACAGCAACAC  
AAAACCTTCAGCAGCAACAACCTCAACAGCAACAATTGCAACAGCAGCAACAGCAACAGCAACAGCTAC  
GTGCCAACAGGCAACAACTCCATCTCAGCCTCAAGCGCAAACTCAATTCAGGAGTTTGGGCTCTGTTTTC  
AACCACAACACAACCTTCTGCTGCTTTAAGAACTCTGAACAGCACCCAAATGACGATAAATCAAGTC  
TAGCTGCTTTCTCATAAGGGCTTTTTTCCAAAAATTAGTTGTTGTGCTAA

MSMPIASTTILAVNNLTNINGNANFNQANKQLHHQAVDSPAKSSMTATIAANSNSNSSRDDSTIVGLHY  
KIGKIGEGSFGVLFEGTNMGVPAIKFEPKTEAPQLRDEYKYKILNGTINIPYAYYFGQEGHIN  
ILVIDLLGPSLEDLFDWCGRKFSVKTVVQVAVQMITLIEDLHARDLIYRDEKPDNFLIGRGPQPDANNI  
HLIDFGMAKQYRDPXTKQHIPPYREKKSLSCTARYKSNTHLGREQSRRDDMEALGHVFFVYFLRGHLWPQ  
GLKAPNNKQKYEKIGEKKRSTNVYDLAQGLPVQFGRYLILVRSLSFEBCPLYEGYRKILLSVLDDLGCT  
ADGQYDWMKLNDRGWDNLNINKPNLHGYPHPNPNNEKSRKHKNKQLQMQLLQMQLLQOQQQQQQYAK  
TEADMRNSQYKPKLDPTSIEAYQHQTQQKYLQEQCKRQCKQLQEQQLQEQQLQOQQQQQQQFATGQP  
PSOPQACTOSOPGARYOPQOQPSAALRTECHTNEQNSLAASHKGETOKLCC

TAGAGCAGATTGTTTTGAGTAGGATTTAGGAATCAAGACCTCCATCTTTGTGCGATTATTCCCTAAATGTAACCGTAACTCGTTTTGATAAGAGAATGTCTAATCGAAGAGAGTTAATAACTTAATAAGCTCTTTTAAAGAACCGATGGCATTATATCGTCTCCTATGCCAAGATAATTACTGGCTCAAAATTCCTCAGCGTTTCATAAAACTTTGATATACATTTCTGCGGCACAAAGCTAACCTTTATGTAGTTCTTACGTAGATTCTTTTTAGCAAGTGCCTGGTAGTGGTTATTACATAAAAGTATCTTTTCACTTTTGTATATTTGATAACAATTTCTTTCAGTAGCATGTCTGTCTAGCACGTGACGTAGAATCTGTGGCTTTTTTTGTGTCTATTATGACAATCAAGATAACCAAAATTCAGTCTATGTTTTAAAGGGGCAAGGTACCATAGATATATATAAAGTCTCAATTTACTATAATTTGCGTATAGAAATCCATTTGTACTTTGCTCTCAATGAACAACAGGATTCATTCTGCAATTTACGAAACCTAATGTCTACTTCCAGACCGAAGTTGTTTGGTCCCAAAATATTTTCACTTCTAACCCTGCTCAAAAGATGTTTGGTGCCTAACCAATGAAGCCGCTGCAAAAGCTGCCAATAACTCCAAAAACCAGGCCCCGAACCTTATTAATTTAGGCCAAGGCTTTTTTTCATATTTCCCTCTCAATTCGCCATTAAAGGAGGCTCAGAAAGCCCTAGACATTCCAATGGTCAATCAATATTTCTCCAACTAGAGGTGACCTTCATTAAATTAATTCCTTCATTAACCTTCTATTCTCTATTTATAACACAGAATTGAAAGCGGAAAATGTTACCGTAACAACAGGTGCCAATGAAGGTATACTTTCTGTGTTGATGGGGCTTTTGAACGCTGGCGACGAGGTTATTTGTTTGTGAACCTTTCTTTTGACCAATATATTTCCAAATATCGAACCTTTGCGGTGGTAAAGTTGTTTAAGTCCCCATAAATCTCTCCAAAGGAATTCGATCAAAAGGAATCTAGACCTGAAGAATGGACCAATGCACTTTGAGCAAGTTCCGAAAAAGCGATTACATCCAAAGCAAAAGGCTGTCAATTATCAATACCCCTCACAAACCCCAATTTGGTAAAGTTTTTCACGCGGAGCAATTAACCACTTTTAGGTACATTTTGGTCAAGCACAAAGCTTGTGATTATATCTGATGTAGCTCTATGAACACCTTTTACTTTCACTGATTTCTTCACTAGAAATGCCACACTCTCTCCAGAAATTTGGGCAACTAACTTAAAGGTGGTTCTGCGCGTAATCGTTTTGCTGCTACTGGTTGGAGAATTGGTTGGGCTCTATCTCTTGAACGCAGAGTTGTTAAGTTATGCAAGCTAAGGCACATACAAGAATTTGTTTTGCATCTCCATCCCTCTACAGGAAGCTTGTGCAAACTCTATTAACGAGCGCTTTAAAAATTTGGGTATTTTGAAAAAATGAGACAGGAATATATCAACAAATTCAAATTTTCACATCGATCTTTCATCAATTCGCACTACCATATACACTCCAGAGGGTACATATTTTGTCTCTGTGATTTCTCTAAAGTGAAAATTTCCGAGGACTATCCCTACCCAGAGCAGATCTTGAATAAGGAAAAATTTTCGCAATTTCTCTACTGGTTGATGAATGAATTAGGTGTGTTTCCCATTCACCAACTGAATTCATATCAAAGCACAAAAGCTGTCTGAGAAATTTGTTAAGTTTGCAGTTTGTAAAGATGATGCTTATCTAGAAATGGCGGTAGAGAGATTAAACTACTCAAGGACTACTTATAA



128/251

YJL060W 444aa public: 1..444 (SEQ ID NO 704)

MKQRPIRQFTKLMSTSRPKVVANKYFTSNTAKDVWSLTNEAAAKAANKSKNQGRRLTNLGGQGFPSYSPP  
 QFAIKEAQKALDIPMVNQYSPTRGRPSLINSLIKLYSPIYNTELKAENVTVTTGANEGILSCLMGLLNA  
 GDEVIVFEPFFDQYIPNIELCGGKVWYVPINPPKELDQRNTRGEWTIDFEQFERAITSKTKAVIINTP  
 HNPIGKVFTREELTTLGNIQVKNVVIISDEVYEHLYFTDSFTRIATLSPEIGQLTLTVGSAGKSFAAT  
 GWRIGWVLSLNAELLSYAAKAHTRICFASPSPLQECANSINDALKIGYFEKMRQEYINKFKIFTSD  
 ELGLPYTAPEGTYFVLVDFSKVKIPEDYPYPEELIKGKDFRISHWLINELGVVAIPPTEFYIKKHKKA  
 AENLLRFAVCKDDAYLENAVERLKLKDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

AAAATTAATCGATGTAACACAAAATATTCCGATTCGATCTTTTCATTCGAATTCGGCGCGTTTAATGCCGC  
 ATATACAAGAACATATACGAGGGATGGTCTATTGGAAGACCCGGATAATGTTAGCTTCCGTGAAGCTCT  
 CTCTGAAGGCCAAGATATTGAAGTCGCCAAGATCTTCAAAGAGTTCACGATCCACATCATGAAAGTGA  
 TGAATGACGTCAGATGAGGTTGAATTACATGTTAATTGGGCCAAGTTGGGTTCTGCTTTATAGAAGC  
 CAATGCGAAAAATATGCGTTTCCGAGTGTTTATGGCCAAATTCGAATTCCTCCCGGTATAATGGAAC  
 CGAGATCAAGAAGGATACTATTTTACAGAAAGGAGAGAATTCGCACCAAGATATGCTGACACTGATAA  
 TTTCTTTGCTACTATGAAGCTAAAGAACCGCTTCTCTTACGATTAAGGAGAAATTAATGTTACACGACAG  
 GTGGTCTGTTGGGACGTATGAAGAATCTCTCTTAACTTTGACAGAGAAAAATTAATGTTACACGACAG  
 TCTTGAACCCGACGATAACAACACCGATAACAATGTTAATAACAACGATGAGAAGCGCTGGTTGCAATGA  
 AAATTCGCCATTATTGGAAGATGATGCCAATAAAGACCGAAAAATTCAAATACCCCCCGTGAAGTATC  
 AGATGGAGCTATCAATAAGAACCCCTAGAAATAAATCTACTAAAAACGTCAAAGAAACAGAGGCAAAATC  
 TTCTAAAAAGAAGAACAGATCGAGAAATAAGAGACATTATGAATTTGGTTTTTTTTTACAATTTACGCA  
 TACACAATATATACATTTCTACTAGCTTTTTTTTTTTCTCAATTCGATAGTTTAG

YKL123W 126aa public: 1..126 (SEQ ID NO 706)

MKESLLTLTEKINFTTVLKPTITTPITMLITMRTLVAWKIRHYWQMAIKDRKIQIPPVKYQMELSI  
 RTLEINLLKNVKETEANLLKRRTDRENKRHYVEFGFFYNLRIHNIYIPTSPFFFPNSIV

YML028W 1091bp CDS: 501..1091 public: 1..1091 (SEQ ID NO 707)

GGTAACGATAGGGTGATACCGCTGTGATAAAGAAGCTTCGTGCTCTTTTGGGTTACACTACTCCCTA  
 TGTGAAGGAGAGCTGGATGATATGTTTGCACAGAGAGCAAGGACCGTGAGCAACCGGCTCCATCTGCG  
 CCAACAGCAGGAAACGAAAGATGAGGCCCTCATATTCCTGACGAGGAAGAACCACCGCCACAGGTGC  
 GCAACCTCATCTCTACATTCCTGATGAAGACTAATTGCAATCCGATGTGGCCACGTTATATAATGCGTT  
 TAAGGTGTACGAAACCCATGCTGTTCTGGCCCCGTGGGTTTTCTGACAAATGTCTCTTTAGGGATTTT  
 TCGGTTTGGCTCCGCTTCGCAAGTCCGCTGCCAACAAACCAGGACATATATAAGGGAGGTAATTCGT  
 CAGATCAATGCCGAACCGTCTTCAACGGGCTTCCCTCCGTTCAATTCGTCACAAUUAUCCAACTAC  
 ATACACATACATACACAATGGTGGCTCAAGTTCAAAGCAAGCTCCAACTTTTAGAAAAGTCCCGTCC  
 TCGACGGTGTCTTTGACGAAGCTCTCCTTGGACAANTACAAGGTAAGTACCTGTCTTACCTTTTATTC  
 CATTGGCCTTCACTTTTCTGTCTGTCCAAACCGAATCATTTGCTTTCTCAGAAGCTGCTTAAGAAATTCGAAC  
 AACAAAGGCGCTCAAGTTCTTTTGGCTTCACTGACTTCGAATACTCCCTTTTGGCATGGACCAATAATCC  
 CAAGAAAGGAAGGTGTTTGGGCCCAATCAACATTCATTTGTTGGCTGACACCAACCACTTTTGTTCAC  
 GACACTATGGTGTCTTGATCGAAGAAGAAGGTCTCGCCTTGAGAGGTTTGTTCATCATCGACCCAAAGG  
 GTGTCAATTAGACACATCACCATTAACGATTTGCCAGTCCGTAGAAAAGTTGACGAAGCCTTCAGATTTGG  
 TTGAAGCCTTCCAATGGACCGACAAGAAGCGTACTGTCTTCCCAAGTAACCGACTCCAGGTGCTGCTA  
 CCATCAAGCCACCGTTGAAGACTCCAAGCAATACTTCGAAGCTGCCAACAAATBA

YML028W 196aa public: 1..196 (SEQ ID NO 708)

MVAQVQKQAPTFFKKTAVVDGVFDEVSLDKYKGYVVLAFIPLAFTFVCPTEITAFSEAAKKFEEQGAQV  
 LFASTDSEYSLLAWTNIPRKEGCLGPINIPLLADINHSLSRDYGVLEEEGVLRSLFIIDPKGVIRH1  
 TINDLFVGRNVDEALRLVEAFQWTDKNGFVLPUNWTFGAATFKPTVLEDSKEYFEAANK

YOL052C A 686bp CDS: 501..686 public: 1..686 (SEQ ID NO 709)

TGGCCACTGAAAAATCCTGGCCAGACCACCCCTGAGCTAAGGGAGTTTAGCCGCTCAAGCTTTTATATTC  
 CTCTGATGTAATAATATCACACACCCAGACACGGTTGCCAAGGCCTCGACGGAAGGCCGCTTCAAGGCAC  
 GCGGCAGTGGCTATCAGAAATACCTTAATATCATCAATATTTTTCAATCAATCGCAAGGTGTCAAACATC  
 AATAAAGGATGATGCTCAAAGGTTTATGCCCGATGTTCTCTTAATCCCCCTTCTCTCTCTAATAAATACC

129/251

TTTTTTTACTCTTCTTCTTTTCCCTTGTTTCCATTMTTGTCTTTTTCUACCCCTTATGGGACATCAATA  
 ATGCAAGTATGTTTATACATTTTTATATAAATGTATATATAAATGCCATTTCTTTACACATAAACCCTCCAT  
 TCTTTGGTTAATTCTTTCTTCATTCTTTTTTTTTTTCATTCTGAAAAAGCCCTCCCAAGCAAGCACGGCTAAT  
 TTAATATCGATTAAACATGAAAGTATCACAAGTTTTCATTCTGCCCATCTCTGCTTCGGGCTCGCTA  
 CTAGCGTAAATGCTCAAAACGCATCCAAACCCACCGAGTAACGCTGCTCCTGCTTTGCACGCTCAAAATG  
 GTCAACTACTAAACGCCCGAGTCGTCGGTCTGCTGCTGGTGGTGGCTTTGGCCCTTTTTCATTTAG

YOL052C A 61aa public: 1..61 (SEQ ID NO 710)

MKVSQVFLSALSIVFLATSVNAQNASNTTSNAAPALHAQNGQLLNAGVVGAAVGGALAFLL

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)

TGTCCAAATATGTTGATGAATTCIGTTTGCAAAGGGGGAACAACTTCAATGAATTGTATTTCGAAAGGTT  
 TGCAGAATGTTACCAAAACAGATCTGAAAATGCCCATGCAGAAATATTTTGTCAACATCTTTGATTCCCA  
 ATAAAAGCGTTGCCCTTTGTGAGCTGTCTCCAGCTAAATTGGAAATCAGTTCAAGAAATCTTTTGAAACTC  
 AAGGTTTTCACCTGTGAAATAGAAGAGCTAGAAAGATGACGATGACGAAATCGATAGTGAAGAAGACGAAA  
 ATGCGTGAATACATGACCTCCATTTCAGCTTCACTTTCAACACAGAAACACTGCGTATTATCTGCAATTC  
 AATAAAATGACAAAAGGAGCATTTGCTCATTTCTTTTTCGAATTCGGGATCTGCCCCTACCCCGCTTTTTC  
 ATTTGATTGATCGAGAATTATTATTATATTATATGAGTACTTGAAATTCCTCAATATTTATTTTAG  
 ACTATTTAAGTAGCTTGATGAAAACATTAGATAAAATTTACTAATTAAGAACCTCTTCGATTTTTGCAGATG  
 AGTTTTTGAAATTTGTTCTCTGTGTTTAGACCTAATCCACGGTAACTTGTCTTTTGGCAATCCCGTTAA  
 CTAATTTACTGGTTAACGGTACTGGAGCAGCGTGTMTMTTGAATTTTGTCTCTTTTGGCAATCCCGTTAA  
 TTTCAAAAATTTCTGCTTGATCTGTGCTCTTAGCGCTATTATCGATTGAGAAACGAATTTGTGCTTTTTC  
 AAATTCATGGAGATTGGCTATGCGTCTCTGGCTTTTGGCGAAGGAGACTTGGAACTTGGAGATCTTTAG  
 GTATGCTCTTTCCCATCATGATCTTCTCTTTCAATTACCTTTTGGTTTCTTTTCAACAGTTCTTTTCT  
 CTATTTTATTTGTATTGGAATTAAGAATTTTTTTTGAGAACAGTAAACAATTTGCTCGTGGCTTTTATTAT  
 CAGTTCUTUAAAAGAAATGACTTTGTA

YOL099C 163aa public: 1..163 (SEQ ID NO 712)

MKTLDKITNYDLDFDADEFLLKFVVFVRNPVTYTCLEGNPLTNLLVNGTGAACFFZFCSLALIKVSKILL  
 ELLLLALLIDSENELCFEIDGDWLCVLGFGEGDLEVGRSLGMLPDDDVHLSITTFWFLCNSSFILFVF  
 ELRIFLRVTNNLLVVFSLVLRNDL

YOL100W 3746bp CDS: 501..3746 public: 1..3746 (SEQ ID NO 713)

TTAACGATCGACTCGACACATTTGTTGATGGAATAATTTGTTUCCCTAGTTAAACAGCCGAGAAATAGCCCC  
 CCAGGATAAATUGGAGAAAAGTCACGTGCAAAAGAAATCATATTGACCGAAATAAACTAGAATAAATTTT  
 TGACGTTTAGCAATAATPACCCCAATGGAAGCGAACATTTCCCGATCCTTTTAGTTTTCCTTTPAAGGCG  
 CTATTGGCAATTCATCTTCAAAGCTTCCGCAACACAGAAATTATATATTCACATTTCTGAGGCAGAGAAAT  
 AGTTTTGACAACGAAACTGTTAATATTTTTACTCCAGTTACCGCCTTTGAAAGTCTGATATTGCTGTACA  
 AAGCTACTTAGGGGTATTTAAGAACAAAGAACTACATAAAATAGTTGCAAAAGGGAACAAAGTAAC  
 ATCTTGATGAACCGAGAAAGCCACTAACTAGTTTAAAAAAGCAAAAGAAATTAATTCCTCCTTTTTTTT  
 TTTTTCATTTCAACCAATGTATTTTGATAAGGATAATTTCCATGAGXCCCTAGGCCGTTATTGCCCAGTNG  
 ATGAGCAGAAGCTAACATTAATCTTCAACGAAAAGCAGAAATTCCTCGCATTTAGACCCCCATTATG  
 ACGCAAAAGCCACTCCACAAAGAAGCACTTCCAATAGAAACGTTGGCGATTTACTTTTGGAAAAAACAA  
 CUGCTAAGCCTATGATTCAAAGGCCCTTACGAATACGGATAATTTCAATGAAATGTACCAATATCAGC  
 AGAGAAAAAATCTTGATGACGACACTATTAAGAAGTAATGATTAATGATTAAGAAACGGAAAAAAGTGTGG  
 CTAGTACCAACGACGGCAGATATGACAACGATTACGATAATTAAGGATAATTAATGACCAAAAAAAGTGTGG  
 ATAATATAGCGGGAAGTCCCCACATGGAAAAAAATCGAAACAAAGTAAGATTAAGACATGACCTTTTCAT  
 UTCAAAAACCAATAGCTAAAGAGTCAATCAAGGCCAAAAAATAAATCAAAAGGGAAATCAAGGACT  
 TTAAATTEGGTAGTGTAATAGGTGATGGCGGCTATCTACTGTAAATGTTAGCGACGTCGATTGATACCA  
 AAAACAGCTACGCCGCAAAAGTACTAACAAGAATATTTAATACGCCAGAAAGTCAAAATACGTTUA  
 GCATAGAAAAAAGCGCCCTTCAAAGCTCAATAAATTCCTCTAGTGTGTGCGATTATTTTCCACTTTTTC  
 ACGATCAATCAAGCCTATACCTTCTCTTAGAGTATGCCGCCAATGCGGACTTTCTTCTTTAATGAAA  
 AATACGCTTCATAGACGAAACCTGCGCAGGATATATGCTGCGCAATAATAGATGCCATAGACTACT  
 TACATTTCAACGGTATTATTATAGAGATAAATAACAGAAAAATATTCTTTTAGATGGAGAAATGAAGA  
 TCAAACTGACTGATTTTGGTACTGCGAAGTTACTGAATCCTACAAATAATAGCGTTTCGAAACCAAGAAAT  
 ACGATTTATCAACAAGTTCGAAATCTTTGCTTGGAACTGCAGAAATACGTATCTCCAGAACTTTTAAATG

130/251

ACAGTTTTACAGACTATCGTTGCGATATTTGGGCGCTTCGGATGTATACCTTTCCAGATGATTGCCCGAA  
 AACCACCATTCAAAGCTACCAATGAATACTTGACITTCCAAASSTAAAGAAAGTTGAGTACGCCCTTTA  
 CACCAGCTTTCCCACTTATATCAGAGATTGGTTAAGAAATCTTACTAAAAAACTTAGACCGGAAGAT  
 TGACGATAAGCCAAATTAAGGAACATCATTTTTCAAAGATTTCAATTTTAAAGACGGCTCTGTTTGGT  
 CAAAAACGCCCTCCAGAGATCAAACCATATAAAATCAACGCCAAAATCCATGCAGGCAATGCCAAGCGGAA  
 GCGATACAAAACCTCTGAAGAAATCAGTCAACACACTTCGCAAAATCCCATCTACTGACTCAAAGGTUAG  
 CTTCAAGTCCCTCTGTTGAGGAACTACTCATTCAACCCCTATACAATAACAATACTCACGCTTCTACTG  
 AAAGTGAAATATCAATAAAGCAAGACACCCACTGATGAAAGAACACCGCAGATACTTGAAATATGCAAGAA  
 AGGGTATAAACAATAGGAAAAATCAACCCAGGCAAGAGAACACCAAGTGGTGCAGCTTCTGCTGCCCTAC  
 CAGCTTCTGCTGCTTTAACCAGAAAAACCATGCAAGGTATCCAACTTCTAGTTCCGAAAAAGTAGCAGGT  
 CAAGCTCTCTGCGACAAACATCAAGACCAAGCAACTTATAAGCGTACCTTCTTACAGAAAAATAAACCAT  
 TTGCCAAATCTCCACCTTTGTGAGCATCAGTTTTATCGTCAAAAGTCCCAATGCCCTTCATACACACCTC  
 CAATGTCCCCCCTATGACACCATATGATACATATCAAATGACACCTCCCTATACGACAAAAACAGCAGG  
 ATTATTCTGATACCGCAATTGCCGCAGCTAAGCCTTGATTAGTAAGCAAAATGTAAAAATAGCACAC  
 ATTCTCCCTTGATGAACAAGCAAGATATTCATATGCTCCTTTTACCTGAAAAACATCAACGAACATGTAC  
 TAAGGACGGAATAAATCGGATTTTGTACCACAAATACGATATCTTAGAGAGAAAAATGCTTAAACTAA  
 ATGGTTTATTTAGATCTCAACTGTCTTGGTAAGCCTAGACATACTTTTTTATCCCAAGTACCTAGGA  
 GTGGGGGAGAGGTTACAGGTTTTCGAATGATCCAACTATGACTGCTTATTCCAAAAACAGAAGATACGT  
 ACTATTGAAAAATATTATCGATTTCGAGCTCTTCCAAGATGATTATCGAATTGAGGAGGTGACTTAT  
 CGGAGTTGCTTACTAACAGAAGCGGAGAGGGGTACAAATGCAATCAAAACAGCTCACCAATGAAAGACG  
 ATGATAAATCCGAATCTAACAATAAAGGAAGCTCTGTTTTTCTGCGCAAGATTAATAAAATTAATTTTACC  
 CTACCTCAGCAGCTGAAACGCTCTCTTCTCTGATGAAAAACCAAGTACTATAAACCAACCATTGTAA  
 TCACATCATTTGCAAGCTTTCTAGTATTTCCCAAGAGGAGCCACCCAAATCCACTTACAAATTTAAAGT  
 ATGAACTAGAATATGACATAAATTTGCGTCAACAGGGTACCAAAATAAAAGAACTAATCATTCCTCTGG  
 AAATGGGAACATAATCATATAGTTGTTGATTACAGACACCTTACAAGTCATTTCTTTTGGAGCACTGATAAA  
 AAACCACGAGCAAAATGTTTTACTGTTCTCAAAAAATTCCTTAATTCGAATACAAATAAAAATAGAGAAAG  
 AACTGTTGCAAGAAACCAAAAGCTAATTGAAGAAGAACATCATCATCCGGAAGAGCCATACCTAAAG  
 ATCTTCCAACCTCCAAGTCTCTTCCGCCAAAACCCAGGACGCATAGCCAACTCCATCAATTTCAAAAC  
 ACAATTGCTTTTCTGAATCGATTAAATAGCGCTAAGAGCAACAGATCAAGCAGAAATTTTGAAACCTTTA  
 TCAATGCCAAGGAACAAATTCAAAAAACACCGCTCCTCCACTACCGTTAAACCACTAAATTAAGTFAACG  
 GATTGCCAAAAAGACAAGTTACCGTGGGATTAGGCTCTAACACAGGAACAAATTTCAAAAACTCATCTG  
 CAAAAATCGAAGAGGTCTGTAA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

KYPDKDMSMSPRLLP\$DEQKLNINLLTKKEKFSHLDPHYDAKATPQRSTSNRNVGDLLLEKRTAKPMI  
 QKALTNTDNFIEMYHNQQRKNLDDOTIKEVMINDENGKTVA\$TNDGRVDNDYDNNNDINDQKTLDNIAGS  
 PHMEKNRNRKVKLEHDS\$SQKPIAKESSKAQKNILKKGIKDFKPGSVTGDGAYSTVMTATSIDTKKRYAA  
 KVLNKEYLIRQKKVKYVSIETALQKLNNSP\$VVRLESTFQDESSLYFLLEYAPNGDPLSLMKKYGSLD  
 ETCARYYAAQIIDAIDYLH\$NGIHRDIKPENILLDGEMKIKLTD\$GTAKLLNFTNNSVSKPEYDLSTR  
 SKSFVGTASYV\$PELLNDSF\$DYRCDIWAFCILFQMIAGKPPFKATNEYLT\$QKVMKVQYAF\$TGFPL  
 IIRDLVKKJLVKNLDRRLTISQIKEH\$FFKDLNFKDGSVW\$KTPPEIKPYKINAKSMQAMP\$GSDRLV  
 KKS\$VNTLGKSHLVTOR\$ASSP\$VBE\$THSTLYNNNTHAST\$E\$E\$SIKKRPTDERTAQILENARKGINNR  
 KNQPGKRTP\$GAASAALAASAALTRKTMQSYPTSSSKSSRSS\$PATT\$RPGTYKRTSS\$TESKPFK\$PP  
 L\$ASVL\$SKVPM\$FYTPPM\$PMT\$PYDTYQMT\$PFT\$TKQDY\$CTAIAAPKPCISKQNVKNSTDSPLMN  
 KQDIQWSFYLNIN\$EHVLRTEKLD\$FVTNYDILEKMKLKLNGSLLD\$QLFGKPRHTFL\$QVARSGGEVT  
 GFRNDPMTAY\$KTEDTYYSKNIIDLQLLED\$DYRIEGDLS\$ELLTNRSGEGYKCNQNS\$P\$MKDDDK\$ES  
 NNKGS\$V\$P\$GKIKKL\$FHPT\$AAETL\$SS\$DEKTKYVKRTIVMT\$FGRFLVFAKRRQPNPVTNLKYELEYD  
 INLRQGGTKIKELIPL\$MGTNHTVV\$QTPYK\$ELL\$TDKKT\$SKLFTVLKKILNSNTN\$KIEKELLQRN  
 QKVLERRP\$SS\$GRALFKDLPT\$SK\$P\$FKPRTH\$Q\$P\$SKHNS\$F\$ESINS\$AKSNRSSRI\$FETF\$INAK\$Q  
 N\$KKHAAPVPLT\$SKLVNGLPKRQVTVGLGLNTGTNPKN\$SAK\$RS

YOR302W 573bp CDS:501..578 public:1..578 (SEQ ID NO 715)

GTGTATGATGTAATCCATCACCCCCTATAAAAAACACCTGTGCACCGCATATTTCCATAGCGCGTGACG  
 CTAAAGTACAAGAAACAGCGAGGGGCCGTTAACTCCAGGCTTTACCGAGGGCGCGCGCTGGGCGCTTCCCG  
 TGGAAGGGTGTTTGACTCATCATCGCATCGCATTTACCTCATGATGAGTAAATAGTTGUGATTTCACCTTA  
 TCACCTCTCGCGGAAAAAAAGCGCATGACATGATATATAAGGCTCTCTCGTAAGACACTTAACATCC

131/251

AACGTCACCTAGATTATTCGGTCAATTTCTTTTTCATGCCCTCCTTTTTCTTTTCTTTTCTTGACTC  
GTCGTTTCCTTTTCTTTTTTTTTTTTTTTTTTTCTTTCAGAACTATAACACATAGATACACTCGAACAT  
CTAATTCCTTAAATACTGCAAAGAATACAAGGTAATCGACTCTTCTACATACCCCTTTTTCGAGATTIGA  
AATAAAAAAACATTATATGTTTAGCTTATCGAACTCTCAATACAUCTGCCAAGACTACATATCTGACC  
ACATCTCCAAAAGTAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)  
MFSLSNSQYTCQDYISDHIWKTSSH

132/251

**Figure 2****Candida spp. homologues**

YBL002W\_homolog 393bp public: 1..393 (SEQ ID NO 397)  
 ATGGCCCCAAAGCAGAAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA  
 ACCGCTTCCACCGATGCTGCTAAAAAGAGAACCAGCTAGAAAAGAACTTATTCTCATATATATAAT  
 AAAGTTTTGAAACAAACACATCCAGACACTGGTATCTCCCAAAGGCCATGTCAATTATGAATTGCTTT  
 GTTAACGATAATTTTCGAAAGAAATTCGACCGGAAGCTCCAAATTAGCTGCTTACAATAAAAAATCCACA  
 ATTTCCGCTAGAGAAATCCAACTGCTGTAGATTAAATTTTCCAGGTGAATTGSCCAACATGCCGTT  
 TCCGAAGGTACCAGAGCCCTCACAAAATACTCATCTGCTTCTAGTTAG

YBL002W\_homolog 130aa (SEQ ID NO 398)  
 MAPKAEKKPASKAPAEKKPAAKKTASTDGAKKRTKARKETYSSYIYKVLKQTHPDTGISQKAMSIMKSP  
 VNDIFERLATEASKLAAYNKKSTISAREIQTAVRLILFGLAKHAVSEGTRAVTKYSSASS

YBL064C\_homolog 732bp public: 1..732 (SEQ ID NO 399)  
 ATGACGAGACAAAAACAAACAAAAAATACTTTTTTTTTCGCCACGCACACTACCATCTCGCAA  
 CAACACCATTTACGTCTCGGATCTACCGACCTGATTTCAAAGCTGATACAACTAACGGGCTATATCTG  
 TTTCACGGAATACATTCGTGATAGCTGGGCTATCTTCTTCACATCCCGCTGCCACACCACTGTGTGT  
 AGCACCGAGCTTTCTGCGTTCCGACGACTCGAACCGGAGTTTACGAAGAGAGGGGTGAAATTCCTTGCA  
 ATTTACGCGGACCCCTGTGAAGCAAATTCGACTGGATTGATGATATGGAAGATTTTAGCGGATCCAGG  
 CTCATATTTCCAAATTATCGCAGACCCCTGAGAGAAAGTTTGCTACCTTGTACGACATGATCCATCACC  
 GATGCCACCAATCTCGATGACAAAGGGCTTCAATTGACAATTCGTGCAGTGTATTATCATTGATCCAAGT  
 AAGAAAATCGAGATTGATCATGACCTACCCCTGCCTCGACCGGTAGAAACACCGCTGAAGTATTGAGAGTA  
 CTCGACTCATTAACCTTCTTCATAAAACAAACCTTATCACTCCAATCAATTCGGTTCAGGTGACGAT  
 GTTCTTGTCCATATGGGTCTCCAGATGATGAGGCAAGAGTTTTGTTTCTAAATATAGGGCTATAAAG  
 CCATATAATTAGATTGACTCCCTTCGAAAACGAAGACAAGTAA

YBL064C\_homolog 243aa (SEQ ID NO 400)  
 MRDKKQTKKKKSEFFATHHTMSQOPHLRLGSTAPDFKADTTNGPISFHEYIGDSWAILFSHPAAHTSVC  
 STELSAFARLEPFTKRGVLLAISADPVEANSWDWIDMEDFSGSRVKFPILADPERKVATLYDMIDHQ  
 DATNLDDKGLQLTIRAVFLIDPSKKIRLIMTYPASTGRNTAEVLRVLDLQLVDKQKVITPINWVPGDD  
 VLVMGVPDDEARVLFPKYRAIKPYIRLTPLEKEDK

YBR149W\_homolog 981bp public: 1..981 (SEQ ID NO 401)  
 ATGAAATTAGCCACTGAAATTGATTTCAAACCTCAACAATGGTAAACCATTCTGCTTAGGACTAGCT  
 ACTGTTGCCCTCAAAAGATCCATAAGATGTAAAGGATCAAGTAATCACTGCTCTTAAAGCAGGATATCGT  
 CATATTGACTACTGCTTGGTTTTATGGTACTGAAAAATATATTGGTGAAGCATTACAGAAATTAATTGCT  
 GAACGAATCATTAAGAGAGAAGATTTATTTATCACGACAAAAATTTTGGCCATCATATTGGGCTAATCCA  
 GAAAAATCTTTAGATCAATCTTTAAAGACTTCCAACTTCATTATGTTGATTTATTTTACAACATTTGG  
 CCAATTGTTTTACATGCTGATGAAATGGATTAACGAAAAATACCTAAGGATGAGAATGGTGAATTCATTT  
 TATGATGATGATCCAACCCCAATGGTACTAAATATATCGACGTTTATCATAAATTAGAGGATATTTTA  
 GAAACAACCAACAAAGTTAGATCAATTGGTGTCTTAATTATTCATTCACAAACTTCGTCAATTTATTA  
 CCTAAAGTTAAAAAACATATTCCTGTTTGTAAATCAAATTGAATATCATCCACAATTACCTCAACAGAT  
 TTAGTTGATTATTTGACTAAAAATAATATCTGATTTCTTGTATTTCACCAGTTGCTAGTTATGGAGCT  
 CCAGTATTGAAAAATCCCATTTAGTTAAGCAATTGGCAGAAAAATATCAAGTCACAGAGAATGAAATTCCT  
 GATGCTTATAAATATTTTGAATGGTAGAGTTACATTACCAAGATCTTCTAATCTTGAAGAATTAAGAAC  
 ATTATTAGATTACCACATTIGACTAAAGGAAGATTTGGATGAATTCATCAAGTTGGAGCTAAAGATCCA  
 CAAAGATATAATTTGTATCTTGGGGGTATGGTATAGGATTCCCTTGGTCGAAAGCCCACTTTAAGT  
 AAAGAATTTGATTAA

YBR149W\_homolog 326aa (SEQ ID NO 402)  
 MKLATEIDFKLNNKTIIPALGLGTVASKDPKDVKDQVITAVKAGYRHIDTANFYGTEKYIGEALQELFA  
 EGITKREDLFITTKFWPSYWANPEKSLDESLEKDLQIDYVDLFLQIDWPICLIGDENGLPKIPKDENGELI  
 YDDEPTPNGTKYIDVYKLEIDILETTTKVRSICVSNYSIPKLRQLLPKVKKHIPVCNQIFVHPQIQOOD  
 LVDYCTKNNILISCYSPVGSYGAPVLKIPLVKQLAEKYQVTENFTADAVNIINGRVPLPRSSNLERLEK  
 IERLPHLTKEELDELQYGVKDPQRYICDPWGYGISPRWKKSDTDSKEFD

YBR289W\_homolog 1389bp public: 1..1389 (SEQ ID NO 403)  
 ATGAAACCAATGCAAAACGTTAAGGAGTGGTCAGAAAAATTGAAACAGGAAGGTAAAGATGCACTCTC  
 CACTTGAAAGTGTATCAAGATTTTCATTACAAAGCAATAGGAATTTGTGGGTAAATTGAATMAACAGCTG  
 CACGACAACAAATTTATTATGGAAAAATTAACAGAGATATCAACTCTTATATCTMAATCAAAACAATCG

133/251

AGGATGAATTCATTCGGTTCCTCCAAACAAGGACATATTAATAACAGTATTTTCGGGGGGAAGGATATCAA  
GGTTATGGCARTGGAATAACAAACTCCAGTACAAAGTTATTTATTTCCCAACAGGGATTTAACTGATAGA  
ATCATCAATGAAGAGTGATGAAAAACAAAAATAAACCAAAACATTATGTACCCATTCCGATTAGAGTTT  
GACCAAGAAAAGGGATCAATTTAATTGAGAGACACATTTCTTTGGGATTTGAATGAAGAGATTATAAAA  
GTGGAAGATTTCACTGCTCAATTGTTAGAGGAATTATAAATTTATCTCCAAAGTTCATTATGAAACAATT  
TTGTCATCTATTAAAGAGCAGATTGCTGACTATCTCCAGAAACCTAGCAAAACAATGGGTCGAATTGAGA  
ATTCCAAATTAAGATCGACATACCCATTAAACAATACACAATTAACCTGACCAATTTGAATGGGATATATTC  
AADAGCCAGGAAGGCGATGCGAGAAGAAATTTTCATCTTACATGTGCGACGAATTTGTGTCTACCCGGGAGAG  
TTTTCGCACTGCCATCGCGCATAGCATAGAGAACAATCGCAGATGTACTATAAAGCATTGAATATGGTA  
GGGTACGGTTTTCGACGGTTCACCAGTACACGAAGATGAGATTAGAAATCATTTTATTTGCCACCTTTTAAGA  
TTAGTATCATCGGACTTCTGGAAATCGTGGATGATTTTTCTCAATTTTAAGAAACCCATCAAGTTTCGCA  
GACTTTTCACCTACGTTAGGTAAATTTGCCAATTTGGAAGTTGAAAGATTGGACAAGGAAATGGAGAGA  
GAAAGTTAGAAAGGAAAAGAAGACACAATTACAAATGAACATCACCAACAGGGTTCTGGTCGAGGCTTCACCT  
TCGAGAAGAATTCAGCTCATGCTGGTAGGGGAAACACCATTCCCGACTTGTCTAGACATACCCCAAGACA  
TTTAGGACGCGCTGCCCGCTCATFCCATATTGCCAGGTGCTGTTGATATGGGTGTACCTGAGGTGTATGAA  
TACAAATGAAGTTTTAAACAATAGAACTCAAGTTAGGAATCCAGATTATAGACCGCAACACCTTATTCGT  
CTTGAAAATCAACTAGCGGATTATAACCATGATCCAATGAAGGTACTTTTATGGTTACAATCAAAATTA  
CCCGTATAA

YHR289W\_homolog 462aa (SEQ ID NO 404)

MKPMQNVKEWSEKLKQEGKDVPLDLKVYEDLIRKDKKEFVGKLNKQLHDNKFIMENLNKDIKSYNQIKQL  
RMNSIALSNKGQYNNSSWCEGYQGYNGCITMNSSTKLFIPNRDLTDRIINERVMENKPKHYVPIRLEF  
DQERDQFKLRDTFLWDLNEELIKVEDFTAQLLEDYKFISKVHYETLLSSIKEQLADYSQKPSKTMGPTR  
IPKIDITINMTQLTQDFEWDLLNSQEGDAEEFSSYMCDELCLPGEFCTAIAHSIREQSQMYKALNMV  
GYGFGSPVYHEDETRNIJLPPTRIVSSDSGIVDDFFSTLRNPSLPDFSPTLGEKLSQLEVERLDKEMER  
ESRRKRRHNYNEDQQQSGRGFTSRRIAHAHAGRGNTIPDLSIPKTFRTAPSSILPGAVDMGVPEVYE  
YNEVLINRTQVRNPDIRPPTPIRVENELVDYNHDPLEGTFMVTIKLPV

YCR004C\_homolog 597bp public: 1..597 (SEQ ID NO 405)

ATGGCACAAAGGAAAAGTAGCAATTAATCAATTTATTTCAATTAATCAATCAATGTTTATGATTAGCGTTAGCT  
GAAAAGCTCCAAATTCAGCTTCCTGGAGGTGTTGCTGATATTTATCAAGTTGCCGAACATTATCTGAT  
GATGTTTTAGCTAAAAAGCATGCACCAGCAAAACCAGATATTCCAATTCGAACATCATGAACTTTAACT  
CAATATGATGCATTTTATTTGTTATTTCCAAACCAGATTTGGTAATTTCCCTGCTCAAAATTAAGCTTTTT  
TGGGATAGAACCGGTGGTTTATGGGCTAAAAATGCTTTAAGAGGCAAAATATGCTGGTGTGTTTCGTTTCT  
ACTGGTAGTCCAGGTGGTGGTCAAGAACTACCATTATTAATAGTTTGAAGTACTTGGCTCAATCATATCGG  
ACTATTTATGTTCCATTTGGGTATGGATATCTCGTATGACTGATTTAGAAACAAGTTTCATGGTGGATCT  
CCTTGGGGGGCTGGTACTTTTCTTCACGTAATCGCTCAAGAAAAGTTACTGATTTAGAAAAAGCTATTT  
GCTAAACAACAAGGTGAAGATTTCTTTAAACTGTCTTCAAATGA

YCR004C\_homolog 198aa (SEQ ID NO 406)

MAQGKVALIITYSLYHHVYDLALAEKAGIEAAGGVACIYQVAETLSDDVLAKMHAPAKPDPIATHETLT  
QYDAFLFGIPTRFGNFPAOIKAFWDRGTGLWAKNALRGKYAGVFSVSTGTGGGQJETTAINSLSTLAHHG  
IITYVPFGYGYPGMTDLEEYHGGSPWCACTFASGNGSRKVTDLKAIKQQGFRFPFKTVFK

YCR013C\_homolog 450bp public: 1..450 (SEQ ID NO 407)

ATGATAACAATGTTACCATTTTTCAGCAGATTTGACAGCAGCATCCAATAAGGATTTAGTACCGTTGGCG  
AATTTTTCAAATTCGAAAACACCTGGTGGACCGTTCCAAACAATGGTCTTAGCTTTGGCAACAGGTTG  
TGGAAACAATTCGACAGATTTTGGACCACAGTCCAAACCCATCCAGTTGTCCTGGAATAUCTTCAGCATCA  
GTAGCAGAAGAACTTTTGGCATCTTTTGTGCAATTTATCAGCAGTGACAAAATCAACTGGCAAGATCAAT  
TCAACATTTGTTTTCTTAGCTTTTTCAACCAAGTGTCAACGTTTTTAGCACCCSCTTCAATCGAAAAGA  
GAATCACCAATTCGCAATTTTGTTCAGATTTTCTTGAAAGTGAAGGCCATACCACCACCAACAATCAAC  
ATATCAACCTTGTCACAACAAGTTGTCAATCAATTGA

YCR013C\_homolog 149aa (SEQ ID NO 408)

MTMLPFSADLTAASNKDLVPLANFSNSKTPGGPFQTMVLATATACWNNSTDFGPGSKPIQLSGIFSSAS  
VAEVLASLSNLSAVTKSTGKINSTLFLAFSTKCTFLAPASSKRESPIGLPKIFLKVKAIDPFTIN  
ISTLSNKLQIN

YDL147W\_homolog 840bp public: 1..840 (SEQ ID NO 409)

ATGGGATAGGAGTTGGGTAGTAGGTGTGCCATAAAGGGTGGTTGTGTTAGTTAGTTATGCCACATGTTGT  
GGTAGTTTGATTTTPTTTTGTGGTTCACACGACATGGCCAAACATTTATCAAAAAATCGAGTTCAACTTT  
TTTTTTTTTCCAGTTGCCACCACCAACTACTTTTACCACCACCTAACACATGTCAAGAGAAGATCCA  
ATTAAGGCTGAAAAAGACTTTCTGCTACTTTAGATGAACAAATTCUCCATTGATTGAAAACATCTCTTGAC

134/251

TACAAGCAAGCATTAGATAAGTATCTTGTCTCTGGAGAAACAAACTCGTCAGTCTTCCGACTTTGGCTTCA  
 TCAAAAAGAGTTCTCAACAAGATTGTTACTGCAATTCGTTGATAATAACGATTGGGAGTACTTGAATGAC  
 TTGATAACTATCTTTGTCAAAGAAACATGCTCAGTTAAAGTCTGTCATTCAGCATTATCAAAGATGCTG  
 ATTGATAATTTGGATAAAATTTGGATGAAAACAAACAGCAACAATACAGATTGAAGATGAAATTTGATTGAA  
 ACTATTTAGAACAGTTCACAGACAAAAGATTCTTTGTTGAAAGTTGAAAGAGCCATTGTTTCAAAGACAGTTG  
 GCCAAATTTTATTGAAACAAATGAAATGATTGGATAAGGCAGTGGAAATCTTGTGTGATCTTACAAGTA  
 GAAACGTATTTCGTTAATGCCATTTCAGTGACAAGATTTCAGTATATCTTAGAACAAATTCAGTTGACTTTA  
 CAAAAGGGGGACATATGGCCCAAGCCAAAGATTCTTTGAGTCGAAAGATTTTATTAAAATCGTTGAAGAATCT  
 TGCCAAAGCTGA

YDL147W\_homolog 279aa (SEQ ID NO 410)

MDRSWVVGCAIKGGCLVSYGTCCGSLTFPCGPHDWPNTYQKIEFNFFFSFSPPTTTCTTTRMSREDP  
 IKAEDFSATLDEQFPLIEKISDYKQALDKYLVEKQTRQSSDLASSKRVLNKIVTALVDMNNWPFVLDN  
 LITILSKKHGQLKSSIQAFIKEDVIDNLEKLDENNKQQLKMKLIETIRTVTDKKIFVEVERAIVSRQL  
 AKIYLNKLNLDLRAVEILCDLQVETYSLMPFSDKIEYLEQLQLTLQXGDYGPSQDFESKDFIKIVEEL  
 CQS

YDR253C\_homolog 1752bp public: 1..1752 (SEQ ID NO 411)

ATCCAAAATACTAACCCTAATAATAGTAATAGTAGTAAGAATAATAGTGAATAATCATCATCAACAACAA  
 CAACGACAACGACAACACAAGTTGATCAATATCAATCTATTACATTACCACCATTACAATATCAATCT  
 AATACTCACGAATCGATAGTACTACCTTCGCCAACACCTAAAAGAGGTCGATCTGAACATTTTAAATCA  
 CAATTCCAACGTAATATAAATTCAGACCACTGTTATTACCAAGTCTCGTGATAATAATAACACCACA  
 AATATACCTATACCTATAAATTTACCAAGTAGTACCAATTTCTAACAATCCAATTAATTTCTAGTAGCAA  
 TCAAGAATGTTTTCCACCTAATCCTCTGAGTCCATTTATATATCCCGTGGTCAACCACCATCATCAGCATTA  
 TCACCACCAACACAACACCATCAACAACAACAGCAACAATTAATAAAAACTCAAAACATCAAAATCA  
 GGTTCCAATATCTCCGATTACTGGTGGTGGAAATGGATCTCTTAGTACTACTAGTTATTTAGCTAATTC  
 GCATAATATCAGTTATACTAGAGTCAACCATTTAAAGATAACAAACCAACCATCTTCCACAACTAAGGAT  
 AATAATAACCGATAATTGAAATGAAGACCAGAAGTTTTTCCGATTAGCAAAAGAAGCATTAGTAGCT  
 AATTGCCAAGGGAGTTAAGACCANTCATTCCAATAATAATGCTAATTTGCTAATAATACTTTCTAAGAT  
 GATATTAATAATCATAATAAGAAACAACAACAACAAATAATGATGGTAATGAAACCATACTTTGATTCTACA  
 ACTGCAGATTTATTAACAGATTACAATATGCTAGTCTCTCATGGTAATCCCATTTGGCCAAATAAGT  
 GGACTTCAAACATAATTTCTAAAGGATTAATTTGAAGTACAGATCAATACTCTAATTTCCCTCATTTACAA  
 AACAATAATTTTTCAAAGTTAATAATGGTGATAATAATAATACTAGTAATAGCAAGTTTAAATAATAT  
 TATCATCATCATCAGGTANTGAACCAACATGGAAATTTTTTACTTCATGAAGCATCAACGAAAACAACA  
 TCAAACAATACACGATCAACAGGAACAACAGGAACAGGAATAGGAGCAACAACCAATATAAATACAGAA  
 TCAGAATCGGAATTAAGAGTGAAACGAGANTCAAGTATTGCCAATATAATCAATCCCTCAACAACAACA  
 AATTTCACAACAACATAATAGAATAACAATAACACTTCATCATCTACTAAAACAGAAAATATTCTCAA  
 GATCCACAAGAAAATTTCCCTTGTGATAAATGTCCTCATGTCATTTTCGTCGATCATCAGATTTAAACCT  
 CACCAAAAACAACATTTAATATCTCCACCTAATATTTGTCAATTTTGTGGTAAAGGTTTGTCTAGAAAA  
 GACGCTTTTAAAAAGACATATTGGGACTTTACATGTAAGAAATGCTGTAAGAAATTTATATATTGAA  
 AATTTAAATTAATTAATAATTTCAAGTCAAGTGAATGATGATGAAGAGGAGGAGGATGAAGAAAGAA  
 GAAGGATTGGAACAGGATAGATTGTATAAGAAGAGGAGGAAGAGTAATAATAATAATCAAAATTAATTA  
 GAAGAAGGATTTGAACATAATCATCAGGATGATGATGATGATCAAGAGGATGAAGTGAAACGAGAAATTA  
 CAACTTATGGATATCAACAGAATTGA

YDR253C\_homolog 583aa (SEQ ID NO 412)

MQNTNRNMSN5SKNNSDNHHQCCQRCRCQOVDQYQSITL PPLQYQSNTHESIVLP5QQPKRGRSEHFN5  
 QFQRNINSREVLUPSSRDNNNTTNIPIPIILPSSNNSNNPITSSNSRMPSNPNVSPLYPVVTPPSSAL  
 SPPTQHHQCCQQLHKKFKTSNSGSNTPTGGGIGSPSTTSYIANSANTSYTHSQPLKDNNTQTSSTTKU  
 NNNTIENEDQKFFRLAKEALVATARKVKTNHSNNNGKFGMNTSKIDINNNHKNMNMKSDGNETILNST  
 IADLLRRLQYASAPHGNPIGQISGLQTN5KGLLEVQDEYSNFPOLQNNNFKVDNIGDNNNTSN5KFSNN  
 YHHPSCNEPCWNPFLDEASTKTT5NKT5STGTTGTGIGATTNI5SESE5ELKVKRESSIANI5NPSTTA  
 TSIT5NNNNNTSSSTKTRKYSQDPTKRFPCDKCPMSFRSSDLKRHEKQHLTIP5NICQPCGKGFARK  
 DALRHHIGTLTCKRNADKKLYIENLKYLN5SQDDDEEEDEEE55GL5QDRLYKKRKSNNNNQ5IK  
 EECFEHNDDEDEDEDEDEVEKREFPTYGYQQN

YDR276C\_homolog 516bp public: 1..516 (SEQ ID NO 413)

ATGTCGTTATGTCCTTTCCGATTTATTTCTTATTATTTCTTCAGTATTATTCCTACCATTAACCTGTTGG  
 ATTAGAAGAGGATGTTGTTTCATGTGATTCAATTAATTAATATTGCCCTATGTAATGTTAGGATACCTTCCA  
 GGGTTAATTCATTTCATGGTATATAATAGCTAAATATTCTCTTATTTATTATCAACAACAACAACAACA  
 CCTAAAGATACCATTTATTATGCTTTATTCGAAGTGATTTAGAAATCAAAACACCAAGAGAGATGCCAGA  
 GATGGGAGAGATGAATGTCATCATGACCACCACCACCACCATCATCATCATCACAACACAGGCAGAAATCA  
 CAAAGTGCGGATTAATAGTTTCTAAACAATCATAATAATAATAATAATAATAATAATAATAATAATAATA

135/251

GGTTCAATCATCATCGAATTTGACTCCCTGTGGCTCCTATTCCCTGTTGAAAATGGAGCTCCACUACUAGUT  
TATACTGAGATTGATAATAAAACACAACATTAA

YDR276C\_homolog 171aa (SEQ ID NO 414)

MCLCLSDLFLIILSVLPPLPVWIRFGCCSCDSLINIALCMLCYFFGLIHSWYIIAKYSSYYVQQQQQQ  
RKDTIYYVYRSDLENQTPRPDGRDGRDECHDHHHHHHHHHQQABESQSAGLTVSNHNNNNNNNYGSSVVE  
GSSSSNLTPVAPTPVENGAPPAYTEIDNKTQH

YEL039C\_homolog 333bp public: 1..333 (SEQ ID NO 415)

ATGCCAGCTCCATTTGAAAAAGGTTCAAAAAGAAAGGTGCCACTTTATTTAAAACCTAGATGCTTACAA  
TGTACACACCGTTGAAAAAGGTGGTCCACACAAAAGTTGGTCCAAATTTGCATGCTGTTTTCGGTAGAAAA  
TCCGGTTTAGCTGAAGGTTATTCTTATACTGATGCTAACAAAGAAAGAGGTTGTTGAATGGACTGAACAA  
ACCATGAGTGATTATTTGGAAAATCCAAAGAAATATATTCCAGGTACTAAAATGGCTTTTGGTGGTTTA  
AAGAAACCAAGGACACAAAACGATTTAGTTACTTATTTGAAGAAAGCTACTTCTCTAA

YEL039C\_homolog 110aa (SEQ ID NO 416)

MPAPFEKXSEKKGATLFKTRCLQCHTVEKGGPHEKVGPNLHGVFGRKSGLABGYSYTDANKKKGVEMTEQ  
TMSDYIEMPKKYIPGTRMAFGSLKKPKDRNDIAPYILKKAIS

YER112W\_homolog 321bp public: 1..321 (SEQ ID NO 417)

ATGTCAGCAGGTATTCCAGTAAGACTTCTAAATGAAGCACAAAGGTCATATAATATCAATAGAATTGATA  
AATCGAGATACATACCGTGGGAAGCTATTGAAATGCAACATTAATATGAATTTATCCCTATACGAGGCA  
ACTATAACACAAGGCAAAATCGGGGAAAGTAAGTCATATGGACCAAGTGTTTATAAGAGGGTCAATGATT  
AGATTTATATCTGTGCCCTGATATTTTAAAGAAATGCTOCTATGTTTTTTATGAAACCTGGAGATAAACCA  
AAACCTCCAATAAGGGGGCCCTCCACCAAAAAGAAAGAGAGTATGA

YER112W\_homolog 106aa (SEQ ID NO 418)

MSAGIPVRLINEAQGHIIISIELINGDTYRGKLLENEONMNLSLYEATITQGKSGKVSHMUQVFLRGSMI  
RFISVPDILKNAPMFFMKPGDKPKPPIRGPPPKRKRIV

YFR010W\_homolog 1239bp public: 1..1239 (SEQ ID NO 419)

ATGGTTTTTAGGCACTCCAGACAAGAATTGCGCTTCAAAAGCCAGTTGAAAAACAAGTTTTTCTCGAAGAT  
TTGAATAAAAAATCAATTGGTTAAAGTTAGTAATGAACCTAGTGGGTTGACCAATTTAGGGGAACACTTGT  
TACTTGAAGCTCAAGTTTACAAACATATTTCCATATTTGATGATGTGAATAACAGGCTTGAAAGATTTACACT  
TTTTGGTGGAGCCAATCAAGCCAATAGTGCCTTTGTGTTGTTCATTGAAAAGTATGTTCCAGCAATATGTCG  
AAAAACAAGAAGTTATAACTCCTTCTACATTTTCTTTCTCTTTTTCAGAGAAGATCTTATCCTCAATTTGCT  
GAACAACAAAATGGTATTTTATAAACAACAAGACCGCTGAAGAAGCATTTTCCCAAAATTTTGAAGCTCTTGT  
AGAAGCGAATTGAAAATAGATGATGTGTTCAAATTTACATTTTACACCAAGACTCAATCCTTGGCTATG  
CCAGAAGATGTCACAGAAGGGTTTGAAGAAGCATATAAAATGGAATGTCATATCGCGCTCAAGACCAAT  
TTTTTTGAGAGATGGATTGTTGGCTGGATTAAAGAAACGATTGAAAAACATAAATTCACATTTTGAATGCT  
GATACTGAGTATCAAAACAACCAAGACCATAACTAGATTACCAAAATACTTTTACAGTACATTTTATTAGA  
TTTTTCTGGAACAGGAGACATCAATAAGAAATCCAAGATTTTGAAGAAAGGTTCAATTCOCATTTGAATTA  
GATTTAGCAGAAATGTTGGATGTATCAATTAAGGCAGATAAAGTTTCCATAGAGATACATTTAGAAAA  
GTTGAAAAAGATAAATTTGGATATGATAAGAGATTTTCAAAAAGACCATAAATACACACCAGTTTAAACACCA  
TTGGAACAACAAGAGGAGGATGAGATGAAAATAACATCAATCAAGAGTAAGTTTAAAGACGACTTGAAT  
AGCGCTTTGCCCAACGTTGATTTTACACACCACCACAGAAAACCTTCTAGTGTGTATGAATTAACGCA  
GTCATTACTCATGCTCGATCATCTGCCGATGCTGCTCATTATAAAGCAATACGTCAAGGATCCACAGAC  
TTGGATGGCGAGAGATGGTGGTTATTTAACCAGTATAAGGTGAGCTCCGTAAACAAGAAAAACATCGAA  
ACTTTAGCTGGCGGTGGTGAAGCGGACTCAGCTTTATTATTGATTTTACAAAGGCTTAGGGCTTAC

YFR010W\_homolog 412aa (SEQ ID NO 420)

MVLGTFDKNLPSKPVKQVFLEDLNNQLVKVSNPSGLTNLGNFCYLNSSLQFIHLLDDVNNRLKDYT  
FGCANQANSFVLSLKSMFQQMSKKQEVITPSTFLSLPFRSYTPQFAEQQNGIYKQQDAEEAFSGQLLSL  
RSELKIDDVFKITFNTKTQCLAIPEVDTEGFEEAYKLNCHIGVKTNFLRDGLLAGLKETTEKHNSTINA  
LNEYELTKTTERLPKYLIVILRFPWKRDLNKKSKILRKVQFPFELDLAEMLDVSIKADKVSNRDITRK  
VEKDNIDMIRDPKRTKNEFSITPLRQQEENFMKCTSTKSKFKDLENLALPNVDNMTTENPSSVYELNA  
VITHAGSSADGGHYKAYVKDPTDLDGERWLFNDOKVSSVNKEIETIACCGESDSATMLIYKGLGL

YFR052W\_homolog 834bp public: 1..834 (SEQ ID NO 421)

ATGTCCTTTACAAAACTCACTGCAGAAATATACTCACTATTTCCGAAAAGCAGATTATCAAGGTTGCCAA  
CAATTACTTGGTCCGATTAAACTAGAATTAGTCAACACATGATTTGTTGGTTTACCTTCAACACAC



136/251

ACCGATAAAAACCAATTAAATGATTTTGAAGATTGCCCAAGAATTTTGGGAATTGGAGCATTATCGTCA  
 TTATTAACCAACAACATATCCGGTTTTCAGAAATTATTTTGGTCAGTTGAGACCATTTTACTCTAAACCC  
 AAATTACATAATTTACAAAAAGTCCATATCAATACCGGATATAACAAAAATCATTTCATTATACCTTGTTA  
 TACTTGTTGAGTCAGGGTTTGAATTCAAAAATCCATGTTGAACTAGAAGTGATTTATAATTCATCACAA  
 TATGATGCCCAACAAGACAGTATTTACAATTTCCAATAAATTTAGAAAACCAATTTAATGGAAAGGTAAT  
 TACA/AAAAATCTGGAAGTTATTAAAAGAAGAGAAAAACTTACCATGTCAGAATAACACCCATTTTGT  
 GATACTTTGATAAATGCTTTACGTTTGGAAATTCGCAATCTTTGGAGAAAACCTACGATTGCAATCCA  
 ATTTCTAATTCGAAGAATTTATTATATTTACCACAAGAAATTTGCCGATGCTAACTTTGAGAAAACTTTA  
 AAGGAAACTTTATCAAGTTGATAATTCGAAATTCGAGGATGGAGTTATATATTTCACTAAGAATGAAAT  
 GAAACCAATGTTGATAACCAATCGGTTATAAGAATTTATTAGGGTACGCTGAACAAATCGAATCCATC  
 GTATAA

YFR052W\_homolog 277aa (SEQ ID NO 422)

MSLQKLTAETYSLFGKGDYQGCQQLAPIKLELVKHDHLLVPLPSNTTDKNQINDIRIAQRILEIGALSS  
 LLTNNYSGFENYFAQLRPFYSNPKLHNQKVHINTDITKIISLYLLYLLSQGLISKFHVELEVIYNSQ  
 YDAQQDKYLQFPINLESNLMEGNYIKIWKLLKEEKNLPCQETHTFVDTLINALRPETAKSLEKTYDSIP  
 TSNCKNLIVYFQELSDANFEKTLKETVQVENWKPFEDGVTVFTKNEKETNVDNQSVTKNLLGYAEQLESI  
 V

YGL080W\_homolog 354bp public: 1..354 (SEQ ID NO 423)

ATGTCATCATTTAAAAAATTCACGATTTTATTTTTCAAAAACAATCCCTTAGATATGCTCTGTACAAC  
 CATTTTGGGGTCCAGTATCAAAATTTGGGAATTCCTATAGCTGCTATTTTAGATTTGAAAAAGATCCT  
 GATTTAATTAGTGGACCAATGACTGGTTCATTAA/ACTTTATTTCTTTAGTGTTTATGAGGTCATTCAAATG  
 GCAGTTACTCCTCAAAATTATTTATTATTTGGGTGTCAATTTTGTTAATGAATGGCACAATTCAGTCAA  
 GGATTTAGATGGGTTAAACATCACTATGATACCTCTTCAAATGATGGTGAAGATACCAAAAAGATAACT  
 CAAAATTGA

YGL080W\_homolog 117aa (SEQ ID NO 424)

MSSEKKFTDFLF3KQSLRYVCTTHFWGPFVSNFGIPIAAILDLKKDFDLISGFMTGSLILYSLVFMRYSM  
 AVTFQNYLLFGCHFVNELAQLSQGFRWVKHHYDTSSTNGSDTKKTTQN

YGR070W\_homolog 4146bp public: 1..4146 (SEQ ID NO 425)

ATGTCGAGTAATAGTTCTTGGTCTAACCAACGATCTTTACCAACTGAGGAACAAATCCTAATAA/CGTAAT  
 AACCATAACCCACATTTAATGTACACAACAACACTACCAATCTGTAATATTTCTTCTCATTTTGTTCCT  
 CAAGCATTTATAGAACAAACAACAACCAACCACCAACCACAACAATATCCGCAAGACGGCCAA  
 GCTCATAACAAAAACCCACCAATCAATANTCGTTTTCATCAATCACAAACCACCA/CAACTGGCGCATCAA  
 TACATCCCATCCAAACAAGAACAAATGCAACAACCTTACCCAACTGCCGAACAAAA/AAATCAACACTCT  
 CCTCCACCACAGGAACATCATATAGTTTTTCATGCACTATCGATCCTGGCTCAGCTAGCAAAATGAUG  
 CCACCTAATTTTTTCACAAAGGAACCAATCATTTTCTGGCTACCAACAACCAACCAACCAACAACAC  
 TATCCGCACTCACCCATAAGGCATATAACCAACAACCCCACTCAACCAAGGTGGAC/TTCAACAGCCA  
 TACATTTGGCCNAACACAAAACTGGCCACCTGGATATATTAACCAAGATCCATATTTCCAGCAAAATAGA  
 TCAGTATCATCTTTGACTCAAGATAGGACAGGAGCACCAGTACAACACCTTTCCTTATCCTGTCAACAA  
 GATGATCCTGGATATCAACTACAACCACTGGCAATTCATTAACACCAACCAACCAACAACAACAACA  
 CAACAGCTTCCACTCCAGACACGTAGACAACCTTCGTAAAGGCCCTTCGAGCAACTTGGCCCCAAT/UA  
 ACTGATCAAGTTTACTATAGCCCTGATGCTAGAGAATTTGTTCCACACCTTACACACCACCAAGAACTT  
 CCCACTCCCATACCACCAAGCTAGAACAAATCACTTACTTCCGCATCAT/AAAACACCAAGAAACAA  
 CCACCTGCAACCTCTCCAACCATATTTCCAACAAATCTCTGAAC/CGCCAGGTAAAGACAGCAACGCTCC  
 AATCCCTCCAGCAGTTCCCTTCATCATACATTTTCCCTTAACCTCAAAATCGCGATCATTTACATCTATC  
 AGCAAAATTGCTGCTCTTCACTCAACTAAGAAATTCGGTTCCTCT/UAATCGGTCAATACCAACAAATTAGAT  
 CGTTATCAATCCAGTGGAACTATTAGAAACAATCAAAATCATTAACCAACCAACCAACCAACTAGCCACAAC  
 ATTCAATTATGCTAAACCACTCAGTATATCCCGCAATTTTATCTGAAGTCCCAAAATTCCTTAAAGAGGCC  
 ATCATTTTGAAGATCAACACCAAGGATGGTTTGGAAATACCATCA/ATTTTACUUGGAAAAATGGCAGCT  
 CATATATTTATCTCCCATTTATTCGAACAATGATCGTAACTTGGCCTTGTTATGGGAAGATCATTAGAC  
 GCTCAGAAGTTTTCATGATGTTACTTACAATCATAGATTAAGGGATTCGGTACATGAATTTATGCC  
 TTTAACAATGCTTATAATGAATTCGATTTTTCACCAAGAAAAATGGAGGAGCTGGTCTGGTTAGCAAT  
 GGGGAAAAATAGTGCATTAATTTCCAACATGGGTCTTTCTTTGATAGCAGCACACAGTTACAGAAATGCT  
 TTCAATGACCAATATCCGATTATCATACCTCACAAAGCACTGGATCATTAACATAAAATTCCTAGTAGT  
 GCCACTGGTAATGGTTCAGTAGCTGCTGGTTAAGGAGTTGAGTGC/CAAGTCAACCAACAGGTGTTAAT  
 GGAGTTTTCACAAATTTTACAGAATGTTATTCGCCCAAC/CTAGCAGAAATAGTCTTTTGTTAACAGTATT  
 GCTGTCCAAAGAAGATTAGAGCAACAACCTAGATTAAATTTGAAACCTCAGGTTGGTTTGCAACGTGCT  
 GTTTCAAAATTTATCAATTCATGATCAGGAAGAAACCGAAACTTTATGGCACAAGACTGTACCTCAATCA  
 GTTTTAGATAAATTAGACAAGCATGAAGAAGACTCGACAAGAATTGA/TTTAAGAATTTGTTTATACTGAA  
 CGTGACTACCTCAAGATTTTGAATTTATGACTGATTTCTACATTA/CGCCCTACGAAATCCTGCCAA

AGATTATGCTCCGTTATGACCAAGGAGGACATTTATTCAGACTGTGTTTTCGGGAGTTGCCGATTGTTG  
AGATTGGCCGAAGAGACTCAGTGAAGCATTCTAACCTCGAAGACAACAACAAAGGCCCGCTTATTGAGACC  
ATTGCTGATGTATTTTATGATTATGTTGGTGATTTTTGAACCTCTTTGTGACATATCTCGGAAATAAAGTGT  
TTTGCTACTTTTGAACATGAAGACCAACACAGTTATATGAAATATGCTAGATTCTTAGATGCCAATT  
GAAAAGAAACCAGAATTGAGAAGACAAGATTTATCATCTTTTTTAATTAAAGGGGTTCAAAGACCAGCA  
AGATAACAGTTATTGTTATCGGGTATTTTGAACAATACCAAGCCAGAGTCAACCCGACTACAAGTATTTT  
ACGAAGACCAAAAGAGAGATTGAGAAATTTATGGTGAAAATCAATATCCAAACTGGGGAATGTACTGAT  
CGACACAAAGTCATGGTTTTCATAGCTTTATTTGGGCAAAACAAATTTGGAATAATGGCTTTAATTTCAA  
TTATCTTACAATAATCGTATTATCTATCAAGTGCATTTGTAATAGAAAGAGGGGATACGAAAAAATTGAT  
TTATACTTTGTTTGAACATGCGTTGTTATTAGTGAACACACAGATTCAAAACAAGCGTGAACAACATAAA  
GTATTTGAAAAACCAATGTATTTACCATTGTTATTGTCAATAGTGGTATGGAGATCCCCACATAATAGA  
ACAATCATGGCTCATAGATACCATGGATCTTTGGTATCTGATACTAGTATAAGACCTCAAACAGCAGAA  
TCTAATTATATTGCTAATACTTTGAATCTTCTTCATCAACACCTAAATTTCAATTGAATTTTTCGGGTTA  
CGTAGTAAATCAAGTTACAGCGCTCATTTATTTGCTGATGACTTGCATTTCAAGAACCAAGTGTGCTGCAA  
ATATCGGCUUUAACAGAAAGAAATTAATCGATGCTAATTCACACTTTTTTCATTGTTGTAATTTGAAACGAGA  
AGATTCACTGGGAATAATAAAATCAACTGTCGCTGTCTCTGTTATGGTGGGAGAAATTTCTGTATGTT  
ACTGATTCAGGGGATGCGGTTAGTACTGTTGTTCAATTAGTGCCACATCTAATGAAAAATCTGTAGT  
GATCCCACTATGTCATTTTCCAAAACCTATGTTCACTCAAAATGAACTGATTTTGAATTTTGAATCTTCTG  
TTAGTATTGAGTGACAAATCATTTATACCTATGTTCACTTTATCTTTGATTTGAGTATCTGATGAG  
AATACCAAACCTGGGAAATTTGCTTTTGAGTCACTGTGTCATTTTCAAAGTTTGGTFTTTGTGAATGGGAAA  
TTGCTAGTGAATGGTGCTAGAACACCGTACTCTGCATTCAAATTTGTATATTTGAGCCTGTTAATCCATT  
GATAAATCGAAATGAAGAAATGAAGAACAAAGAGATTAGAAATCAAGAAATTAATTTACGTTCTGATCCAAAT  
TCCATCTCAATTTTGAAGACATAACTCTGTTATTTGGGCTGCTCAAAGGTTTTCGAAATTTTATCTCTTCTCAA  
ACAGGAACCAAAAGATCGATTTTGGATGAGCAGCACCTTCAATAGATTTTTCGAACACAAAGAGAAAGT  
GTGACACCACTTAGCAATTCATCGATTAGGAGCGGATTTCTTTATTTGTTTATTCTGAATTTTGTATTTT  
ATCAATCGAAATTCATGCGACAACAAATCATGATTTGGGGATATTTTGGGAGGTAATCCACAAATGTT  
GUGATTTTCTTCCTTACTTTGCTATCAATTTGAACCTGATTTGTTGAATTAGAGATTTGCATACAACT  
AATTTTATTAAGAGCTTTTAAACGGGAGAGAAATATTAGATTTTTCATTGCAACGAACATGAAGCTATGTTT  
CCTTCTGAAGAAAATGGATATGATATTTATTTCCATTGATTTCTTGAATTTGAAACCAAGTCTCCA  
ACATAA

YGR070w\_homolog\_1381aa(SEQ ID NO 426)  
 MSSNSSWSNNDSYQSRNNPNNGNNHNPHLMSQQIISQSVNIPSHLLPQAFTRQQQQPPQPQPQQYPQDGO  
 AHNKNPPIINRFHQSQPPQSRHOYIPSKQEQMQQPYPTAKCNQNHFFPPQERSYSZPSTMDPGSPSKMT  
 PPNFSQRNQSGFCYQYQPPPPQQQQYPCSPHKAYNQQTHTHGGGLQQPYIAQPNMPPGYINQNFYSQQN  
 SVSSLTQDRGTAFVQHLPIPVNNNDDEFGYQLQPSAIQSHHPFQQQQQQPPQLQTRRLKAPSSNLPPIQ  
 TDQVYYSFDARRIVSTPIHQNNFPTPEARTKSLTSASLKHQKQSPQSPYVQQLSESPGKDSNAR  
 NSSSSSLHHTFSLTSKSRSTSTSKTSSLSTKTKFGSSSSSVNTNKLDRYQSSGTIRNNHNNHNTNQTSN  
 LHYAKPSVYPALLSEVAKLFKEAIICTNTKDGLEYHDTFTGKMAVDILCRITNTDRNLALNIGRSLD  
 AQKPHHDTYNNHRLRDSVIEIYALNNVYNDVDFNENNGGAGSVSNGENSALNSKHGSLDSSTQLQNA  
 LNDHISDYHTSQSSGSIKTXASSAANGNSVGVAGKELASQCTGVNGVFTILTCEYSPTCRSNLSLCYSI  
 ACPRLREQQARLNLKPQCGLQRAVSKLSLHDQETETLWKEITVPQSVGLDKLKDKEHTRQQLBELIYEFVYE  
 RDYVKOLEFMTDFYIMPLKNPANNLFPYQRTSIQTVFGGVDLLRLAKRLSEALTRQQQQKPKVIEI  
 ICDVFLDYVGDPEPFTVYSGNKVFAFTEHERQQQVNMKYARFLDALEKKPESHKQDLSSFLIKGVORPA  
 RYQLLLSGILKFTKPESPDYKYLTAKKEETELKLVKINIQTCECTDRHKVMVIFRLLGKQTLNRFNFK  
 LSYNNRLLYQVTLNRKRONEKIDELYLFEIALLLVKKHIQMKRQHKVFEKPMYLLPFVNSGMETPTNR  
 TIMPHRYHGSLSVSDTSIRPQAESNYIGTNLNSSSSTFKPQLNFFGLGSNQVHASL/ADDITIONQVLSQ  
 ISAQQKLLIDANDIFSLCAKFETRRFGNNKINCAVPCYGGKLLYGTDSQVWVSTVRSISATSEKIES  
 DPTMVISKTYVITQLEVVEYSKLLVLSDKSLYEFDLSDTDSLHVKNTKSGKLLLSHVSPFKVGVCDGK  
 LLVIGARTGSSHSICTFEPVNPFDKSNVKNRKRLEIQEINPSSDPISTISFLTKLKCIGCAKGFELSSQ  
 TGTKESSILDEADPSLDFATQRESVTPLAIZHLGRDPLLCYSKVFVLINRMGWRNTNHDWGIFWEGNPQNV  
 AIFFPYLLSFEPEGFVETLDIITTNLLRALTGEMIRFLASNEHEAMFACEENGVDIIISIDFTNLKPKSP  
 T

YGR132C\_homolog 956bp public: 1..956(SQ ID NO 427)  
 ATGCTCATTTATTGACACCAAAATAAATTCTTCACCTTATTATTTCCTTTCTTTCTTCAAGACAAC  
 ACAGTTTCCTTCCCTCTGCTACTGCTAAACGTCCTAATCAACACTATGTCCACAACGAATTGCAGATTTT  
 GTTCTATAAAATAGCCTTGCCAGCTGGTAATCAACCAATTGCATTGGCACAATCAGCCTTGTATGATGTTCC  
 GGGGGTAAGCGTGCCAGTTATATTTGACCGTTTAAAGGGGGTCAAACAGCGAGTTATTGGCGAAGGTAAC  
 CACTTTTGTGCTGCCATGGTTTACAAAAGGCGAGTATATTTCATGTTTAGAGTTGAACCCACGAGTAATTA  
 ACCATTACAGGATCTAAGGATTATACAGAACTTTTCATATGACATTTGAGGTTGTTGAGTAGACCCGAA  
 AGAAATTTGCCCTACTATTACCAAACCTTGGGGTTTGGATTACCGGGAAGGGTGTGTTGCCCTCCATTC  
 AATGAAATTTTGAATTCATTTGTGGCACAACTTTGATGCTGCTGAATTGATCCACCCAGAGAGAGGTTT

138/251

TCTGCCAGAATAAGACAAAGAGTTGTCAAGAAGAGCGCGCAGAGTTCATATAGCAATTGGCAAGATGTCTCG  
ATTACACATATGACATTTCTAGAGAGTTACCAAAAGCCGTGGAAAAGAAAACAAITGCACAAACAGAT  
GCAGAAAGATCAAGATTCTTGTGGAGAGAGCAGAACAGGAAAAGAAGGCTGCCGATTATCAGAGCTGAA  
GGGGAGGCTGAATCAGCAGACGTTGTTTCCAAAGCGGTTCGCCAAAGCTGGCGATGGGTTATTGATGATC  
AGAAAGATTGGAGGCATCAAAAGACATTGCATCAACATTGGCCAACTCACCAAATATCACTTATTTACCT  
AATCTTGGCGCTGGCGGCAGCGATAGCCAGCGGTCCAAAACCTCATTATTGTTGAATATTXGCGGTTAA

YGR132C\_homolog 321aa (SEQ ID NO 428)

MLCIDTKIISSPFFSFSFPPKTSVSSPSLSLNVQSNMTMSQRIADFVSKIALPAGITIALAQSALYDVP  
GGKRAVIFDRLKGVKQGVIGEGTHFLVPWLQKAVIFDVRVVEPRVITTTTGSKDLQNVSLTLRVLSRPLV  
RKLFTLYQTLGLDYGERVLPALIGNEJLKSIVAQFDAARIITQREVVSAIRQELSRRAAEFNIEIFDVS  
ITHTFTGREFTKAVEKKQIAQQDAERSKFLVERAEQEKKAATIRAEGEAESADVVSALAKAGDGLLMI  
RRLAASKDIASTLANSPNITYLPNGCAGGSDSDGSKNSLLLNIGR

YGR135W\_homolog 756bp public: 1..756 (SEQ ID NO 429)

ATGTCAAACAAGATACGATTCAAGAACCCTATTTTTTCCACAGCAAGCTAGATTATACCAAGTGGAAATAT  
GCTCAAGAAGCCATATCCAATGCTGGTACAGCCATAGGGATATTATCTCTCGAAGGTGTCTGTTTTAGCG  
TGTCAAAAGAAAGTCACCTCCAAGTTATTGGACGATGATGGATCAGCTGAAAAATTATACATTATCAAC  
GATCAAAATGATTTGGCGTGTTCGCTGGTATGACTGCCGATGCATCAATTTCTCTGAATAATGCAAGAATT  
CAAGCCCCAACAGTATTTGAAGTTGTACGACGAAGACATTCTCTCTCAAATCTTGATCAATCGTGTTCGT  
GATGTCAAAACAAGGTTATACCCAAACATGGTGGGTGGAGACCATTTGGTGTAGTTTCTCTTATGCCGGG  
TATGATGACAGATATCAATTCOAATTGTTTACATCGAATCTTCTCTGTAATTACAGTGGTTCCGAAGGCA  
ACTAGTATTGGTGCTAACAATTTCTGCTGCTCAAACTTTATTGAAGAAAGATTACAAGGACGATTTGACT  
TTAAAAGATGCGATGCCAAATTGGCTATCAAGGTTTTATCAAAACATATGGATGCTTCAAAACATAAATAGT  
GAAAAATTAGAATTGCTACCTTAACTTTCGCCAAAGACAACAAGTGTGTCATAAAATTTGGAACGAT  
AAAGATATTGACATCTTAATTAAGGCTTCGGGGGTTCGAAACGAAAAAATAGCGATGATGAATAG

YGR135W\_homolog 251aa (SEQ ID NO 430)

MSRRYDSRTTIFSPDRLYQVEYAQEAISNAGTAIGILSPEGVVLACEKKVTSKLLDDDGSAEKLYIIN  
DQMLCAVAGMTACASILWMNARIQAQOYLKLYDEEIPCEMLINRVCEVXQGYTQHGGLRPFVGSFLYAG  
YDDRYQFQLFTSNFSGNYSGWKAISICANNAAQTLKKDYKDDLTLKDACELAIKVLSKTMDASNINS  
EKLEFATLSLGLKDNKVLHKIWNOKDIDILIKASGVLNEKNSDDE

YGR155W\_homolog 1491bp public: 1..1491 (SEQ ID NO 431)

ATGACATCTACAAACAAACCACAGCCTTAAAAGAAGATATTTAGAACTTATTGGTAATACTCCATTAA  
GTCAAATTGAACAAAATTCACAAATCGTTGGGAATTAAAGCCAAGCTCTATGCCAAAGTTGAATTATTC  
AATGCCCGGAGGATCAATTAAAGATACAAATTGCCAAAATATGGTATTGGAGCCGAAAAACAAGTTAA  
ATCAAAACCAGGCTATACTTTGATTGAACCAACCTCAGGTAACTACTGGTATTGGTTTGGCTTTGGTTGGT  
GCCGTTTCGTGGATACAGAACCATCATTAACCTTACCACAAAAAATGTCAAAACGAAAAACTTTCTGTTTTG  
AAACCTTTAGGTGCTGAAATCATTAGAACTCCAACTGAAGCTGCATGGGACTCTCCACAATCTCATATP  
GGTGTGGCTAAAAATTCGAAAAAGAAATACCAAACTCTATTATTTGGACCAATATGGTAATCCCGACC  
AAGCCGATGCTCATATTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG  
TTGGTTTGTGGTGGTGGTACCTGGTACCATCACTGGTATTTCCAAATACTTGAAGAAAAAAATTCT  
AAGATTCACTTTACTGGTGTGACCCAAAAGGTTCTATTTTAGCTGAACCAGAACTTTTAAATAATTCC  
ACCGAAGGTTACTTGGTTGAAGGTAATGGTTATGATTTTATTCAGATGTGTTGAACAGAAAAATATGTT  
GATGATTGGATCAAAACAGATGATGCTGAATCTTTAAATTTGGCTAGAACAAATTATTAGACAAACACCT  
ATTTTGGTGGTGGTTCCTCTGTTCTGCTTAAAGCTGCTTTTAAAGTACCTTAAAGACTTACTGAA  
GACGATACCTGCTGTTGTTGTTTTCCTCAGATTCATCAGATCTTACTTGTCTAAATTTGCCGATGACGAA  
TGGTTAATCTCCAATGGATTGAAAGTTGAAGATTCACCGGCTCTTAAACAGGCTGACGAATTTCTTGAAT  
GGTAAGACTATCAAGGATTTGGTTGCTGGCAAGCTCCAGTTGCTCACTGTCACTTTATCTGACACAGTT  
GCCAAGACTTTTGATTTATTGCAATCCAATGGGTTTGATCAATTTGCCAGTTTTCGAATAACTCTGCAAGA  
TTAGTTGGTTTGATCACTTATCCAAGATATTGAAATCTTTATCCACTAAAAAGATTCAAAACGACCAT  
TCAATCACTTCGATCATCATTTGATTTCAAGAACTTGGCTGATTTTGAATAACTTTTCAACCATCAATA  
AAATCAGGATTCACTAAGAGCAAGTTATGAACCAATCAAGTTGGACACCCCCATTAGCTGCTTTGAATAAA  
TTCTTTGAACCAATTCAAATGCTATAATCAGAGATGATGAATTTGAACCAAGTTCAATTTGTTACTAAG  
GTCGATTTGCTTTCCTATTGACTAAAAACCTACTTTTAA

YGR155W\_homolog 496aa (SEQ ID NO 432)

MTSCNKPFAI KFDJLELTGWTPLVKLNKIQSLGIKAKVYAKVELEFNACGSIKDRIAKNMVLEAEKQCK  
TKPCYTLIEFTSGNTGIGLALVGAVRGYRTIITLPEKMSNEKVSVLKALGAEIIRTPTEAAWDSPESHI  
GVAKKLEKEIIPNSIILDQYCNPNPNDAHXYSTGYEITWEQTEGKITHLVAGAGTGGTITCTSKYLKEKNS  
KIHVTGADFPGSILAEPESLNNSITPGYVREGIRYDPIPDVLNRKYVDWIKTDDAESFKLARRIIREEG  
ILVGGSSGSAALQALQVAKDLTSDDFVWVFPDSTRSYLSKPADDEWLTSGGFEVEDSPGANKADEFLN

139/251

GKTIKDLVAGKAFVVTVTLSDTVAKTFELLLQSNQFDQLPVLNNSGRLVGLITLSKILKSLSTKKIQPTN  
SISIIIDFRKLADFEKSEFTITKKSGFTKRSYEFIKLDTPLAALNKFFETNSNAIITDDELKVFQIVTK  
VDITSYLTKNASF

YHR138C\_homolog 384bp public: 1..384 (SEQ ID NO 433)  
ATGAATCAAAATAAGAAATTAACCTGGTCTTAAATATTATTAGCGATTATATCAATCATTACTTTATTCAAC  
TTTAAACAATTTCCCAATAACTGCCATCAGATCATTGTCTCCCTGCCCTCTCCACCGCTACTAAT  
ACTAATACTAAATCAACAATGTCAGATTCCAAAGGTTACATTATCACTTTGAAAGATACTTGTGCTGAT  
TCCGAAGCTAGTTCAATTAATCAAGATTACTGAATTGGGAGGTAAGATCACTAATGAATTTAGTTTA  
ATCAAGCATTTTCTGCTCAATTGCCAATATCCATGCTGAAGCTTTACCTAAAGATTTTGTCTGGTATT  
GCCAATATTGAAGAAGATGCTGAAGTTCTGTACACAATAA

YHR138C\_homolog 127aa (SEQ ID NO 434)  
MNQNKKLTLGLILLAIISITLFPNFKTISQITAIRSFVSPASSTATNTNTKSTMSDSKGYIITLKDTCAD  
SEASSLRKSLTELGGKLTNEFSLLIKGPSAQLPTTHAEALPKDFAGTANTFERDGRVRTQ

YHR179W\_homolog 1212bp public: 1..1212 (SEQ ID NO 435)  
ATGACCAATCGATAACGAAGGCATTTGTCATTAACCATTTGGGTTCAACAAAATTATTCCACCAATAAAAA  
CTTGGTTTTAACACTTTATCACAAGAATAGCATTGTGCACCATCCACACGTTATAGAGCAACCAAAGAT  
AATATCCCTACCGATTTCATTTAGAGTATTATTCTCAACGATCAGAATATCCTGGAACTTTAATCATT  
ACTGAAGCAACTTATACATCACGTCAGGTTGGATTAGTACCATAIGTCTCTGGGATTTATAATGATGCT  
CAAACTAAAAGTTGGAAGAAAATTAATGATCGGATTTCATGCCAATGGAAGTTTCAGTTCACTTCAATTG  
TGGTATTTAGCTAGAGTTGCTAATCCTAAAATTTGAAAGATGCTGGATTACCATTGTGTTGGAGCCTCA  
TCAGTTTATTTGGAATGAAGAAAAGTGAAAAATTTGGCCAAAGAAGCTGGAATGAATTGAGGGAATTGACA  
GAAGAAGAGATCCATCACATTGTTGAAGTTGAATATCCGAATGCTGCTAAACGTGCCATTGAAGCAGGA  
TTTGATTATATCGAAGTGCATTACCTTCATGGTTACTTGTAGACUAACTTTTAAATCTTGCCTCTAAT  
AAAAGAACCTGATAAAATATGGTTTGTGGTAGTATTGAAAATCGTGCTCGTTTATTATTAAGAATTATTGAT  
AAATTGATTGATATAGTTGGAGCTGAAAGATTAGCTATCCGTTTATCACCATGGGCCACGTTCCAAAAT  
GTTGACCTCGAAGGAGAGAAAATTCATAGTTATATCATTTGATCAATTACAAGAAAGGGCAAATTTCTGCT  
AATGAATTAGCGTATATTTCTCTTGTGTAACCAAGCTGTTCAAGCAAGTTGGGATATTGCTAAAGAGAAT  
CAAGTTGGCTCAAATGAATTTATTTTGAACATTGGAAGGGGAAAGTAATTAGAGCAGCTACTTATGCT  
CATGAATTAATAAATAATTAATGAAGATATTAATAATGATAGAACTTTAATTCCTTTTCAAGATTTTTC  
ATTTCTAATCCTGATTTAGTGAAAAAATPACATGATGGGATTTCTTTGACTCCTTATGAAAGAGCAACA  
TTTATATATCATGATAATTTTGGATATAATCTTGGATTAATATGAGAGAAAATAAAGTTTTCAATCAA  
CAAGAAGAAAGGAAAAAATTTGGGTAAACCTTTAGCTTAG

YHR179W\_homolog 403aa (SEQ ID NO 436)  
MTIDNEGIVIKPLGSTKLFQPIKLGFNFLSQRIAPSTRYRATKDNTPDLQLEVYSQRSEYPGTLII  
TEATYTSROGLVPYVPGIYNDAQTKSWKKINDAIVHANGSFSSVOLWYLGRVANPKNLKADGLPFGAS  
SVVWNEESKLAKEAGNELRELTEELDHIVEYEPYMAAKRAIEAGFTYIEVHSANHOYLLDQPLNLASN  
KRTDKYVCGGSIENRRLRLRLIIDKLIDIVGAERLAIRLSPWATFQNVVEGEEIHSYIIDQLQERANAG  
NELAYISLVEPRVQASWDIAKENQVGSNEFLKHWKQKVIKAGIYAHENLNKINEDINNDRCLIAFSRFF  
ISNPDTAKKTHDGTSTPYERATFYNHDMFGYNFTWIKYGENKVFNEQEERKKLGLKPLA

YIL074C\_homolog 1392bp public: 1..1392 (SEQ ID NO 437)  
ATGTCATCTCCTCAACAAATGTCAACTCATTCCAACAAGCCTTCGAATTTATCAACCATCTCCAAAATGCT  
GTTTCTACATCACCAACTCAATCATTTCTTGAGTCAATATGTTCCAAGCAAGCCAGCTAAAGCTTTGAAA  
CCTTTTCAAAAACCTGGTGAATATCAAAAATTTTATTTATTTGGAAAATGTTAACCAAAATGCCAATAAAATTTTC  
AAAAACCAAGGTTACCAAGTTGAATTTTATAAATCATCATTAACCCGAAGATGAATTATTAGAGAAAATCC  
AAAGATGTTTCATGCCATTGCTATTAGATCAAGAGCAATAATTAACAGAAAAAATCCTTAAGCTGCTAAA  
AACCTTGGTGGTGAATTTGGTGTGTTCTCTGTAATGGTACCAATCAAGTTGATTTGGAATTTGCTGCCAAATCA  
GGTATCGCTGTGTTTTCAACTCTCCATTTTCAATTTCAAGATCAGTTGCTGATTTAGTCACTTGGTGAAGCC  
ATTACTTTGGCTAGACAAATGGGTGATCGTTCAATCGAATTTGCACACTGGTACTTGGAAATAAGTCAGT  
GCCAAATGTTGGGAAATCAGAGGTAAACCTTTGGGTATTGTAGGTTATGGTTCACATTGGTTCCCAATTA  
TCCTGCTTTGGCTGAAGCTATGGGTATGAATGTTATCTATTATGATGTCATGACCATTATGCTCTTAGGT  
AATCTGAAACATGTTCAAACTTTGGACGAATTTGTTGAAAAAAGCCGATTTCTTACTTTGCACGTCCTCA  
GCTACTCCAGAAACCAAGAACTTTGAGTGTCTCCAGAAATTTGCCGCTATGAAAGATGGTGCCTACGTT  
ATAAATGCTTTCTAGAGGTAATGTTGTTGATATGCCAGCTTTTCTTTCAAGGUCATGAAAGCCGGAATAAT  
GCTGGTGCCGCTTTAGATGTTTACCTTCATGAACCAGCAAGAAATGGTGAAGGTTTATTCAGTGATAGT  
TTGAATGAATGGGCCAGTGAATTTGTTTCAATTGAGAAATGTGATTTTCACTCCACACATTGGTGGTTCTT  
ACCGAAGAAGCCCAATCTGCTATTGGTATTGAAGTTGGTAATTTAATTGAACCAATACATCAACGAAGGT  
GCCTCTCAAGGTGCTGTIARCTCCCAAGATTTCTATTGAGACCATTAGACTTGGATCAACAAAATGTT

140/251

GTCAGAGTATATATATATCCATCAAAAACGTTCTCTGCTGTGTTGAAAACGTCACAATATCTTATCCAAAT  
CATAACATTCAGAAACAATTTCTCCGATTCTCAAGGTGATATTGCTTACTTAATGCCCCATATTTCCTGAT  
GTTCGATATUAGOGATATACAGTCATTATATGAACAATTAGAACAACCTCCATATAAAATTCCTACTCGT  
TTGTTGTATTAA

YIL074C\_homolog 453aa (SEQ ID NO 438)

MSSPQQIVNSFQQALNLSGSPNAVSTSPQSFLSQYVPSKFAKALKKFFKTGDIKILLLENVNOTAINIF  
KNQGYQVEFYKSSLPEDELLEKIKDVHAIGIRSKTELTEKILKAANKLVVIGCFICIGTNQVDLEFAAKS  
GIADVNSPFSNSRSVAELVIAEIIITLARQLGDRSIELHTGTWNKVSAKCWEIRCKTLGTVGYGHIGSQL  
SVLAEAMGMNVIYYDVYTIMSLGNSKQVESLDELLKKADFVTLHVPAFTPETKNLLSAPQFAAMKDGAYV  
INASRCTVVDIPALVQAMKAGKTAGAALDVYPHPAPKNGEGLFSDSLNEWASELCSLRNVILTFPHIGGS  
TERRAQSAIGLEVGNLSLTKYINEGASQGAIVNFPEVSLRPLDLDDQONVVRVLYIHQNVPCVLKTFVNNILSN  
HNIEKQFSDSQGDIAYLMADISDVDISDIOSLYBOLEQTPYKLAIRLLY

YIR037W\_homolog 436bp public: 1..486 (SEQ ID NO 439)

ATGTCTCAATTTTACGAATTAGCTCCAAAAGACGCCAAGGTGAACCATATCCATTTGAACAATTGAAA  
GGGAAAGTTTCTCTTATCCTCAATCTTCTTCCAAAATGTGGATTCACTCCTCAATACAAGGGTTTAGAA  
GAATIGAATAAGAAAATTTGCTTGATCAACCAAGTACAAATCTTGGGTTCCTCATGTAATCAATTTGGCCAC  
CAAGAACCAGGTAGTAACGAAGAAATTGGATCATTCTGTTCATTGAACCTACGGTGTACATTCCTCACTC  
TTCCGATAAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAAATATTGTGAATACAAAAAGAGT  
GGTGTTTTCGGGATTGACCAGAATTAAATGGAATTTTGAAAAATTCCTTGATTGACCAAAATGCTAAAGTT  
ATTGAAAGATTCAAGTTCATTGACTAGTCCAGAAAGTATCGGTACCAAGATTGAAGAATTGTTGAAGAAA  
TAA

YIR037W\_homolog 151aa (SEQ ID NO 440)

MSQFYELAPKDAKGRPYPPRQIKGKVVVTVNVAASKGGFTTQYKGLEELNKKFADQPVQILGFPCNQFGH  
QEPGCSNEELGSGFCSLNYGVTFPVLDKIEVNGDNTDPVYKYLKSQKSCVLGLTRTKWNPFKFLIDQNGKV  
IERFSSSLTSPESIGTKIEZLLKK

YJR096W\_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTTCATATCGATTAAATCAAACTCAATTCUGGTUATACCATTCCATCAATTGGATTAGGATGTTATGAT  
ATCCCAAGAAATAAAAACGGTTTCCGGTAGTTTATGAAGCTTGTAAAGTTGGATATCGTCATTTTGATAC  
GCAGTGTATATGGAAACGAAGAAGAAGTCATTGAAGGTATAAGTAAATCTTACCAGAGAACCCCAAT  
ATACCAGGATCTGAGTTTCTTTTACACCACAAAGCTTTGGGAATTAATCAATTTGGGTACTTCAAGCACTAAA  
CAAGCCATTTCAACAATGATGGCTCAAGTTGGTGCATAAATTACAATATATTGATTTATTTATTGATTCA  
TCTCCATTACCAGGTAAGACCAAAACGTTTAGAAAGCTGGAAAGTTTTCGAGGATGCTGTGGAAAAAGGA  
TGGATTAAAAACATTGGGGTTTCTAATTATGGTAAACATCATATNGAAGAATTGTTGACCAATGCAACG  
ATCCCTCCAGCTGTCAATCAAAATTGAAATTAGTCTCTTGGTGTATGAGACAGCAATTTAGCTTACTTGGTGT  
TTAAGTAAAGGTATCAATGTTGAGGCATATGCACCATTAACCCATCGCTAACAAATTACAAGTCAACAAT  
ACTGAATTTCAAGAAATTATGCAAAAGTATAATAAATCAGCTGCTCAAAATATNGATTAAATGGTCACTTA  
CAAAAAGGTTATATACCATTACCAAAAACAAAACCTCCATCTCGATTAAAGGAAAATCTTTCTGTTCAT  
GATTTTGAATTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATCAACCAACAGATTGG  
GAATGTACTGATGCTCCATAG

YJR096W\_homolog 232aa (SEQ ID NO 442)

MSYRLIKLNSGHTTPSTGLGCDIPRNKTVEVVYEACKVGYRHPDTAVLYGNEEEVLEGISKFLRENFN  
IPRSEFFYTTKLWNNQLGTSSTKQAISTMMAQVGDKLEYIDLILIHSPLEFKTKRIEHWKVLQDAVEKG  
WIKNIGVSNYKGKHIEELLFNATIPPAVNQIEISPWCMPQDLATWCLSKGINVEAYAPLTHGNKLQVNN  
TEFQETMQKYNKSAAQILIKWSLQKGYIPLPKTKTPSRLEKNLSVDDFELTNEEIKAIQDPDAYEFTDW  
ECTDAP

YKL196C\_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATGAAGATTTATTACATTTCCTATTTTAAAGATCAACTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA  
GATTTATCACAGTTTTCTCTTTTCGAAAGAAATGGGGTATCCCAATTCATGACTTTTTCGCGAGAAACC  
GATCCCAAGAACTCAACCTGGACAGAGACAAGTGTGTAAGAAGGTAATTATATTGGTTCATACTTAT  
ACCAGATCACAAAGGAATTTCTGGTATCATTATACAAGGACAAAGATTACCCGTGAAGACCAAGCATATACA  
TTAATAAATAAAATCTTTGGAAGAATATTTATCATTTGCATCCTAAATCTGATTGGGAAACATTGATAAA  
GCAATGAAACTTTACAATATGGACAATTAGGAACCATATTTGAAAAATATCAAGATCCCACTCAAGCT  
CATTCATCATGAAACTTCACCAACAATTACATGATACTAAGGTGTGTTTACACAAAACCTATTGAAGGG  
GTTTTACAAAGAGGAGAGAGAAATTAGATTTCATTGGTTGACAAATCAGAAGCATTCCTCAAGTTCTTCAAGA  
ATGTTTTATAAACAAGCAAGAAAGAAACCAATTCCTTTCTGATTATGTGA

YKL196C\_homolog 200aa (SEQ ID NO 444)  
MKIYYIGILRSSGDKALELTSARDLSQFSFFERNGVSQFMFFAETVSQRTPQPGQRQSVVEGNYIGITY  
TRSEGISGLIITDKDYFVRPAYTLINKILIEEYTSHPKSTWRNTDKANEPLQVGQLEAYLKKYQDPTQA  
DSINKVQGEIGETKVLHKTTEGVLORGEKLDLSYDKSEALSSSSRMFYKQAKKTSNCCVIM

YKRC7SW\_homolog 256aa(SEQ ID NO 446)  
 MNDKQWRFPPTKPELTKLTEDDISLGTPDHNVYDFSLRRELYFKAEPEYEGRFVTPVLWDKKKEGTIVNNE  
 SARIIRMLNTEFPNSILFSEYAEVLDLPVKOLESDIDELNSQITVDNINNGVYKAGFASKQEVYAKEQNVF  
 DILDKVEAITELKCHNGSKKGRFVYIGNQITFEADIRLYTTTIRFDPVYVQHFKCNIGTIRTHYPYIHWLR  
 LLYWKIPGFEQETTKFEHLYKRYTXSHIKINPEYGITELGRVNIIPLEEK

[illegible]

YLR043C\_homolog\_312bp\_public: 1..312 (SEQ ID NO 449)  
 A1GGTTTCACGTTGTCACTGAAGTTAAACGATTCCAAACCCTTTTAAAGCAAAACAACCTTACTTATTCTT  
 CACTTTTTTCCCACTTGGTG1GGTCCATGTAAAATGATTGCTCCATTATTAGAAAAATTCCAAAATGAA  
 TATTCTAATATTAAATTTTTGAAAATTGATGTGATCAATTGGGTTCTTTAGACACAGAATATAA1GTT  
 AGTTCTATGCCAACTTTGATTTTATTCAAAATGGTGAAGAAGTCAATCGTGTCATTGGTGCTAACCCA  
 GCTCCTATTAACAAAGCTTTGGGCTTCTCTTGCTCAAA

142/251

YLR343C\_homolog 103aa (SEQ ID NO 450)

MVHVVTVEVNEFQTLLENLVIVDFPFWCGPCKMIAPLLEKFNQNEYSNIKFLKIDVDQLGSLAQEYINV  
 SSMPPTITLTKNGEPVNRVIGANPAATKQATASIA

YMR273C\_homolog 4938bp public: 1..4938 (SEQ ID NO 451)

ATGTCACTGCCCCAACACGGTCAATCCCATAGUGAATTCAAAATTTTGAATCAGCTGTACAAGATCTTGAAACAA  
 GAGAAGAAAATGGTGGCAGCCCTTAAAGAGACTATCTATAGGTCATATGATGCCAATATGATCCCGACTTG  
 CCAACCAGGCAGTATGGATGATATTGATCCCTTTGCCAAACAATAACAACAACAGCAATACCGCTAGTAAC  
 AATAACCACTATAATGGTCATACCAGAGATCACACCAGCAACAACAACAATACACACAATCATTCCTCC  
 AACTCAAAATTTGAACCAACATCGTGGTCAAAGTCCTTATGATGAAGATTTAATTCACACAATATCCAC  
 AGATCACACTCAACTCGATCAGCATCAAAATCAGATTCAACTTCTCCTTCTACTTCGCTTCAACACAAAG  
 CAACAACAACAACAACAACCGCAACCTTTTCCACATGAACCAACAGACTCCCTCCATATAACAATTCACCA  
 AGCCCACTCAAGAGACGTAGTTTTTACGACAAATTCACGCTGTGTGACCTCAGAAGTCACGATATTTTT  
 TTCCGATGCCGAGGATGAAGTTTATGATAGTTTCATCCCTTTGTGTGGGTACCAGCTAACCTCTCATCCT  
 CAAGTGAATCCTGAATCGTTCAAGAGTTTAAATCAAAATCAAGTGAAGAGATATTGGAAAGAAAGCTA  
 TCTCGAAAGTCAACTATTTCAAGAAAGTCAACTTTTATCACCGCACTCCCTCAACCAAGTACUAAAGAGACA  
 TTAGCCCCAGAACCCAGAAATAGTCCAGAACTGGAAATGTGATGTGTACCTCCTTCTCCAGTAAGAAATA  
 TCTTCCCTTGTCTTCGTCTCAACAACAATCAAAATGAAGACGTTTCTCGAAATCGTCTCTCTCTCTCT  
 TCTTCAACTTCTCCACAAGAGATCCAGCTAAGAGAGAAATCTTGGTACCTTCAACCACTCAAAAAGATAC  
 CTGAATCCATCATTTCCACAGCTAACTTTCAGAAATGGAGCAGTTGTCAAAATGGCGGGGATGGACAAG  
 AATGACGCGAGTAACCTTTGGCAAGAACTTTGTGGCCACAATCACTGGGGTATACAGATGTCCAAAAAATA  
 GCAATTTGACGAATTAGATAGTTTCACTAACCAACCCCTACTGCAACAACACCCCAATTCACCTGGGTCTCCA  
 GGAAGTTATGACTCTGCAAAAUUACCTCGCAACCAAGACCTTGCAATTTACAACAACGATTAACAACATCAA  
 TTTCAACAAGCTCAAAATCAAGGCAGAAAGGGAGGCAGAAAGATCGACAAGACATCAACAAGGCAACAA  
 CAGTGGCCAGTATCGAATGACGATAGTCAAAATCTCTGTACAGTTTACAGCAAGTGAAGGAGCTTCT  
 ACTGCTAATGCTTTTACCAGTGTCTCCAGTGGTGTGACTTTTCCCTTGAACCGAAGTAGAAGAACTGAT  
 TACCGGAAAAAGGAAACAGATTGGAACAACAAGACTTTTCAAAATATTCGCTCTTACAACAAGTACAAT  
 GTCCGGAATTCACAGTTGTATTTAACTACAAGAAACCCAGTAGATTCTCTCTCTCTCTCTCTCTCTCTCT  
 TCACCATCTACATCTCAAAGCATGATGGGTACAGGGGTGAACACAAGAAATCTCAAAGCCATTGGAA  
 GCAGCAATTCGCTTAUUUUAATGATGGATGGTTCAAGATATTTACATAAACCCGTATCCCCACCTTCAACC  
 ACTATTGATTTTCACTGCTATGGGTGCTAAGAAATCAGCCAGACAAATCACTTACCTTCCAGAGAATGCAATG  
 GATGGCAGATCTCGAACAAGCCCAAAACAGACTCATCTGTGCTATCTGCATCAAGAAAGGTCTCAAT  
 CCTTATCATCAACAACCACAGCCTCAAGTGCACCTTCAAAACCCGCCAACCACTTCCACCAGCACAACAA  
 GCTCATAGACAAATCGACGAGACAAACCCACAATCATCCGAGCACAGGAGTTGAAAGGCAATCACCGACAG  
 GATAACAAGCGTGTAAATGCTGTACAGCTTTCTAAATACAGACATAAATGATTTTATGCTCAACTGAATCAA  
 TTTTCAAGACTAATGCAACAAGAAACCAATCGATATGACAACCTCCUATAAAAAGGATAAGACTCCATTTTGTG  
 CCAATGAAGACCAACCAAGCTAAGTCCCATTCGACAAGAAATTCAAATGTAAGAAATTTGTCTTCTCTCTG  
 TCTCAACAGCAATTTACATCAACCCGTATCTGACAACTTCTGTGTGCGCCCAAGTCAAGTCAACTACATCAA  
 AATTTAGACAAGTTGAGATCCGAGATCAATGAATTTAAGGAAAGCTTGAATTAATCGGAATTACCTGGT  
 GAGGAATCAAAAGAGAACACACACACTGCGTCAAGACCAAGCACCACCAACAACGACAAAGCAGCAGCA  
 TCACAGCAACCAACTTGAGCCTCGCAATTTACAACTCAATAGCACCCTCACCAAGCAACAGCATGAACA  
 GTACAACCCCAACAAGTCCAGCCCCTTACAGTCAAGATACTAGTTTGTGATATCAGTTATTAAGATTTTACG  
 GTTCAAGATCAATTTGGTATTGAACAGGAAGCATTTGAGAGAAATAGGCAAGGAAAGGCGCATTTCTCAT  
 GAGATTGATATAGATGAATGATTTTGTGATGAATTTTAAATTTCTGCTTATCAATGAACGACATGGCTCT  
 CAATTCACACTTGTATCATGACATTTTGGACAGCTTTAATTTGGTGAATTAATCAGTTGGTGTGATCTGCA  
 GATGAAGGAATTTGATAATTTTCAAGGCTAAGAAATGAATATCCCTTGGGCGACAACAACCAACAACAA  
 CGTCAACAACCAAGAGCTGCTTCCGCCCATCTCTCACAGCAGTACTTGGGCGCATGATCAATTGCACCTTG  
 CAACAAGGTAAAGATACAAATAAAAAAGTTGGTCTCTGTTTAAGTATTGATACATTTGCAGAACAAGCC  
 ATTCACCCCTGACGAAACCTGCAACTGGATTTGGAAATGAATGCTTACCTTCCCTTACCTTGCATTTAGAT  
 GAATCTCAAAATAGCACTCTCTGGACATCTGAGAAAGGCAAGCAATTTCTGCAAGCTACGACGATTACTAT  
 AATATAGCTGACAAATCATCTACTGCGGGTACCCCCAAAACAAGAGAGACCAAGCTTAAACCGAA  
 TATCTCAATTAAGACCCCTAATTTGGAGATTAATAGACTCTGATAACTATAAGGAACAAAATGGUATTTGAG  
 ACATCTAACAATAAAAAATTTGAAABGAAGAATCTTTTGGTTTCTCTTAGTACAAACATCATCTGTGGGA  
 GCAAAATGATACATTTGAAATTAAGGCGCCCAAGAAATTTGAAABGAAGAAAGTCTGTGGGCTCTGTGCGG  
 GAGCCTTCTGCCAGTGCCTCTGCTGTCAGATATCAACAAATTTCCCGCTTTGCTCTTTGATAAACTACCT  
 ACAAGATCATTTCTCAATTCGGAAACCTCAACCTGACCAACACCCAGAAACATGATCTTGAGAACCGTTCA  
 GATCTTGAACGTTGAATTTGGAACACCAACCTTGAATTTGAATTTGAGTTGGAGCTGCTCTTGAATTTGA  
 TACGAGCAACCAAGAAAGCAACCAAGATGCTTCAATTTGGTAAATGATTTCAAGCTTTTGAATTTGATCT  
 TCTATGAACTCCACAGACAAAGGAAPACCTGTCTTTCCAAATTTTTCAGAAAAAAGCAAAAGGTACCGG  
 CCAAGCTCACAGTCAATTTTTCAATTTGAATCAAAAGCTTCAGGCGCCAGCTGTGACTATGAATCCGAC  
 AACGACCGCAAACTGATCAAAAGAAAGGGCAACAATAGCAAGCAAGTTTCAAGAAAGAAATCAAGGSCC  
 AATTTGTGAGAACAAACAAATTCAGTGAATTAAGGAAAGCTTCGACCTTTGAATTTTGTGTCAACCGAA  
 TCGCAGACGATCGAAGGAAAGAGAAATTTGUGACAAACTAATCCCACTCGTAAGGCAGAAAGAGCTGAG

143/251

AGTCAAGAGCAACAGGAGGAACAGTTCCTGTAACTCGTCCGGATACATCAATTCAACATTGAACA  
 UTCAACACGACTTTCTCACTCTTTGGGGAGAAAGACGATGTTTATAGATTCTCCTACTGATGACTTGGGTT  
 GAAGATGTAAAGATCTCGTAACATTCAGAGCACAAATAGTTATTTGTTGATGAGGATGAAACTTCTATTTCAA  
 AATAACAATGATAACAAGATTGTTGGGGATGCTAAAAAGTTGACGAATTGTCCAAAAAGAAATCAATTAGC  
 AGGMAAAACGGAAACAATATCCAAAAGAAAGAACCTTTCTACTGAACCTTACTGATACAAACAAAGAGGTA  
 GTAGAGGAGGTTCTTGCACCTGAGCAAAGTGTCAAACCAAGCCAAAGGGGAAGATCTTTTGTCTA/CAAT  
 GAAGATAAAGAGAAATTAGATATCCAAGAAAAGTTGAAGAAATCAAT/AAAACGTACATCAAGGGCCAC  
 CAGCCTATTGAGTTTACTGATTACAGCCTTTTGGGTTCCCTTGCCACCACCATCTCAATCAACTTTAGTG  
 ATGCTTGACTACAGATTTCCAGTTCACTGTGAGCGTCCCATTTATAGA/TGT/CACACTTGAAACTTGCT  
 AACCTTAAGCGTTCACTAAGAGAGCAAGTTTTGT/TTGTGAAATTTTATGSTATGCCACCTCAACTTAGTT  
 GATCATACATTACATTTAGAGCAACAAAATATGAGCAAGTAGGATGGCGATCAGATGGAACCTGACGAC  
 GACGACAAAGAAGAAATGACTGACACTGATGACAAAGACATGATTTTTGACACAGTAATATTGCCGAT  
 GAGGATGATCTTATTCCTGAAGAAGCAATGGTGATTGCGATTGGGATTAACCTTAGATATGCGATCTTTA  
 CATAGGAAACAGCATCAT/CAATCTGGAA/CGAAGTAT/AG

YMR273C\_homolog 1645aa (SEQ ID NO 452)

MSSPNTSFHSDSNFESAVQLEQEKKNVAALKRLSLGHMMQYDFDLPPGSMDDIDPFANNNNNNSNTASN  
 NNHYNGHTRDHTSNNNNTHNHSNPSKINHHRGQSPYDEDLTPQNIHRSHSTRSRFSKSHSTSPSTSPQHK  
 QQQQQPQPFPFHEPQTPFPYKSPSPVKRSPYDNSVLTSESHDIP/DAEDEVYDSSSPLLWV/PANSHP  
 QVNPESFKSLIKTOVEEILERKLSRKSTISRKSTLSRSSSTSTKETLAPEPEISPESECDVSPSPSVRK  
 SSLSSSSQQNQNEVDVSRKSSSVSSTSPQKPAKRESWYFNNSKRYSNP/SLRELTSLEBQ/SLK/MAGMDK  
 NDAVTLARTLSAQSLCYTDVEKLAFCLELSSQMTATATT/NS/SGSPG/YSANFPRTTTLHLQQRLQHQ  
 FQQAQ/IKAREALERS/THQC/SEQQ/PVSN/DSHK/SSQLT/ASEGGSTANA/TSAGSGADPALKRSRR/TD  
 YRKKETDSKQKTSNNS/P/TKY/NVRNSQLL/FNYKK/PVDS/SSSPSPSPST/SQSMGHRV/KHKKSQK/PLE  
 AALANPHMDGSDMSHNPYPTASTTILFSRMGA/KKSARQ/SLSPEN/AMDCR/SRTK/PENK/THRCY/SHQFRSII  
 PYHOOP/POPOVOPOTR/QQLPPAQQA/HQSTRQ/THNHPSTG/VEKHHRQ/DUNKR/MSSAS/NIDIND/MAQSNQ  
 FQTNGTNRNHRYNLHKKDKTAF/LPNE/NIQRKSHSTRNS/NVRNLS/SSSQ/HLIQ/PYST/TSVAPKSRQLHQ  
 NLDKLRSEINEFKESLNKSELPGEE/SKREHRSR/HQHHQ/RQRP/APSQ/HQL/PRMY/NHND/RHQ/ROQ/EEH  
 VQPOQVQ/PLQSD/TSFD/LSYQDLS/VEDQLG/IEQ/ALRELGKEK/HSHEID/DADFDENL/KXSP/INER/HS  
 QFTLDH/DILDSFNLVDNQLVGS/AD/EGID/MLKGK/NEIPVGR/QQ/PQQ/RQ/PRAAS/P/SSQOYLGH/DELHL  
 QQGKDTNKKVGPRLSID/TLCKP/PIHPEETATGFG/MNALP/STLH/LESQNSTP/GHSR/KASNS/ASYD/NY  
 NIADRSS/TA/TFK/TKETKVK/TKLFN/KUPN/LEIDSDNY/KEK/IGIETS/NNEKL/KKKKSP/GLLSTTSSVG  
 AND/PS/NEG/P/KK/KKKKSWG/LRERSAS/ASSAD/INNL/P/LELDKLP/TSR/STNP/ETSTD/QI/QK/HD/ENG  
 DLERELEHEFELELELES/DELFDYEQQR/KHQD/ASMV/NDSS/FAVD/SISMK/STDKEN/VLSK/P/KK/KA/KV/G  
 SSSQSVF/SFESK/SGSASVDYES/DNDAK/SIKK/KGNSSR/LFKKK/RAK/SEQ/NSV/NKEK/LRPLN/LVSNE  
 SQTIEEKENL/RQ/SNGTR/KAE/RVES/QEQ/EEQ/FPVT/SSP/HLQ/FNIE/HLK/D/VP/LG/KD/VD/LD/SGT/D/LV  
 EDVRSRNIQ/STIV/IVDE/DETP/IQ/NN/NK/DL/MLK/VDEL/SKKK/SISR/KK/RNM/MQ/K/NLSTEL/TDTN/REV  
 VEEVLATEQ/SVK/PSQ/EDLL/SKNECKE/KLDIQEKL/KKSIKRTSRANOPIE/FTDS/AFGF/PLPP/SQ/STLV  
 MLDYRFPVH/VERATYR/LSH/KLAN/PK/SLRE/QVLLSNFMYAYL/NLVD/HTL/SL/EPQ/NMS/SEDGTQ/MER/D  
 DEEBENTDT/DEKDM/IFGES/NIADDE/ELIPEE/AN/CDS/ICIN/LDM/DGLHR/KQ/HQ/SGTEV

YNL112W\_homolog 1332bp public: 1..1332(SEQ ID NO 453)

ATGTCATACAATAACCGAGGATATAATAATAGAAACCGAGGTAGTTACGGTGGAGGCTACCCCCCTGGT  
 GGTAGCAGAGGTGGAAGAGATGGCTACAGTGGTGGTGGCAGAGGCGGTGCTACGGTGGTGGTGATAGA  
 GATCAAGCTGGATACAGAGGTGGAAGATTCAAGTGGTGGTGGCCGTGGTGGTGGTAGATT/TAAT/GAT/TCCT  
 CCAAGACAAGAAATTAATGCTTCUACAATGGGATTTAGAACAAATTCGCAAAATTTCAAAAAAATTTCTAT  
 TCAGAACATCCAGATGTTGCTGCCAGATCTGATAGAGACATTGAACAAATTTAGAAAAGAAAATGAAACG  
 ACAGTTAAAGGTCATCATATCCCTCATCCAAATCACCACCTTTTGATGAAGCTGGTTTCCAGATTATGCTT  
 TTACAAGAAGTCAAAGATCAAGGTTTCCCTAAACCAACTCCTATT/CAGTGTCAAGGTTGGCCPATGGCT  
 TTTGAGTGGTAGGAGATATGAT/TTGGTATTGCGCGCCACTGGTTCCGCTAAAACCTTTATCTTAT/TTGT/TTACCA  
 TCATTTGTTCATATTAATGCTCAACCCACAATTACAATATGGTGTATGCTTCCAAATTCCTTTTGGT/TTTAGCA  
 CCAACAAGAGAATTTGGCACTGCAAAATCAAACCTGAATGTTCCAAATTTGGTAAATCATCAAGAATTAGA  
 AACACTTGTGT/TTATGCTGTGTCACCAAAAAGGTTCC/TTCAAATTTAGAGATTTAGCCAGAGGGGTTGAAAT  
 TGGATTTGCCACTTCAGGACATTAATTCATATGTTTGAAGCTGCTAAAPCTAATTTGAAAGAGAGTCACT  
 TATTTGGTTTTAGATGAAGCTGATAGAAATGTTAGATATGGGTTTGAACCACAAAATTAGAAAAATTTGCT  
 GAT/CAAATTAGAAC/TTGAT/CTCAAAC/TTTGATGTGGTCTGCTACTTGGCCAAAAGAGGTGCAACAAATTC  
 ACTAGAGATTATTTGAACGATCCTATTCAAGTCACCATTTGGTTCA/TTGGAATTTGGCTGCT/TTCT/CA/TACT  
 ATTACTCAATTTGCTTCAACTCAITTCATCAATTTTCCAAAGAGAGATAGATTAGT/TAACATTTGGAAATCC  
 GCTTAAATGAAAAAGATAACAAAATATTGGTTTTTTGCTTCTAC/TA/TAAGAACTTGTGATGAATCAACC  
 ACTTATTTAAGATCAGATGGTTGGCCAGCATTAGCCATT/CATGGT/GATAAAGAGCAAAATGAAGAGAC  
 TGGGTTTTAGATGAATTCAGAAAGGCTAA/AACTTCTATTATGTTTCCAACTGACGTTGCTGCTAGAGGT  
 ATTGGTATGTATAATTTTAA



144/251

YNL112W\_homolog 443aa (SEQ ID NO 454)  
 MSYNNCGYNNRNGGSYGGGYGGGGSRGGRDGYSGGGRGGGYGGGDRDQGGYRGGRFSGGGRGGGRFNDA  
 PRQELTAQWDLQLPKFEXMFYSEHPDVAARSDRDIEQFRKENEMTVKGHDIPHPITCTFDEAGFPDYV  
 LQEVKDQGFPPKFTPTCCQGWPMALSGRDMIGIAATSGSKTLSYCLPSIVHINAQPOLQYGDGPVILVLA  
 PTRELAVQIQTECSKFGKSSRIIRNTCVYGGAPKGPQIRDLARCVELCIATPGRLIDMLEAGKTNLKRVT  
 YLVLEADRMMLDMGFEPQIRKIVDQIRPDQTLNWSATWPKEVQQITREYLNDFIQVTCGSLLELAASHT  
 ITQLVEVIDEFKRDRLVKHLESALNBKDNKILVFAS TKRTCEITTYLRS DGWTPALAHGDK EQNERD  
 WVLDEFKKGKTSINVAEDVAARGIGMYNF

YOL151W\_homolog 1032bp public: 1..1032 (SEQ ID NO 455)  
 ATGTCAACACCAATTACTGTTATTGTTTCTGGAGCCACAGGATTTATTGCTCAACACCGTTGTTAAACAA  
 TTATTAGCTAAAAACTATCAAGTCATTGGTACAGTTAGATCAACAGCCAAAGGTGATCATTTATTAAAA  
 TTATTCAACAATCCACAAAACCTTATCTTATGAAATTTGTTGAAGATGTTGGAACATAAAGGTGCTTTGAT  
 AAAGTATTACAAAAACATGGAGAAGCAAAAGTGTTCCTTACATTTAGCTTCAACCATTCCTATTAAATGTC  
 ACTGATGTTGAAAAAGAATTGTTATTGCTGCTGCTGTTGATGGTACTAAAAATGTATTACAACCAATTTAT  
 AATTTTGGTAACAACTATGAAAAAGTGGTTATCACTTCATCTTATGCTGCCATTAGTACCGCTTCTTAAA  
 GAAGCTGATAAAAAATGCAATTTATTACAGAAAAAGGATTTGGAATGAAATCAGTTGSCAAGATGCTTTACTT  
 AATCCAGTTAATGGATATCGTGGATCCAAAAAATTTGCTGAAAAAGCTGCTTGGGATTTTATAAAAACT  
 AATGATAAGGTTAAAACTTTCATTGTCGACAAATTAATCCATCATTTGTATTGTTGGTCCACAACTCATTTGGT  
 TCAGAAATTAACAAAAGTTTAAACACTTCTAGTGAAATCATTAAATCTATTTTGAATTTGAAATGAAACCAAT  
 GATTCCAATTCCTTGGCTCAAAAGGAGGTTGGGTTGATGTAAGAGATGTTGCCAAAGCTCATATCATTTGCC  
 TTTGAAAAATGAGGATGCCAAAAATCAAGAATATTTGTTGAATTCAGGTAGATTTACATCTCAATCACTT  
 GTTGATATTATTAATGATAAATTTCCAGATTTGAAAAGGAAAAATACCAGTTGATTAACCAAGGTTTCAGAT  
 AAATCTGTTATTGCTGAAAGTTTGGCTACTATTGATGATACCAAAATCTGTTGAATTTATTAGCATTTCGAA  
 TATTATAACCTTGAACAATCAGTTTATGATACTGTTGAACAAATTTGTTAATGCTCATAGTTTGTA

YOL151W\_homolog 343aa (SEQ ID NO 456)  
 MSTPITVIVSGATGFIAQHVVKQLLAKNYQVIGTVRSTAKGDHLLKLFNNPQNLSYEIVEDVGTGKAFD  
 KVLQKHGEAKVFIHLASPFHFNVTDVEKELIIPAVDTGKNVLIQATYMEGNNTREKVVITSSYAAISTASK  
 EADKNAILTEKDWNEISWQDALLNPNVNGYRGSKKFAEKAAWDFIKSNDNVKPSLSTINPSFVFGPQSFG  
 SEIKQSLNTSSEIINSILKLPND SIPASKGWNVDVRDVAKHIIAPENEDAKNQRIILLNSGRSTSSSL  
 VDIINDKFPDLKGKIPVDEPGSDKSVIAESLATIDDTKSRELLGFVYNLEQSVYDITVEQIVNAHKL

YOR286W\_homolog 546bp public: 1..546 (SEQ ID NO 457)  
 ATGTTTGCATTTAAAAAATCTACTACTTCAATTCCTCAAAACAGTCTCTGCCCCCAACATCATCTCGTTAT  
 TTATCCACCGTCACTAATAAGATCAATCCCAAGAACATTTCCATAATGCCACATAAGTTTCATTATTCAAT  
 GCATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAAATCTCCAGAGGCCAAAGTATATAAATAT  
 GCGGATGTTAAGGATGTGGCCGTACACCGCTGAAAACCAACCGCTGATTCTGTTTTACTGGATGTTAGAGAA  
 CCAACTGAATTTGGAGATGGTCAATATACCAGGAGCTTTGAAATATTCATTAAAAAGTAGTTCUUGGUCBA  
 TTGCTATTGTCACAAAGAAGATTTCCAGAACATTTTGGCATTTCCCTAAACCAAGTACTGATAAAGAACTG  
 ATPTTCTATTGCTCTTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCCAATACTTTTGGTTATAAG  
 AAAAGAGGAAATTATCTTGAAGTTGGGAAGATTTGGGTAAACATGAAAATAAAAGAACTAA

YOR286W\_homolog 181aa (SEQ ID NO 458)  
 MFAPKKSTTSILKTVVAPTSSRYLSTVTLRSLPRTFHINATKVSLEKGLRIITPRPYSVLITSPBAKVYKY  
 ADVKDVAVHPENHPUSVLVUVREPTPEGDCHIPCALNIPPKSSPGATLISREDDFQEHGFPKPSDTKEL  
 IFYCLGGVRSAAEELANTFGYKKRCNYLGSWEDWVKHENKKK

VPL078C\_homolog 702bp public: 1..702 (SEQ ID NO 459)  
 ATGTCCATGATCAACAGAACTGCATTGAGAAGTGCTCGCCCAAGCCATGCCAATGGCTTCCGCTCCAGCC  
 CCAATTGGTTTTCAGATACTGCTCTGCTCCAGCTGACCCAAAAACAAAAGGCCAAATTCUATTCATTGATCCA  
 TTACCACGTAACAACTTATCTATCTAAGACTGGTCTTTTGGCTACTTCAGCCGCTGCTGCCATCTATGGT  
 ATTTCCAATGGATTATTTATCTATACACGATGAACCCATTTTGGCTTGTCACTTTTGCAGTTTTCACAGCT  
 TTGGTCCGCAAAATTCGTTGCTCCCTTTATACACTGAATGGGCCGATGGTGAATCAAAAAAGTCAACGAT  
 ATATTGAATCAATCTAGAACCAACCATATCGAAGCCGTTAACAAGAGAATTGAAACCGCTTTCAGAAATTA  
 AAAACGTTGTTTCAACCACTGAAGATTTCTTTGCTTTATCTAAACAAACCCCTCAATTCGAAGCTGAC  
 TCATTTTGAATTAATAACAAAAATTTGGCTGTTTCTCAGGAAGCTAAATCTGTTTGGACTCTTGGGTAGCA  
 TTTGAACAACAACAAAGACAAATGGAACAAGAACAAATTTGCCAAAGAAGTCATTGATAAAGTTGACAAA  
 GAANTTCTAATCCAAATATCCAAGACAAGATTTGGCTGAATCTCTTAACGAAATCGAAAAATTTGTT  
 GCTAAAAACCTAG

145/251

YPL078C\_homolog 233aa (SEQ ID NO 460)

MSMINRIALRSARPMGMARFPAPIGLRYLSAPADPKQKANSIIDALPGMNLLEKTCVLATSAAAAIYG  
ISNGLFIIHDBTILLVTFASFTALVAKFVAPLYTEWADGEIRKVNIDILNOSRTNIIIEAVNKRIETVSEL  
KNVVATTEDLFLSKETACFTEDSFELKQKLAVSHEAKSVLDSWVRFEQQQRQLFQEQLAKEVIDKVDK  
EIANPKFQDKVLAEISNFTKTFKKN

YPL085W\_homolog 2490bp public: 1..2490 (SEQ ID NO 461)

ATGTTCTCCTTAAAGCTGAAACATGCATTGACCTTAGCTGATTATGGATTGATCAATGAATCACAGAGA  
TATATTGATCATATTAAATCTAGTATCAAGACATTGGGTAAACAAATCACCTTTTGGTCACCGCTAATTTTG  
CTTCATGAGTTTTCAGAAATTGATTATGAGAATCACTGAAGCTGGATCTGGAGATCGATCAAAACAACTGG  
TTTCCCGCTAAGATTAGTCCGACTCAATCTTGATAAGATCTGGGGACAAATTGATAAATTTATTGTTGGT  
GGAGATGAACCTGAAAAATGCTAACAAATAACGATGGTAAATGGAACTGGCAATGCCAAGTCTACTGTTTTC  
AATAAAATTAGCCCCCTCCGTGTUGAGAAATGCATCAAGTGTGAATTTACACAACCTATGTACAACCTTCA  
ATGATTAGGCAACCATCACATTTACCATATCAACCACAACAACACCGCAACCGCAACAGCAATTATTG  
GATCAAGTTCCACATTGAAAGAAAACCTACAACCTGGATTCACCTCCGCAACACCAACCACTTAGTTGGTCA  
CCATCAACGACATCAGTTAATAAATATTCTCCAAGTATTAAATCGAGTCTCTCGTCAAGCACAACTGAAT  
AAGTTTGA AAAATATGCCCCAAGCAACAATTTCATCTCATACAATCTTAGTCTTGTTGAAGAAAGGTCA  
GCTGTTACTAGTGTGATGGTCTGAAATACCTTCACCAACCAACACCAACAGAGTATCAATGCCGTCAACA  
GTTCCCGGTGCCACTTCCACCAACCAACCAACCGCTAAGCACGCCACAACATGTATCTAGGTCTCCACGT  
AGCCATCAACTGCACCAACCAACCAACATTACCACCACTGCATTACATCATGTTCAACAACCATCTGAGA  
GATCCGTCACCAATTAGCGACACCAATCTACCTTTATAGCAATAGTGTGGCGGACAAATTTCTACTACG  
TCAGTGGGTTCCTATTCTTAGTCAAAATACCACTTGTGACAGACTCATGGGAAACAACCTTCTATTTC  
AGTGTAAATTTCTGGAGATAGTATTGCAACAGTTGGTTTAGGAGAACAAAGAGAATGTTTTACCCCCATCA  
ACCGGACAAACAGGGAAAAACCTACAACTGAAGTGAATACAAATGAGGAAGGTTATGGATTTCGCGGT  
CACTATCATCATGATCAACCTGAAACATAACCGGAATCTCCAGAAATTAAGAGGCTTACAAACAACCAAG  
TCCACCTAACCAAGAAATAGTAAAGACATTTCAAAATGATGTAGCATTGGATAGTGCTAAGATAACAGAA  
CCTTCCACAGGAACCAAGAAAGAAACCGAAGCAATCAGGTAATGTGGCAGCTGCTCCACCACCTCTACCT  
GCTCCAGTTTCGACCTCTAGAAAAACAAATCTTCTAGATCTAATCCATATGCTCCATCTACAGATATT  
GGTCTTATCACTAATGCAACCATCAGCAATAGGACAAACACCTAGTGGGAAACCAAGTGTAGAAATCA  
GGAUCAAGAACTAACAGATATGGACCACCAACAGGAGTTGGTAAATAACCAACCACTATTGATGTTTCG  
CCACCTTCCTGCTACTAATAATACTGGTAATGAAGATTCCATTACTATCTTTTCTATGGTGCCTATCAA  
AATGAGTCTAGTCTCTCACTCAACCAACCGTCACAATTTGATCAGACTGCAGTTGCATCTGCCCTGCT  
CCACATCCATTACCAACCAATTTGGCGGTTCACCAAAACAGTTCCAACTAAAAATGTGCGCAATATTGAT  
GATGATTTTGTATGAAATAGTTTAGCAGCTGATACATTAACAACITACAATAAATAATATGGTAAATATA  
CCATATCCACTGTCACTAATGCGGACCACTGTTTGCACCTAATGAGACCTGGATCACTTCTGACACCT  
TTGATTTTAAATCAAGGTTCTGCAAAATATGAATTTATCAAAATCTCAGTACTATTACTGTCACTGGAACT  
GGAGCCGGAAGTCTTACTGCGACTGGTGGAGCATTGATGGATTTCCTATACCAGGATCACTTGATCAA  
ACTACTCGACCAAAATCTATATTGGTGGTCTACTAGAGGATTATTTCTTCAAGATTATCAGAATCA  
CAAAGTGTATTATATCAACAATATGCAATTGCTGATGATACAGTTGGTGTATTATTTCTATTATGGA  
GAAGAT  
CAAGATTTGAT  
GGT  
AAAGTTTATAAAGCTCATTTAGGACAAAAGAACTTTTGTGTTTATGATGAAAAATTGAAACGTTGGATA  
GATTAA

YPL085W\_homolog 829aa (SEQ ID NO 462)

MLSLKLKHALTLADYGLINESQRYIDHINSSIKTIGNKS PFVTPNELLHEFQNLIMRITVVGSGDEONNW  
FSGKISRVLNLDKIWQQIDKFIYGGDESKNGMNDGNGTGNWGGSVFNKFSVSVSRNASSVNLHNYVQPS  
MIRQPSIILPYQFQQQPCFQOQLLDQVHIERKPTTGFTFPQPPPLVGHPSSTSVNKYSPSIKSSPROAQSN  
KFEKYAPSNKSSHHNLSLVEERSAVTSADGPEYPIIHQHQQSINASTVFPVPLPPTFTVSMPOHVSRSR  
SHQSHQPTLPPSHHHVQQPSRDRSPLATRIYPYNSVGGQISTTSVGSIPSQIPLGRQTHICKQPSYS  
SVISGDSIAAVGLGEQLNVLPPSTTCQTKGTATSEVNRNEEGYGFGGHYHHDQPETITESPELRGTQQDQ  
SSEAEISKDTSNDVATDSAKTPEASQRPREFYDSGNVAAAPPPLPAPVAPPRKTKSSRSNMYAPSTDI  
GATSNAPSAIGQTFSGKFSVRKSGSRTRRYGPPPGVGNKQPTIDVSPPSATMNTGNFDSISMF SYGAYQ  
NESSPPLKQPSQFDQTAVASAPAPHPPLQPOLAVFERVPTKTVANIDDSFDENSLAADTLTTYNNMFMK  
PYGSSPMGPTVATNGPGSVTSTPLILNQGSANMKLSNLSTLSVLTGAGTVITGIGGAFDGFPIPGSPDE  
TTRPNSIFGGHTRCLFSSRLSESQSVLYQQYATAADTVGDYIPIMEFEDDEDEDEQAKQKQKKEKEAQE  
QELKRKQEQCCQKAAAKNNNSGGGGGKFFSLPGGGGNKKQDNEAKVYKAHLQKQNTFVYDEKIKFWI  
D

YPL190C\_homolog 396bp public: 1..396(SEQ ID NO 163)  
ATGCCAAGTACAAAAAGATCATCATCTACTGAATACTCCCATAAAGACTCTAAAAAGAAAGTCAAACTA  
GATTATGTAAATCTCAAAACCATCAAAACCTTATATGTCAAAAATCTAAATACCAAAATCAATAAGAAA  
ATTTTATTGCATAATTTGTACCTATTATTTCTGCATTTGGAGATATCATTCTCTATAAATCTACAGAAT  
GGTTTGGCCCTTATAAATATTTAGTAAATTTAAATCTGGCTACATTTGCCGTTTGACAAATTTGAAAAATCAA  
GATTTTTTGCACAAACCACTTGTATTAAATTTATGCTGTCAAGGAATCTAAAGCTATTTCTCAGTAGAAA  
CAAAAATCATACAGATGAAAATGATGAAGAAGTGATGCCACTATGAATAA

YB8112C\_homolog\_3243bp\_public: 1.3243(SEQ ID NO 465)  
ATGTATGCGACACCCCATACAATTAAACAACAACAACAACAACAACAACAATCCACCACCACCTTTA  
AACGGTGGACTACATGCAAGTGGGGCTCCTCCAAATTCCCATGAAGCAGCAGCTATTGCTCAGCAACAA  
CAACAACAGCAGCAACACUACAAATGTCCTGGTATGATTGTTCGCCGAGCTGCAGCTTCTGCTAACCAA  
CAAGCTTCTCCAGCCACACCCCAACAACAACAACAACAACAACAACAACAAGCTTACCTTAGTTCAGCTGCT  
CTAATGAAACTACAGTATCAACTTGGTTAGCCATTGGTTAGCTTAGCCGAGAGTTTAGGTGCACATGTAA  
CGTGGCAGAGCTTCTTACAATTCCGCTTTGAGACATTCACCAAATAAACCAGATATTTTAGTCAAAATA  
GCAAAATACATACCGTTCAAAAGATCAGTTTCTTAAGGCTGCTGAATTGTATGAACAAGCTCTTANTTTC  
CATGTTGAGAAATGGTGAAACTTGGGGATTATTGGSTCATGTCTACTTGATGTTGGATAAATTTGCAAAGA  
GCTTATGCTGCTTATCAACGTCATTCTTTTACCTGGAAAACCTTAACGTTTCCAAAATTTGTGGCACGSA  
ATTGTTATTTTATATGACAGATATGGCTCATTTAGAATATGCTGAAGAAGCTTTGTGAGAGTTTGTGAT  
TTGGATCCAAATTTGACACAAGCCTAATGAATTTATTTCCGTTTAGGGATCATTTATAAGCATCAAGGT  
AAACTACAACCAGCATTAGAATGTTTCCAAATACATTTTGAATAATCCACCACACCCATTAACTCAACCA  
CATCTTTCGTTTCAAAATTTGGTTTCACTGTATGAACAACAAGGATTGGAATGGTGTCTAAGGATGCTTAT  
GAAAAGTGTTCAGATTAATCTTCATCAGCTAAAGTTTTCGAAACAAATGGCATCTCTTATATCCCAA  
CCAGAATCAAAATCCATCAACACCAGCTAATGGTGTCTGCACCCACACATAAGUCATTUAAACAAGATTTC  
ACCATTTGCTTTTAAATATTTTGAACAATCTTTTGGAAAGTTTGATCAAAAGTGATGCTCATTCATGGTACT  
TTGGGTAGAGTAGAAATGATTAGAGGTGATTTCACTGCTGCTTATGAAGCTTTCCAAACAACCTGTCAAT  
CGAGATGCAGAAACCCAACTTTCTGCTGTTCAAATTTGGTGTTTGTACTATCAAAATAAGCCAATATCGT  
GATCATCTGGATGCTTATACAGAGCCATTAGATTTAAATCCTTATATCAGTGAAGTATGGTATGATTGTTG  
GGGACTTTGATGAGACTTGTATATATCAAAATAGTGTGATGCTTGGATGCATATAGACAAGCAGAAGA  
TTGGATCCAAATAATCTCTATATATAGGCAAGATTGAGCAAAATGACAAAGTATCAACAAGAAAGGTAAT  
ACTCACCCACCTCAAAUACCCGCCAAGTTCTCAACAACCTAGATTACCTCAAGGAATGGTTTTTGAAAGT  
ACTCAACAACAACAGUAAACACAAACCACCACCACCTCCACACAACAACAACAACAACCTTCAACACCAA  
CTGCAACTGCAACTCAAACTCAAAACACAGCAACCCACCTCAAAACCAATCACAACCACTGTCTACTTCAACACCAA  
TCTCATTGCTCTCTCAACAATCAAACTTACATCAACAAGCTGCAAAAGCTTTAGTGAATCAAAU  
CAAGGTTCACCAACCACCTCACTTGTATGAACCTTGGGACAAACCGGGGCAACAACAACAACAATTTGCCACCA  
CATCTTCCACCACTATCCAGCAACCTTCTCAAAATCAAGAAAAGCTTCAACTCAAGAAACAACCCAT  
TATCAACACCTCCACCTCCACACACATCAACAGCAATCCGATTCGCCAACCGCAACCTCCACACCAACCT  
CAACACACTCAAAATCAAACTGCTCAATATGCTCAATTTGCCACCAACCTATCTTAATCTCCAGCTAAG  
CCACATGGTGCACCTCAACAAGAAGCTGGTTTACCGGATTTATTAACAACAATCTGCTACTGCTATCATATCA  
GCTCCATCACAACCTACCTCAACCAACAACAACAATTAACAACAACCATATTTGCACCTGTTAGACAAGAA  
CAAGTTAACCATGTCTCTTCAAAATTTATTTGGCTCTTAGACCAACTGAGACAAACCTTCTTCAAAATCAAC  
AACCCAAATGAGTCAACCAACAACAAGTTCCACAACCTCAAAAGCAAGGAACCTTAAACCAAGAGGCTACT  
GTTCTTCTTCCAGTCTCTGAGGCTATTAAGTTCAAGATCAAGTGCACAATTAAGGAGTCAAGCACCAGCA  
GCAGCAGCAGCTGTTCAGCACCAGTTCTGCTCCAGTTGGTGTATATAAAACAGATACCTGTATCTACT  
ACTACACCTGCTACTTCAACCACTGCAGATGCTTGGCCAGTCTGTGTCTCAAGTTGGTGAAGCACCAC  
AATGTTGTTCAAGACAAGAAAGTTCCCGACACCGAGCAGATCGTTTCAACAAGTTGAAAAACCGTGGAG  
TCACAACCAGAAGTTACACCAGCTCCAACACCAGCTCCAGCTCTTGAACAGCACCAACTGAACCTGCA  
CTTACTGATATAGGACGTTGTAATGGCTCCAAGTAAAAGTGCAACACCTGTCTCTCAAAAGTATTGTGCA  
CAGAACAACAGAGTATCTGCAACTCAAAAGCCACCCAGAAATCCAAATGGTAAACATGATTTAGAAGACAAG  
AATGATGAAGAAAAAATTTTAAAGAGGCCAAGCTGTGAACAGCATCTGAATCTGACCAAGTTAAACCA  
CTGTGTTGAGAAAAAAGTCAAAAGTTGAGGTACCACCGCCCTGGAACAACCAAGTTCAGAAAAAGACA  
GAAAAACAAGTCAACCGATCAATTAAGAAACCATTTGAAAAATGAAAGTAAGGTGATATTTCTTCAATTC  
TCATCAAAATACACAGCTCAAAATGAAGAAGCAAAATCTGGAGAACAACTGAAAAAGATACAAACCAAG  
ACAAGTCCAGCAAAAACAAGUGGAAGTTAAGGAAGTAATACCATCATCTACAGAAACCTGTATCAAAACCA  
GATGTTGAAAAAGCAATTAAGAGGAAGAACAAAGATGAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT  
AAAAAAGATGAAAAATCCAGTACCTCCATCAGAAAGNTTGAAGAGAGATGAAAAATATGATGATGATGAATG

147/251

YBR112C\_homolog 1080aa (SEQ ID NO 466)  
 MYATAHTIKQQQQQQQQCHPPPLNGGLHASGAPPNSHEAAAIAQQQQQQQQQHNGPQGMIVAAAAASANQ  
 QAVQARAQQQQQQQQRLPSSAALNETTVSTWIAICSLAESLCDIERATASYNSALRHSNNPDILVKT  
 ANTYRSKDKQLRAELYEQALNPHVENGETWGLLGHCYVLMNLQRAYAAYQALFYLENPNVPKLWHG  
 IGILYDRYGSLEYAEEAFVRELDLDFKFKANEIYFRIGIYKHQSKLOPALECFQYILNPNPHPLTQT  
 DVWFQIGSVYEQQKDWNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAESNFPSTPANGAAPPPIKPFQQDL  
 TIALKYLKQSLVDQSDAHSWYVLCRVEMIRGDFPAAYEAFQQAVERNDRARNPTFWCSTGVLYYQISQYR  
 DALDAYTRAIRLNPYISEVWYDLGTLYETCNQISDALDAYRQAERLDPNPHIKARLEQLTKYQQECN  
 THFPQFPSSQQPRLFCGHVLESTQQQQQQQPPPPQQQQQQQLQHQSQSQPQPQPPQTQSQPSLLQHO  
 SSLPQCQIQPLHQQAAPLVNQQQSFPPPHLMNLGQPQQQPQQLPPLPHPTQQPSQIQEKPPTQEQPH  
 YQPPPPPPHQQQSQSQPQPPHQFQHTQNSPQLAQPLPHHSNPPAKPHGAPQQTGLPDLHNSANIIS  
 APSQVFPQQQYQOPHIAFVRQEQVNHVPSIYSAPRFTETTLPOIMNPNESITTVQVQLKKEEPKPEAT  
 VSAFVFEATKVQDQVTIQESAPAAAAAVSAPASAPVGDIKTITVSTTTTATSTTADAVPVSVSQVGEAP  
 NVVQEKKVPDTEQIVSQVEKPVESQPEVTPAPTAPALATAPTPEPAPTDKDVVMAPSASATPVTQSIVE  
 QNTRVSEATKAPESNGKHLEDKNDDEKILKRPTVETTTESVVPVNPVEKENEKVEVPPPPSEQPSSEKR  
 EKEVNGSILKKPLENESKVDLPOFSSNLTACNEEAKSGEETKKITPKTSPAKQGEVKEVIPSSSTETVSKP  
 DVEKDNKEKDKDEDEVMADDDVKKDENPPEPMRKIEEDENYDDE

YDR145W\_homolog 1536bp public: 1..1536 (SEQ ID NO 467)  
 ATGGAAGAGTTCAATCAAAATTAGACAAAACCTCACTGAAGTTCAAAGGAGGGTTCAAGTTGTTGGAACAA  
 ACAAGAAAAACAGGAAATGTTACTCCAGAGCAAAATCAACACATTGATAAACAATAATATGAATGCAAG  
 GCAAACTTCCAACAGTATCAAAAAGTAGGGATTATATATAGAAATCAGTTGGTTCTTCAAGCTAAAGCA  
 CAACAACACAGACAATTCGAACAGCGACAGCAACAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA  
 AAATCAGCTCAGAACCAGAACCCAGAAATCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC  
 CAATACAAAGGAGTGCATCTGCTGAGCAACACCTTCAAGCAACAGAGCTTTTGGCCACAGTTGCAGGCT  
 GTACAACAACAACAATTTTGGGCAACCTGCAACACACAGCAGCAGCAACAACAACAACCTTAGAAAT  
 GCGAATAAAAGTGCACCTCAAGGTCAAGCTCCTTCACAGCGCGCCACTCCTTTACCTCTTCGGCCAAACA  
 CCTCAGAGTCAACCTACAGCACAAGCGGGTGTGCTTCACAGGCAGCTACACCAAGGATTTCAGAGCTTCT  
 CAACCCACACCATCGCAAACTTCGAGAACTGGATCAGCTCTACAACAAGGGCCACCAAGTCCGACAGGCA  
 TCTTCTACACCGCAATCTCAATTCCAACCACCAATTCACACTGCAGAGTCGACATCCTTCTGCAACTACA  
 TCAGAAAAGGCCACTTCCCCAACAACCTGGAAGCGGAACAGCGAAGAGTCTTAGTGTGCTGCTACTCCT  
 CCTCAGATAATGGCACTGTAACTGCCCGGTTCGCATCACCCTGTTGCAACTACTACAGATAGTGCCTACA  
 ACTGGAAGCTCAGGAACTCCCCAACAACAATCAAGGTCACGATCTGGATCATCGTTGAATTTGCCCTGGC  
 ATTACAGTCTAGTCTGTCCCATCATTCGCCAATTTTCGAGTTCATTAATGTAACAACACCCCAACAATCACC  
 ACATTTAATGATGATCAATGATACGAGACCCAGTTTGACGGCAGCAGCTGCCAATCCTATGATATTTTA  
 TTAGATACACCAGCGATCACAAAATTCCTTACTTTTGATATCGAAGGACACACTGCTCATTTGATTCT  
 AGTACCAGTGGACGAGTTTTTAATAAACGAAAATTAGGTGATTTGATAAATACAAATAGGTGTTGATGAA  
 GGGGATGGTAACACCAAGTATTCATCGCAATCTCGAGCAATTTTTCTTTGGATTTCGCTGATGAATTTAT  
 CATTACGTGACAAGTTTTGCTTGTCCGTTAGCAAAACATAGAAAGGTGGATAGTATAGAGGCAAGAGAT  
 GTTCAACTACATTTGGATAAGAATTGGAATATCAAGATTCTGTTTATGCAATGGATGAGATTGCAAAAC  
 ACAAGAAAATACAAACCTAGTAATAGTTATAGTCAGAAAGTACAAAGCTCTCCAAGTTTCGAAAGCTGTG  
 AATGATGATAATGCTTAA

YDR145W\_homolog 511aa (SEQ ID NO 468)  
 MERFNCIRQKLTEVQRRVQLLEQTKKTGNVTPEIQIQIDKEIIECKAKFQQYQKVCIIYIRNQLVLQAKA  
 QQQRLQQRQQQQQQQQQNNNLKSAQNQNQNQNQNQNQNQNQNQNQIQGVQSAGQTPQQQSFSPQLQA  
 VQQQFMGNSQQQQQQQQQLNANKSALQGAPSQAPTPLEVRPTPQSQPTAQAGVASQAATPGERAS  
 QPTPSCTSRGTSALQORAPSRQASSTPQSQFPPLPSESRIIPSAITSEKPLPQQPGSGTAKSPSVAAATP  
 AQNINGTVTARSASPVATTTDSATTGRSGTPQQQSRSRSGSSIMLAGITRQSVPSLPISSSINVKQPTIT  
 TFNSINDTRPSITGGGAANPMSITLDTPTTKLPTFDIEGDTGVLDSSSTSGRVLNKRKLGLDLINPLQVDE  
 GDGKTSIDGNVEEFLDLADEFIHSVTSFACRLAKHRKVDSEAROVQLHLDKNNMIKIPGYAMDEIRN  
 TRKIQPSNSYSQRVQGVSEVSKAVNDDNA

YDR154C\_homolog 333bp public: 1..333 (SEQ ID NO 469)  
 ATGATGTGCTCCAAAGACTGCTCAAAATTCAGAGCTTATGTACTGGTGAAAAAGGTTCTTGGTTACA  
 AAGGTTCTATCTTCCACAGAGTCATCCCACAATTCATGCTTCAAGGTGGTGATTPCACCAACTTAAAGG  
 GTACTGCTGGTAAAAGTATTTACGGTACCAATTTGCTGATGAAAACCTTTGTCAACAGACATGACAGAC  
 CAGGTTGTGTGCTATGGCCAAATGCTGGTCCCAACCAACCAATGGTTCCCAATTTCCATACCACCGTTT  
 CATGCCCATGGTTGGATGGTAAACACGTTGTTTTCGGTGAAGTCACATGATGGTTAG

YDR154C\_homolog 110aa (SEQ ID NO 470)  
 VMSEFQRSSKISELYVSVKVLVTKVLPSTESSHNSCFKVVISPLIVSVVAVFVFNLSMKTLSRDYTD  
 QVCCLPMSVQCPMVPNSSLPFPHAGWVWNTLFSVKSSNV



149/251

YDR216W\_homolog 1418aa (SEQ ID NO 472)  
 MISPTHQSQYLNYFVNZVLMTESGDIIDSVTGTMTTAMMSNTTIDAPTFASTTKNYKEKKQNTNTGTS  
 MSPSNSTNSTNNNAAAAAATTTTSKRSKDTPIELTAFTGTTTSGKPRIFVCCQVCTRAFARLEHLRRHERS  
 HTAKKPFSCGVCORKEFSRDLRLRHACKLHAGCTDAITRLRSKSIKKSQDGDGDDDDDDDDDEEMANSED  
 ENHDHDESGNASTKNGKKDKKDPPEFNLNLFNSKQKPTKANTTKSKVARLSITSRKNSTNFTKNSSS  
 LHKQVLDQRQKAAVNTRIVSESTKIVSGTWSGVSTFTSRHGASFSQAQSGANYAINIPEFNDIYPOSDW  
 VEPSTPQFLPSLDNEMTWLNNIPNIEGLSDSVSAANLMRQNSITNSADIVEPPVNVSQHGSPSHQSTF  
 SATDMGQTRSESVNSLNTPTFGSYMMPTVTISNQETQNGVAAHHHHQOQQQHQOHHHQHPNQSSSLGLS  
 RNDMLSEDHYGYSFYDIPENILNFMESISTTSNAMSSGPIONFKPLSPITQETIEHEITPRIDGRIGDF  
 QNNNNNTNDNP I HQNINNYDINFIHTIDETGQDVT SKEMPOCYSPYCDMNVSATSSANDYNSPNNIVSTSQ  
 OMNQPALHNQSSHPSCASPHLNQAMMNKMR LKNYSSNKLFTNHIRKHMINKALGKYPISGIMTPTTIPSNF  
 KLDPYLSVFIQSPFLAILPFIHPSKLNVEIMAMTGMEDINNESARVCLFLTATWGALLANNKNDAEHL  
 VFAARRTYHTYLFESRKTNTSTNDKNYKNGKDKSSSGNPLWLLQSLMLSVLYGLFSINENNVIIVLRQLNA  
 LNSLVKTSIFKNGPIFFSNNGEDEELYNKLNSHDNGTSLFSNNLNDEMRYKNMINMQSQTRIVFIYRL  
 TWPLMMYNVPLTFSINDINGLAVISKDEETLWNPKNYQEFQEFSHKNNKTLDDYLNKNKNEPIIFRELL  
 LTVTKPGTISDSNISPETEKKVTHQLQNLCKYGFNCLVREGLYELKOYQEMKEVDTEKVLDTKFPYPTND  
 GLGFNCFRLPANKDLEKIDYALLVEFTKISSIIDLKLKESQSWLKNYQDLTQNYHRELLDAHSTGNPLNS  
 INDYDYLKLANDUCISVLKLILFKVEDSNSNSNRKSKNDPTNEINNKLNMMNNNNNNNNNSNGDQLIS  
 AFOTDFGYLNMNDNGYAKKEEFLRFTLDELRYDKENTMSYFDKILKLIIFEEVEKSSNLIQAQMLFHAF  
 SVLSIFSVMRKNDNNSSPFANTGLIFELNHRYSMVLRLLERIETFIKLRVQTSAGGGGGGVNNNNNN  
 ALSIKLEQEFINLYLYNGNVLSHDNTNTNTNTITTTTTDNGTKQNHHSQDFGLEKTLYLKMGEN  
 VLNYIYDNLKVCVFKKLGDSLSERKYLIDNESTLNG

YDR224C\_homolog 393bp public: 1..393 (SEQ ID NO 473)  
 ATGGCCCCAAAGCAGAAAGAAACCAGCTTCCAAAGCTCCAGCTGAAAAGAAACCAGCTGCTAAGAAA  
 ACCGCTTCCACCGATCGCTGCTAAAAAGAGAACCAAGCTAGAAAAGAAACTTATTCCTCATATATATAT  
 AAGTTTTTGAAACAAACACATCCAGACACGCGPATCTCCCAAAAGGCCATGTCAATTATCATATTCCTTT  
 GTTAACGATATTTTCGAAAGAAATTGCCACCCGAGCCTCCAAATTAGCTGCTTACAATAAAAAATCCACA  
 ATTTCCCGCTAGAGAAATCCAAACTGCTGTAGATTAAATTTGCCAGGTGAATTGGCCAAACATGCCGTT  
 TCCGAAGGTACUAGAGUCCTCACAAAATACTCATCTGCTTCTAGTTAG

YDR224C\_homolog 130aa (SEQ ID NO 474)  
 MAPKAEKKPASKAPAEKKPAEKKTASIDGAKRKPKARKEPYSSYIYKVLKQTHPDTGISQKAMSIMNSH  
 VNDIFERATEASKLAAYNKKSTISAREIQAVRLILPGLAKHAVSEGTRAVCYSSASS

YDR342C\_homolog 1653bp public: 1..1653 (SEQ ID NO 475)  
 ATGTCATTAGATAATTCAACAGAAAACCGTGAATTTGGAAGAAAAGGAAGAAATTCCTAAAGCAACGAACAT  
 AACGAACAAGGCGAACAAAACGAGAACAAATGAGCATATACCTACTTTGCAAGATTAACCATTTGAAGGAA  
 TATATAGGTATTAAGTATTTTGTGTTTCCCTATTGCTTTTGGTGGTTTCCGTTTTCGGTTTCGATACCTGGT  
 ACCATTCTCGTTTTCATTACATGACTGACTTTTGTAGAAAGATTTGGTGGTACTAAGCTGACGGTACT  
 CTTTACTTTTTTCCAACGTTAGAACTGGTTTATTGATPAGTTTGTTCATGTTGGCTTGTCCCATTTGGTGA  
 TTATTCTTGTCTAAAGTCCGTTGATATGATATGATGTAAGAGTTTGTATCATGACTGCTATGATCATTTAT  
 ATTCTTGGCTATTATTGTTCAAATTGCTTCTCAACATGCTTGGTATCAAATCATGATTGGTGAATTATC  
 ACTGGTCTTGGCTGTTGGTATGTTATCAGTTTGTGTCCATTATTATCTCAGAGGTTTCTCCCAACAT  
 TTAAGAGGTACATTAGTTTATTGTTTCCATTGATGATTACCTTGGGTATTTCTTGGGTTACTGTACC  
 ACTTAACGCTACTAAGAAATATTCTGACTCCAGACAAATGGAGAAATCCATTGGGTTTATGCTTCTCTGG  
 GCCTTGTGTTTGGTTGGTGGTATGGTAAGAAATGCCAGAAATCTCCAGTTACCTTCTCGGTAAAGATAGA  
 ATTGACCATGCTAAGATTTTCACTTGGCAAAACTAACAAGGTTTCTCCAGAGGACCTGCATTTATACCGT  
 GAACTTCAAATTAATCCAAGCTGGTGTGTAAGAGAGAAAGATTGGCCGGTAAGCCATCTTGGGGTGTCTTA  
 ATCAGTGGTAACCAAGAATCCCTTGAAGAGTTATTGTTGAGCTATGTTGCAATCATTGCAACAATTG  
 ACTGGTGAATAACTATTCTTCTACTACAGTACCACCATTTTCAAGTCTGTGGTTTAAATCATTCCTTTC  
 GAAACATCTATTATCCTTGGTGTCTATCAACTTTGCTTCCACTTTTGTGGTATTATTATGCCATTGAAAGA  
 TTGGGTAGAAGACTCTGTTTATTAACTGGTTCCGTTGCCATGTCCATTTCCTTCTEAAATTACTCATTG  
 ATTGGTACTCAACATCTTTTACATTTGATCAACCAAGGTGGTCCAACCAAGAAACCAGATGGTAACGCTATG  
 ATTTCATTACTGCATTTTATGTTTTCTTCTCGCTTCTACACGGGCTGGTGGTGTACTCCATTGTT  
 TCTGAACTTTATCCATTAAAGTCAAGAGTAAGGCTATGCTTTTTCATTAATGCATGTAACCTGGTTGCTGG  
 GGTTTCTTATTCCTTCTTCACTTCACTTATCACTGATGCTATCCACTTCTATTATGGTCTTTGTGTTT  
 ATGGCTGTGTTTATGTTTCCATTTCCTTGGTTTACCTTATGATTTAAGAACTAAAGGCTTACTTTTA  
 GAGGAAAATGATGAATTAATCTCTACCAAGGTTGTTCCATGGAATCAGCCGGTGGGTAACACCTTCT  
 GACGAAGAAATGGTTTCTGTGCAAAAGGCTATACTGGTGTATCCACCTAGATGAAGAGCAAGTTTAA

150/251

YDR342C\_homolog 350aa (SEQ ID NO 476)  
 MSLDNSTENRDLBEKEEIPKNEHNEQGEQENEMNEHIFTLEDKPLKEYIGISILCFLIAFGGFVFGFDTIG  
 TISGFINMDFLRFRFGGTFKADGTLYFSNVRTGLLIGLFNVGCAIGALFLSKVCDMYGRRVGINMAMITY  
 IVGIIVQIASQHAWYQIMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGLTVVYCFQLNITLGLFLGYC  
 SYGTRKYSDSRQWRIPLGLCFAWALCLLGGMVMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR  
 ELQLIQAGVERERLAGKASWGALITCKPRILERVIVGGMLQSLQQLTGDNYYFFYYSTTIFKSVGLNDSF  
 ETSIILGVINIASTFVGIIYAIERLCRRLLCLTGSVAMSICPLIYSLIGTQHLYYDQPGGPTRKPDGNAM  
 IFITALYVEFFASTWAGGVYSIVSELYPLKVRSKAMGFANACTNMLWGFLISFFTSFITDAIHFFYYGFVF  
 MGCLVFSIFFVYPMIYETKGLTLEEIDELYSTKVVFWKSAGWVPPSDEEMVRAXGYTGDIHADEEQV

YDR343C\_homolog 1641bp public: 1..1641 (SEQ ID NO 477)  
 ATGTCACCAAGACAACGTCCTCATCAACATCTACAGCTGAGGCTGTAAATAATGAAATCAAAGTCAAACAT  
 GAACTTCGACAAGAAGAACAAGCTCATACTAGTTTAGAAGATAAACCTGTGAGTGCCATACATGGGTATC  
 ATCATTACGTGTTTCCCTTATGCGCTTGGTGGTTTCGTTTTCTCTTCGATACTGGTACTATTTCCCGT  
 TTTCATTAAATATGTCTGACTTTTAGAAAGATTGGTGGTACTAAAGCTGACGGTACTCTTTACTTTTCC  
 AATGTCAGAACTGGTTTAAAGATTGGTTTGTTCACACCTCTGTGTGCUATTGGTGCATTATTCTTGTCT  
 AAAGTCGGTGATATGTATGGTAGAAGAGTTGGTATCATGACTCCTATCATTGCTCTATATTGTTGGTAT  
 ATTGTTCAAATTCCTTCTCAACATGCTTGGTATCAAGTCATGATTGGTAGAATTATCACTGGCTCTTGCC  
 GTTGGTACTGTTATCAGTTTAAATGCTCTTGGTTCATTTCGAGGTTTCTCCAAACATTGTGAGAGGTACT  
 TCCGTGCTGCTGTTTCCAAATGATGATTACCTTGGGTATCTTCTTGGGTATTGTACTACCTATGGTACT  
 AAGAGTACTCAGACTCTAGACAATGGAGAATTCATTAGGTTTATGTTTTGCTTGGCTTTAAAGTTTG  
 GTTGGTGGTATGGTTAGAAATGCCAGAAATCTCCACGTTACCTTGTCTGTAZACACAGAAATGAAGATGCT  
 AAAATGTCACTTCTCTAACTAACAAGTTTCCCCAGAGCACCACGCTTATACCGTGAACCTTCAATTA  
 ATTCAAGCTGGTGTGTAAGAGAGAAAGATTACCGGTAAGGCATCTTGGGGTACTTTTATTCAATGGTAAA  
 CCAAGAATCTTTGAAAGGGTGTGTTGTTGGTGTCAATGTACAAAGCTTACAACAATTGACTGGTGATAAC  
 TATTTCTCTTACTACAGTACCACATCTTCAAGTCCGTTGGTATGAATGATTCTTTCCAACTTCTATC  
 ATTATTGGTGTTAATAACTCTGCGTCCACTTTTGTGGTATTATGCTATTGAAACAATGGGTAGAAGA  
 CTTCTGTTTGTAACTGGTTCCGTTGCCATGTCTGTCTGTTTCTTAATCTAATCCCTGGTTGGTACTCAA  
 CATCTTTATATTGACAAACCAGGTGGTGCTAGTAGAAAACAGATGGTGATGCCATGATCTTTATGACT  
 TCACCTTAATGTTGTTCTTCTTGTCTTCTACATGGGCTGGTGGTGTCTTACTCCATATATTTCTGAACCTTAT  
 CCATTGAAAGTTAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCAATTGGACCTGGGGTTTCTTAATT  
 TCTTTCTTTACTTCTTTTACTGATGCTATCCACTTCTACTACGGTTTCGTCTTTATGGGATGTTTA  
 GTTTTCTCCATTTTCTTTGTCTACTTTATGGTTTACGAAACTTAAAGGTCTTACCTTGGAAAGAAATGAT  
 GAATTGTACTCCACCAAGTCCCTCCATGGAAATCAGCTGGTGGGTGCCACCTTCCCAAGAAGAAATG  
 GCAACCTCTACGGGATATGCTGGTGAATGCCAAACCAGAAGAGGAACACGTTTAA

YDR343C\_homolog 546aa (SEQ ID NO 478)  
 MSQDNVSTSTAEAVNNEIKVKDEFQEEQAHSTLEDKPVSAIYIGIIMCFLIAFGGFVFGFDTGTISG  
 FIMMSDFLRFRFGGTFKADGTLYFSNVRTGLMIGLFNAGCAIGALFLSKVCDMYGRRVGINMAMITY  
 IVQIASQHAWYQVMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGLTVVYCFQLNITLGLFLGYCTTYGT  
 KSYSDSRQWRIPLGLCFAWALCLVAGMVMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL  
 IQAGVERERLAGKASWGTLFNGKPRIFERVVVGVMQLQALQQLTGDNYYFFYYSTTIFKSVGMNDSPQTSI  
 TIGVINPASTFVGIIYAIERMGRRLCLLTSVAMSICPLIYSLVGTQHLYYDKPGGASRKPDGDAMIEMT  
 SIVVEFFASTWAGGVYSIISELYPLKVRSKAMCLANASNWTWGFLISFFTSFITDAIHFFYYGFVPMGCL  
 VFSIFFVYPMIYETKGLTLEEIDELYSTKVLFWKSAGWVPPSEEMATSTGYAGDAKPEEEHV

YDR544C\_homolog 1700bp (SEQ ID NO 479)  
 CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAGAAAGGAAAAATTCCTACTGGA  
 CCTGATTCAATTTGCTGAAGATGAATCATTATCTGAGGTTTCTTTGCCACCTACAAGAACT  
 AGGAATTCATCGGTGTTGTCTCCGAGTAACTCAACTAGAGATCTTTTATTGACCGCTTC  
 CATAGAGATGAGTCTAGCACTGGCAATAGCAGACAACATGAGCAGCACCACCACTCTTG  
 AGTGATCCTTTGCCCTACCGCAGAGAAAGCTTCAACCGAAATTCCTCAATCACCAGAAGCT  
 CCACAGGCCAATCACTAGAGCTCTATCAGAAATCTAAAGAACTGTTCCTACCTATG  
 CAAACCGGTTCCGAAAGGAAAGGTCAAAATCAGCAGTCGAGAGTTGATGTATCTCTCAA  
 AACTTGTCAACAGTTACTCTTACTCAGGATGGATTTCGTGGTTCTGTAAACCTATACCA  
 GAACCTGTTGATTTCTCCAAATGTGATTAAATACAAATGACTCGGAAGACTCTTCTACASAA  
 GAACCTAGAGCTCGTTACTTGAATAACACAAATTTAGAAAGTACAACTGTATCTTCCCA  
 TTCCTACTCTAACCCGCCAGCACCTGTGCCACAAAGATCCACATCTACACAAAGCAGTGA  
 GGCATTTACTCGTTTGAAGCGGGTGAATGATTCCAACTCAATCTCGGCTACTCCAAGATCC  
 GAGCAAAATGTGTTTGGACAGATGCCAGACCTCAAAATTTGTCTCTGAAAGAACTCTGCT  
 CCACCACCACCACTTTCGAGAAACTTTTGCACCATGAAGAACCACTGTAAAGGATTC

151/251

CCTCTTTTCCACAATTTACCTGCTGCCTCCCATTTCTGGAAGAGACTCGGTAATGGCTCCA  
 TTAGCAAGTCAAGACAGGGSTCATTGCTTGTGAAAAATGATTTCAAACACGAAACTTGG  
 GCATCCACCCCTCGGATTEAGCTCTTCTATTGCTGAAGTCATCAATGCCAGCTTTAAGGAT  
 GGACAETTCATTAAATCACAAGTAGTTGGTGAAGTCCCTTCAATTATAATGGTAATGCT  
 TCCGATCCACTTGTGGTCACTATTCCCTAATAGTTTTCGATAAAGTACTCGTGAACAAGACT  
 TTTATTGAGCATTTTAGGTCAAAGCAAGTATAAACTGAACCCAACTTCAATTACGCTCTAAA  
 ACTCTTGGTGGGTTGAAATATCTTTTGAAACCAACACAGGTACCAGTGATTAATCAACAA  
 ATATGGAAATTTGAACCTCATCAGTCAAGTTTGATGGTTAGCATTCGTTCAACTACAGCT  
 TTGGTATTGGAAAAATTTTGTGTCTCTGTAGCTTTGAATCAAGACATTGAAGCAACATCT  
 GCTTCTCTCAAAGCCTCAAGGTGCGTTTAATAAAGAGAAAAACAGAATAACATGGAGATAT  
 CCACAGTCCCTCGCATTGGAATGGTGTAGAGCGTTTGATAGCTAGATTTATGACTAATGGA  
 TTGGGTTCCGAACATGAGTCTGGTGTGCAGATTAAATTTCAAGTTAAGGATCCACAGTCT  
 AACTACTGTAGTATTTACAGTGAGAATGCCGAAGAGATTCTACGTTTAGAATTTGGTT  
 AGCGGTAGTTATAGTGGTCTATCTTAAAGTTATCTGTTTTGAGATTAGTCTCTTGTGAAAT  
 TGAAAAAAGAAAAACGTGA

YDR544C\_homolog 548aa (SEQ ID NO 480)

LKSKVCSIFCRKKKKEKFTCADSLAEDESLSEVSLPPTRTNRNSSLRSNSNSTRRSFIDRF  
 HRDESSTGISROIHQHQPLSDPLPIAEKFPQPEIPQSPEAPQAKSLEPVSEVLKELFPPM  
 QNGSERKGENOOSRVDVSSOTLSPVTPTHDGGFGSVKPLPEPVDSPNVIKYNDSDOSSTE  
 ERRGSLLEKHNLEVQPVSSPFTTQPPAPVPQESRSRQSSDGIYSFEAGDDSNPISATPRS  
 EQNVFGQMFDPNLSPEKTIAPPPPSRKVLHHBEPTVRDSALFINLPAASIIISGRUSVMAF  
 LASQDRGMSLLKNDFKHENLASTLGLSSSIAEVINASFKDGLIKSQVVGZVAFNYNGNA  
 SDPLVVTIPNSFDKVLVNKTFIEDLGQSKYKVNPTSTTSKTLGGLKYLKPTQVPVLIQQ  
 IWKFEPHQSSLMVSIRSTTPLVLENFVVSVALNQDI EATSASSKPOGAFNKEKNRITWRY  
 PQSLALNGVERLIARFMTNGLGSEHESGVQIKFQVKDPQVKYCSZYSENGEBIPTFRNLV  
 SGSYSGHL

YEL071W\_homolog 1584bp public: 1..1584 (SEQ ID NO 481)

ATGCACAGCATTAGTACACACTGCTCCGTATTGTATTAGACGAAACAACGTGGCATGTAGATTCACT  
 CGTTATAATGGTTTGGCUGTTGCATCTTATCTACAAAAACAGTACCTTTTACCCGAGATACCTTATTCC  
 CAAAAAGTCCAACTGATGCAAAATCCAAAGCAACTTGAATCTCAAGACATCCAAATACCTTAAAGTGTA  
 TTACCTGAGAAATCCATTATTACTGATGAAGAUGACTTATTGTTTTTCAACGAAGACTGGATGAGAAAG  
 TATAGAGGTCAATCACAATTGGTTTTGAAACCGAAAACCAACGACAGTCCGTTCTATCTTAAAGTAT  
 TGTAAATGATAACAGCTAGCTGTTGTACCACAGGGTGGGAATACCTGGGTGGTAGGTGGATCTAAATCCA  
 ATTTTGAATGAATCATCATTTCCCTTGTCCGCCATGAATAAAATCAGATCGTTTGAATCTCTCAGCGGT  
 ATATTGAGATCGAGCTGGTGTATTTTGGAAACAGCTGTATCAGTATTTGGCTCAGCGGCTACATT  
 TTCCCGCTCGACTTGGGAGCTAAAGGGTCTGTGTCATGTTGGTGGCAATCTTGCATGTAAATGCTGGTGT  
 TTGCTTTTGTACGATACGGTTCTTTGCATGGTCTGTGTTTTAGGTTTGGAAAGCTGTCTTGGCCGACGGT  
 ACAGTTTATAAATCTATGCAATTCATTGCGTAAAGATAATACTGGTTATGATTTGAAGCAGTCTCTTAT  
 GGATCTGAAGGTACTTTGGGTATTATAACTGGTGTTCGATTCTATGTCCATCAAGACCACAAGCGCAA  
 AATGTGGCATTTTTAGCTGTATCGAGTTATGAGCCGCTTCAAAGGTTTTTGTCCAGGCTAGAAAGGAC  
 TTGCAAGAAATTTTATCGGCTTTTGAATTCATGGACAACACCTCACAAAAGCTTGAATGCTAAGCATTTA  
 GGTTTGGAGCACCCCTATTGAAAGCGGTGACTTCCCATTCCTATGTGTTAATTGAACCTCTGGCTCCAAC  
 AAAGAGCACGACGACGAAAAATTGGAAACATTCTTCCCGAATGCAATGGAAGAAGGTTTAGTCGACGAT  
 GGGATTATTGCACAAGATGAGGCTCAAATACAATCATTTATGGTCAITGGAGAGATCCATCCCTGAAGCA  
 ACCACTATTGGAGGCGGTCTTTACAAGTATGACGTTTCTTATCCATTGGCAGATCTTTACGGGTGAGTT  
 GACGACATCAATACCAGTTAAATGATGCTGGAATCGCCAGCTTGGACGATGAATCGAAACTTGTGCTT  
 GCTGCATTTGGTTATGGTCAATTTGCAGATGGGAATTTACACTTGAACGTTTTCTGTGACAAAGTATTCT  
 CCTGAAATTGAAACTATCTTGGAGCCATTGTTCTATGAATGGATCGCAAAAAAATGGATTCATTTCC  
 CTTGAACATGGCTTGGCATTCCAAAAGAAAACTACATTGGGTATTCCAAGAATGAGATTGAGGTCAAA  
 PTAATCAAGAATCAAAACACATTACGATCCAAATGGAATCATCAACCCATATAAATACGTGTAA

YEL071W\_homolog 527aa (SEQ ID NO 482)

MQRRLVQTASYLIRRNNAVCRFSRYNGLPVASYSTKTVPFTADTYSQKVORDAKFKQLESQDIEYFKSV  
 LPENSIITDEOLLFFNEDWMRKYRQSSQLVLKPKTTTEQVASILKYCNENKLA VVPQCCNTYGLVGCNSP  
 IPDEIIISLSAMNKIRSFDPVSGILKVDAGVILETADQYLAEQGYIFPLCLGAKGSCHVGGNVACNAGG  
 LRLRLRYGSLHGSVLGLEAVLPDGTVYNSMHSRLKDNCTCYDLKQIFIGSEGTGTTGVSILCPSRPQAG



152/251

NVAFLAVSSYLAVQKVFVQARKELQEILSAFEPMNTSOKLTAKHLGLEHPIESGTFPFYVLIETSGSN  
KEHDEKLETF LGNAMEEGLVDDGIIAQDEAQIQLSWRESIPEATTIGCGVYKYDVSIPLADIYGLV  
EDINTRINDBACTASLDDESKLVLAALGYGHIGIXNLHLNVSVRKYSPEIETILEPFVYEWIAKKNGSIS  
AEHGLGFQKKNYIGYSKNELEVKLIKEIKQHYDPNGIMNPKYKVV

YER177W\_homolog 795bp public: 1..795 (SEQ ID NO 483)  
ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAAGAA  
ATGGGTGAAAACATGAAGCCCTTGCCTTCTCTGGCCAAGAATTGTCTGTTGAAGAACGTAATTTATTTA  
TCTGTCTCTTACAACAATCTCATTCGCTGCTGCTGCTTCTTGGAGAATTGTTTCATCAATTGAACAA  
AAAGAACGACCCAAAGCAAAATGAGAGSCCAAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT  
GAATTGTCTAAAATTTGTGAACATATTCTCTCTGTTGAGCGACCATTTAATTACATCTGCCCAAACCT  
GGTGAATCAAAAAGTATTTTACTACAAGATGAAGGTGATTACACACATACTTGCTGAATTTGCTATC  
GCTGAAAAACGTAAGGAAGCTTCTGATTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTCTCTC  
ACCGAGTTGCCACCAACCCATCCCAATCAGATTAGGTTTAGCAATTGAACCTTCTCTGTTTTCTACTATGAA  
ATTTTGAACCTTCCAGATAGAGCTTGTCTATTAGCTAAACAAGCTTTTCGATGATGCTGTTGCTGATTTA  
GAAACCTTATCTGAAGATTCATACAAGGATTCAACTTTGATTATGCAATTTATTGACACATAACTTGACT  
TTATGGAACCGATTATCTGAAGCCCTAGCTGCCACTGAAGAACAACAACATCUAGTCAAGCTCCAGCT  
GCTCAACCAACAGAAAGGTAAGGCTGATCAAGAATAC

YER177W\_homolog 264aa (SEQ ID NO 484)  
MFASREDSVYLAKLADQAERYBPMVFNMKAVASSGQELSVEERNLLSVAYKMWIGARRASWRIVSSIEG  
KEEAKGNESQVALIRDYNAKIEAELSKICEDILSVLSDHLITSAQTGESKVFYKMKGDYHRYLAEFAT  
AEKRKEAADLSLEAYKAASDVAVTELPPTHPIRLGLALNFSVFFYBILNSPDRACHLAKQAFDDAVALL  
ETLSEDSYKOSTLIMQLLLRDNLTLWIDLSEAPAATEEQQSSQAPAAQPTGKATQE

YGR192C\_homolog 1008bp public: 1..1008 (SEQ ID NO 485)  
ATGGCTATTAATAATTCCTATTAAACGGTTTCCGGTAGAATCCGGTAGATTAGTCTTAAGAGTTGCTTTGGGC  
AGAAAAGACATTGAAGTTTGTCCCGCTCAACGATCCATTTCCTCCAGACTATGCTGCTTACATGTTC  
AAATACGATTCTACTCACGGTAGATACAAGGGTGAAGTCACTGCTTCTGGTGACGACTTGCTCATTCAT  
GGTCACAAGATTAAAGTTTTCCAAAGAACAGACCCAGCTAACATTCCATGGGGTAAATCTGGTGTTGAC  
TACGTTATTTGAATCCACCGGTGTTTTCCACAAACTCGAAGGTGCTCAAAAACACATTGATCTCTGGTSCC  
AAAAGAGTTTATCATCTGCTCCATTTGCTGATGCCUUAATGTTTGTGTCGGTGTTAAACGAAGACAAA  
TACACTCCAGACTTGAAGATTATCTCCAATGCTTCTTGTACCACCAACTGTTTGGCTCCATTAGCTAAA  
GTCTGCTAACGATACTTTCCGTATTGAAGAAGGTTTGATGACCCTGTCCACTCCATCATCTGCTACCCAA  
AAGACCGTTGACCGCTCCATCCCAAGGACTGGAGAGGTGGTAGAAGTGGTGGTGAACATTATCCCA  
TCTTCCACTGGTGTCTGCTAAAGCCGTTGGTAAGGTTATTCAGAAATTGAACGGTAAATTTGACTGGTATG  
CTTTTGAGAGTCCCAACCAACGATGTTTCCGTTGTTGACTTGACTGTGAGATTGAAGAAACCTGCTTCT  
TACGAAGAAATTTGCTCAAGCTATCAACAAAGCTTCTGAAGGTCCATTGAAAGGTGTTTTGGGCTACACT  
GAAGATGCTGTGTTCTCCACCGATTCTTGGGTTCAAGCTACTCATCTATCTTTGATGAAAAGCCGGT  
ATCTTGTGTTGCTCCCAACTTTCGTCAAATTGATTCTCTGGTACGATAACGAATACGGTTACTCCACCAGA  
CTTGTTCACTTCTTGAACAACGTTGCTAAAGCTTCTCTTGA

YGR192C\_homolog 335 aa (SEQ ID NO 486)  
MAIKIGINGFGRIGRLVLRVALGRKIEVVAVNDPFIAPDYAAVMFKYDSTHGTRYKGEVTA SGDDLVID  
GHKIKVFERDPANIPWGKSGVDYVIESTGVPTKLEGAQKHTDAGAKKVIITAPSADAPMFVVGVNEDK  
YTPDLKIIISNASTTNCLAPLAKVNDTFGLREGLMTTVHSITATQKTVDGPPSHKDWRGRTASGNIIIP  
SSTGAAKAVGKVIPELNGKLTQMSLRVPTTDSVVDLTVRLKKAASYEELRQAIIKKA SEGPLKGVLCYT  
EDAVVSTDFLGSSYSIFDEKAGILLSPTFVKLISWYDNEYGYSTRVVDLLEHVAKASA

YGR243W\_homolog 399bp public: 1..399 (SEQ ID NO 487)  
ATGGCTTCAACAGTTCAACACCGCATCCAAATTCACACGTTTTTTAAATTCAGAGACGGTCCCTAGAACC  
GTGCATTTTTTGGGCTCCAGTGTTCAAAATGGGCCTTAGTTGCTGCTGGACTTAATGACATACAACGTCCT  
GTTTAAAAAATTTAGCGGGAACCCAAACAGATAGCATTGTTTGGCACTGGTGCCATATGGACTAGATGGGCC  
GGGTTTGTATTAAAACCAAGGAACATGCTTTTGGCATCAGTGAATTTCTTTTTGGGTGGAGTTGCTGCT  
TACCAATTTGTTAAGAATTGTCAACTACAGAAGAGATTGGGTGATTCCCAATCCAAGTATTTAATTAT  
ATCTTGAACGGTGATGCAGCTGCTGTAAAAGAAACUAGAACCAGCCAAAGAATTAA

YGR243W\_homolog 132aa (SEQ ID NO 488)  
MASTVQHASKFQRFLNSETGPTVIFWAPVFKWALVAAGLNDIQRFVEKLSGTQQIALFATGAIWTRWA  
GFVFKPRNMTLASVNFPLGGVAGYQLRIVNYRRDLGDSFPMQVFNYILNGDAAAVKEPEPAKN

153/251

YHL021C\_homolog 1224bp public: 1..1224 (SEQ ID NO 489)

ATGTTAAGACACCATTACGCCAATCCGTTTCCACTCGAAATTGGCAGGATACAAACAGCAAA  
 GAAGTCACAGTCACCCATCAACGCCAGAACCTGTACATTCAACCAACCTGTTTGTGAGAGACGCATGCCAA  
 AGCCCCAGACTCGGTAGACCCCATTTCTAGCCAAAACCTATTCACTACAGCAGATGCAGCAACCGGCTTG  
 CAAATTAACGCACCCCCAGTGGTAGAGGATTCCTCATTTGAAATCCAAATTAAGCAACAATGGCAAACTC  
 ACCAACTCAGTCTACUUCGTGTCTATTCTTAGAAAACCTCTCCACCAACAAACGACTCGGCCAAATCTTTT  
 GACAAAGNTAGAACTTATCGGACAAACAAGAACTCGAAAACAACCTTTGCCCTCCCTCAACATGGGACTAC  
 GACGACATTTCTCACCACGACAACCTCTTTCTTCCAGACGTTGTACAACTTGAATACCTACGGGTTAAACA  
 TTTGTCAACAACATCCCCACCCACAAAATTTCTGACATGACAGAGGACAAACGCCAACGCAATGGUCAGTC  
 TACACATCGCCCCAAAAGTTTGGCTACATCAAGAAAACATTCTACGGGACATTTATCGACGTCAAGAAC  
 AAGAAGGAAAAAGCAACCAACATTTGCCATACCAACACGTTTCTTCCATTTGACATGGACTTGGCTCTAC  
 TACGAGTCACCCCCGGGATTACAGTTTGTACACGCTATCCAGAACTCTACGTTGGGCGCGGAAACATC  
 TTTCTGTGACTCGTACCTTGGCTGCTGAGCATGTCCCGAAAACCGACCCAGGCAATACACGGCACTCAAC  
 CAGACCCCAATCACCTTCCACTACGACAACAACAACAGGACTACTACTACTACAAGCGGCGGTTAATCGAT  
 GAAGACCCCGAGGTTGGCGACGGGTTCCCGAAAAATCGCGTCCATCAACTATGCCCGCCATTCCAGCGG  
 CCATTCGAGGTTGACCCCCACCCAGACTTTATCCCGGGAATGCAATTTATTTGAAACCTTCATCAACGAC  
 CCGGCAAAACCACTTTGAAATCAAAATGCCAGAGGCACTTGTCTCATTTTCCGAAACAGAGAAGAGCCCTT  
 CACTCGAGAAACGCATTTCCGACCTGAACAACCGCGACAGATGGTTAATGGGCCTTATGTTCCACGGC  
 GACAGTTTCTAGATCAAAATTAAGTATAGGCTCTAGAAAAAGTACATACCTAA

YHL021C\_homolog 407aa (SEQ ID NO 490)

MLRQPLRQIRFHSLALACYNSEKVTVTINGRTCTFNNVFLHDACQSPDSVDFISSQKLFTTADAATGL  
 QINAPFVVEDSSLKTQWSNNGKLTNSVYPVSFLFNYSTNKRIGKFFDKDRKLWDKQLEEDNMFASLNMEDY  
 DDILINDNSFFQTLYNLNRVGLTFVNNIPTPQLSDMTEDNATQWPVYKIAEKFGYIKKTFYGTLPDVKXN  
 KKEKATNIAYINTFLPLHMDLLYYESPPLQLLHAIQNSTLGGENIFCDSYLAAEHVRKTDPRAYTALT  
 QTPITFHYDNNNFYYYYKRPFLIVEDPEVGDGFPKIASINYAPPFQGPFEVDPHIDFIRGMQLFETFINJ  
 PANHFELKMPGTCVIFENRRALHSRNAFSDSNNGDRWLMGYVDGDSFRSKLRIGYRKVHT

YHR162W\_homolog 354bp public: 1..354 (SEQ ID NO 491)

ATGTCATCATTEAAAAAATCACTGATTTTCTATTTTCAAAAACATCCCTTAGATATGTCTGTACAACCT  
 CATTTTTGGGGTCCAGTATCAAAATTTTGGGATTCCATATAGCTGCTATTTTAGATTGAAAAAGATCCCT  
 GATTTAATTAGTGGACCAATGACTGGTTTCATTAATACCTTTATTCCTTTAGTGTTTATGAGGTAATCAATG  
 GCAGTTACTCCCTCAAAATCATTTATTATTTTGGGTGTCAATTTGTTAATGAATTGGCACAATTGAGTCAA  
 GGATTTAGATGGGTTAAACATCACTATGATACTTCTTCAATGATGGTGAAGATACCAAAAAGATAACT  
 CAAAATTTGA

YHR162W\_homolog 117aa (SEQ ID NO 492)

MSSPKKFTDFLFSKQSLRYVCTTHFWGPVSNFGIPIAAILDLKDPDLISGPMTGSLILYSLVFMRYSM  
 AVTPQNYLLFQCHFVNELAQLSQGFRWVKHHYDTSNDGEDTKKITQN

YLR109W\_homolog 531bp public: 1..531 (SEQ ID NO 493)

ATGACTGACGGTAAATTTCCCAACTAACATGAACCAAAATACATTCCTTATTCTAAAGATCATGCAAGT  
 TTAAGTGTCTGTCTCTAATCCAATACCATTTGGATTTAAATCTTTATTTCCAAATAACTACTGTTGATGTC  
 ACTGCTGTGCGCGGTGCTTTTACCCCAACTTGTACTGAACAACATATCCCTCATTTATTTGAAACATTTG  
 AAAGATTTCAAAGACAAGGGCGTCAAAAAAATCATTGTTTATCTCCCAATGATCCATTTGTAATGGCA  
 GCTTGGGCTAAAGCTTTGGGTTATACTGATGAACAAAATTATGTTTATTTTGGCTACTGATCCCTAATGCT  
 TCTATTTCTAAAGAATTGGGTGATGGATTGTTGCTGATTGACTCTGGCAGGATGGGATTAACATTA  
 CAAAGATATGCTAGTATTGTTGTTAATGGAGAANTCACCTTATTTGGAAACTGAAGATAGTTTGGGATTC  
 CTGGAATTTCTAGTGCTCAAAACATTTTAAAGAGAAATCCACAATTAA

YLR109W\_homolog 176aa (SEQ ID NO 494)

MTDGKFPNTNRPKYIPYSKDHASLTACANPIPLDLKSLFPNNVTVVVTAVIDGAFPTCTEQHIIIPDYLXHL  
 KDFKDKGVKKIIVLSANDPFVMAAWAKALGYTDEENYVIFATDPNASISKELGDCFVADITSAAGMGRRL  
 QRYASIVNGEITYLETEDSLGFSEISSAETILKRIHN

YLR206W\_homolog 879bp public: 1..879 (SEQ ID NO 495)

AAGAGAAAACAAAATAACAATTTATGGATTTGAATGATGAAACACCACCACAACAACCTCAATATATAT  
 TTAGCAACCGGATTCTATCAACAACAACCACAATTTTATGCUUAGUAACUTCAATGGCAACAATTCCAA  
 CAATATGATATGTTTCCCAACCAATACAGAATCCAATGGACACAGGATTATATANTCAACAGGCCTAT  
 TATCAACAACCACAACAGCAGCAACAACAGTTTCAACCAACCAAGTTTACTGGTTTAACTATGGACAA  
 CCACAACAACCACAAGCGCAACCAGAACCTTTACAACCATTTGAAACAGGATCCATTAATCCATTTGCC  
 ATGTCCTTCTGGGTCAAGACAATACCAACAAGCCACCAACTCAATCCCTTAAACAGTTTAGCTGAACAGCAA

154/251

CAACAGCAACAGCAGCAGCAACCACAATTCTTTTACTCAGCCAACTACTGCTCCACTCAAAACAACAAAAC  
 ACATCATCATCAAGGTTTAAATGAAACTCATGAGTTGAATGATTTTATTAAGTCAAGGAACTGGATTAGAT  
 ATATTGGGTAACTACTGGAGATACTAGAATCCCACATCAACATACAAAGACACAAAATTTTATTAATTC  
 AGAGGAACTGGATATAAACAACTGGTAATGAACCAATTAGATTAGTTCTTAATGCTACAGGTAATCCA  
 TTTCTTAATACCTGGTATTGGATATCAAGCTGCTACACACAGCAAGTGCCACAAACAGCAAGTGCCACAA  
 ATCAATCTGCTTATACTGGGTATGGATTTGGTAACGCTCAACCTCAACAAACACAGCAATACCAACAA  
 CAACAACAATCACGTAATGGTAATGATGGCCCAAGTTTAAATAGATATTTAA

YLR206W\_homolog 292aa (SEQ ID NO 496)

MRKQNNLLDLNDETPPQQPQYVLAIFVYQQQPQFYAQQPQSQQFQQYDMFGNPTQNPMDTGLYNQQAY  
 YQSPQQQCCQFQPNQFTGFNYGQPPQPOAQPEPLOPLKGTSSNPFAMSSGSDNTNKPPTQSLNSLAEQQ  
 QQQQQQQFQFFFTQPTTAPLKQQNTSSSRFNETHELNDLLTQGTGLDTFGNTGDTRIPIQITKQTNQFINS  
 SGTGYKQTCNEPTRLSSNATGNPFLNTGTGYQCATQQQVPPQQQVPTNPAYTGYGFGNAQQQQHQQYQQ  
 QQQSRNGNDGPSLIDI

YMR043W\_homolog 789bp public: 1..789 (SEQ ID NO 497)

ATGGCTATTAAAGAAGAAACAATGAATTTAGTCAAGGTAATGAGGGGAATTCCTCATCAACCAATAAC  
 AACAAATAACAGCAACAACAGCAACAGCAACAACAATGCTGATGTTTCTGACUAGTAGATGATGACGAT  
 GATGACGATGGTACTTCTCAAGGTAAAACTCAAAGGAAAGAAAGAAATGAGATCAAAATTCATTCAA  
 GAAAATCAACAGCTCATATTACTTTTTCCGAAACAAAAGCTCGGATTATGAAGAAAGCTTATGAATTA  
 TCAGTATTGACAGGTACTCAAGTGTTATTATTAAGTTGTTTCAGAACTGGTTTGGTTTATACTTTTACC  
 ACTCCTAAATTACAACCTTTGGTCACTAAATCTGAAGGGAAGAACTTGATTCAGCATGTTTGAATGCT  
 CCTGAAGAAGGATTTGGGTGATGATCAAGAGAATCAAAGTGATGGAAATCAAGGAGATTCACTGATCAA  
 AGCCCTGCTCCAGCAACCAATCCAAATGTCAATGGGTGCTGCAGGTCATGCTCATCACATTCAACAACAA  
 CAACAGCAACAACAACAAGCTCAACAGCAAGCTCAGCAACAATGCGCACTCACTTCTCATGGTTTA  
 CCTACACATTATTCCTCACTCAAGGAGCTGCTAATCCTCCTCTACCTCTCAACAACAAGGTCACAT  
 CAACCTGGTATTCCATTACAAGGTGGTTATAGTGATCAATACCCTGTATTTTGGTAAATATTCAAAATAAC  
 AACATACCTAATCAACAGCAATATCAATGA

YMR043W\_homolog 262aa (SEQ ID NO 498)

MAIKKEETNEFSQNEGNSHSTNNNNNSNNNSNNNADVSAFVDDDDDDGTSQGKTQKZRRKIEIKYIQ  
 EKSRRHITFSKRKAGIMKKAYELSVLTGTQVLLLVSEIGLVYTFITPKLQPLVTKSECKNLIQACINA  
 FEEGLGDDQENQSDGNTGDSFDQSPAPATNPVNGAAGHAHHIQQQQQQQQQAQQQQAQQQMAPMPSHGL  
 PTHYSNPQAGNPGVPPQQQQQHQPGLPQCCYSEQYSYFCNIQNNNIPNQQQYQ

YMR256C\_homolog 330bp public: 1..330 (SEQ ID NO 499)

ATCAATATCAAAACAACAGACGACCAAAAGTCTGAGAGAGAGAGAGAGAAAAAATATCGGCTCATTATT  
 TTCAATTCACTTTTAAATCCTAGTTAACTACTATTTACTTTCTTTCTTCTAACTATCCATCCCACCATCCT  
 ATCTATTTCAAATTATGAATCCACAAAGAATTATTGAATTACAAAAACATTATCAAAATACTCCTAAACCA  
 TTAATGGTTAAGAGGTAGACAATCCCACTTTTACTTTTATCCATTATTAATGCTTTATTTGCTGTTAGTACT  
 GCCATCCCATTATATTATAGTGTTAGAGCTGTTGCTGGTATAAAAGATGAATAA

YMR256C\_homolog 109aa (SEQ ID NO 500)

MRMKQPDQKSEREREKKYRIITFNSLLIANTYIFLSSKVPSSHPIYSIMNPQRIIEQLQKHVQNTPKP  
 LNLGRGRQSAFLVYFFYALFAVSTAIPLYYSVRAVAGIKDE

YOR267C\_homolog 2091bp public: 1..2091 (SEQ ID NO 501)

ATCCAGATAAACATAAACTCAAACATATTCGAAAAAATAAACACGACAAAGATGACGAAATGTCTTTG  
 TCAACCTCAAAACCATTTCTACGGAAGTACACGGAAGTTTCTTAGGATTTTATATTGGAAGACATGAATCG  
 GCGGACTCGTTGACTTCTCCAGTTATGAGCAATTCATCCGAAAGTCATCATCACAGCCATCACCCCTCAT  
 CAAGCCAAATTCAAGTGCAAAACCATCTGAACCTTCTCCAGTTTATTCCAATATCGGTACTGCCACTACC  
 ATTCATCAATACAAATCACCAACCTCAAGCATCTGGATTACACCGCGGGGACTCCGATAAAAAATCA  
 TCTGGGTCAAGTTGTTGATTTGAAAAAATCTTCAAAAACAAGAAAACTTCAATTCGAAGAAAGGAACGA  
 CATAGTATTTTGGGACAATATAGCAATCAGTTCATTTCAUACUACCAATGGCGCAGGTTTATTCCGCT  
 GGTGCAGCGTGGGGAAACGGCAGTGCCTTGCAATCACGTGAACAATCATCTACGTCAATAGCCACTTTA  
 ATCAATCAAAACATCTTCTCAACTTTTGTACAATGCTTCACATTTCTGTCAATAGCAATCGAGATCCCTTC  
 ACGGACGACAACCTCTCATTGTTGGAAGAATATGGAAGATCGGGAAGAGTTGGCCAGTGGAGCCGGT  
 GGTTCGCTCAAAATTANTCACGAGGCCAGTCACTGCAAGACCTTTGCTGTTAAAGAAATTAGAGCGGAA  
 AGATCTACTCAATCATTCGAAGGATTACACTAGGAATGTACTGCTGAGTATTTGATTGGTTCTACTTTG  
 AGGCACCCAAACATCATTAACCATCGATATCATCCATGAAACANTCGTTATTTTGAAATTTATGSA  
 TATGCACCTATAGATTTCTTTGCTGTTGTTATGAGTGGAGAGACGTCTCGAACGGAAATCAATTGTTG  
 TTAAGCAATTTATCAAGCTGTGCCATATTTACACAAATTAGGGTTGGCCCATCGTGATTTGAACATG  
 GATAATTGTTTATAACGAATGAAGGATTTTGAAGATATTCGATTTTCTAGTCTGTCTCATTTTCAAG

155/251

TATCCCTACGAACAGTTTGGTAACACAAATTCATTTCAGCCGCTTCATGGTATTGTTGGATCTGATCCT  
 TACTTGGCCCCCGAGGTTTGTGAATCTCCCTAATAGCTACAAACCCACACCTGTGGATTTTATGGTCTATT  
 GCCATAATTTACTCTTGTATGACTTTGAAGAGATTTCCTTGGAAAATACCTAGTCAAGAAAAGGATAAC  
 AGTTTCCGACTTTTATTGTCATGTATGATGATAATTTCCATGATTATTATTGTGACTAACGAATGTCATAAA  
 CTTTGTGTGCAACAGCGTAAACTAAAGAATACAAATGTTAGACTGAACAAAAGGAAAAAGCAGCTAGAA  
 GAGGAAAAGGCGGACAAGCCTGAAGAAGACGAAGAAATGAAAGATGCCGATAGTGCACCACAGCAACAT  
 CATCATTTCTCATGATGTAGAGCTGGGAAAACTGSTCGATCTACCGTTCGCAAGACAACTCAAATGAA  
 GCTGTACCGTTTAAACAGATGAGCAAGCAGAAGAGATTATGCCACAATTAATGAGATTGATAGAAAA  
 CTACAAGAGTTTGAAGATAAAAGAATCAACTTAAAGAGAAATATGAGGCTTTGCCAGATGCTGATCCT  
 AGATATCAAAAACAGTTGGCACAAATTCACGAAGAGGAAGAAAAGCAAAGACTAAAAGATGCCGAGCAC  
 GGTGCCGATGAGAAAAGAAATCACATCATAAACAGATTTCATGCTCCGTATAGATTGATGAGATTCTTG  
 CCACATTGCTGCTAGACCAGTCATATCAAGATTATTGGAGGTTGATCCAAAGAAAAGAGCAACTATGGAA  
 GAAATTCTAGAAGATGAATGGATTAAACAAATTCAATGCTGTACAGTTAAGCCACTTTCAAAATCAACA  
 GATGCAACATTAGATTTTATTTGAGGATGAGGACGAAGCTATGGTGAAAGGAGTACCTCCACACGAGCAT  
 ACAATTTGTCAAAGAAGGTTGA

YOR267C\_homolog 696aa (SEQ ID NO 502)

NPDKHLKLFQGNKHKDELSISTSNHSHGSTRKFLGFHIGRHESQDSLSTSPVMSNSESSESHHHSEHDE  
 QANSSANHRNFSFVHSNTGTAATTIPSISQSPQFQASGLHRGDSDEKSSGVSVDLKFFFKTKKTSNPRKEG  
 HSILCQYSNQLHSPPPMAQVHSPGAGSGNGSALQSRHQSSSTSLATLINQTSQLLYNASHSVNSNRDFF  
 TDDNSPLVKYKGLCKEIGSGAGGSVKILTRPSDSKTFVKEFRKRSTESLKDYTRKCTAEYCIIGSTL  
 RHPNIIKTIIDILHNNRYFBI MEYATIDFFAVVMSEGMSRTEINCCLKQIEGVAYLHLKGLAHRDLKY  
 DNCVLTNEGILKTIIDFGSAVLFKYPYEQFGNNNSIQPCHGIVGSDPYLAPEVLKSPNSYNPQPVDLWSI  
 ALIYCCMTLKRFPWKIPSQEKUNSFRLYCMYDDNFHDYLSNECHKILQOKKLKNTIVRSNKRKKQLE  
 EEKCKPPEEDEMKGADADAPQOHHHSHDVESGKKGSTVYKDKSNEAVTVLTDQAEELMAQLNEIDRK  
 LQEFEDKKNIATKYEALRDAAPRYQKQLAQIHBEFFKQRLKDAEHGADEKKKSHHKQIHGFPYRLMRL  
 PHAARPVISRLLLEVDPKKRATMBEILEDEWIKELQCCTVKPVSKSTDATLDFI EDEDEVLVKGVPPHEI  
 TTVKSG

YOR374W\_homolog 1500bp public: 1..1500 (SEQ ID NO 503)

ATGTTTAAAAAGGCCTTACCATTAGTCAGCAAGCTCACAAACACCAAAAGGATACACTTATAACCAACCC  
 CTTGGGTTATTTCATCAATAACGAATATGTTTCAACCCAAAGCAACAAAAGACATTTGAAGTTATTTCTCCA  
 TCCACTGAAGAAAAAATAACTGATGTTTACGAAGCTTTAGAAGAAGATATTGATACTGCTGTTGAAGCC  
 GCACAAGCCGCATACCACAATGGTTGGGCTCAAGGGCCACCAGAACAAGATCAAAAGTTTGTGTCAAA  
 TTAGCCGACTTGATTGAAGAAAATGCCGAATTATTAGCTCAAAATGAAACITGGGACCAACGGTAAATCC  
 TTACAAAATGCCAGACGTGATGTGGCCTTGACAGCTGCTTACTTCAGATCCCTGCTGGTTGGCCGAC  
 AAAATTTTGGGTTCCCAAAATCAATCTGCTAACACTCATTTCAACTACACTCAAGAGTCCCAATTAGTTC  
 TGTGGTCAAATTATTCCTTGAATTTCCCAATTATTCATGGCTTCTTGGAAAATGGGACCAGTTCTTGCT  
 ACTGGTTCTTACCCTGTTTTGAAGACTGCTGAATCCACCCCATTTATCTGCTTTATATCTTTCCCAATTTG  
 TTAGTCGAACCCGCTATGCCAAAAGCTGTATCAACATTGTTTCGCTGTTTTGCTGCTTACGCTGGTGGCT  
 GCCATTGCTTAAACATCCAAAGATTGAAAAGTTGCTTTTCACTGGTTCTACTGCGACCCGTA AAAATATC  
 ATGAAATGGCTGCTGAATCAAACTTGAAAAAAGTTACTTTGGAATTGGGTGGTAAATCTCCAAACATTT  
 GTTTTCAACGATGCTGATTTGGACAAGACTATTCAAAACITGATTGTTTCTATCTTCTACAAATCTGGT  
 GAAGTCTGTTGCTGCTGCTTCTGCTCTTTGATTCAATCCGGTGTTTAUGACCAAGTGTTCGAAAAATTC  
 AAAGAAGCTGCTGAAAGTCTCAAGGTTGTAACCCATTGACGCAAGACACTTTTATGGCTGCCCAAGTT  
 TCTGACGTTCCAAATTGTCCAAAATTTTCAAAATACGTTGAATCTGGTAAATCTCAAGGTGCTACTGTTGTT  
 ACCGGTGGTGGTACAGCTGATGGTAAAGGTTACTTTGTTGCTCAAACCAACTATTTTCGCTGATGTCAGAAA  
 GATATGGATAATTGTACAGAGAAGAGATCTTTGGTCCAGTTTGTCTCACTTTGATCAAATTTGATACTGTTGAC  
 GAAGCCGTTGAATTGGCCAATGATTCCGATTATGGTTTGGCTGCTGCTATTCACTCTGCTGACGTTAAC  
 AAATGTATTGATGTGGCCAACAGAGTTAAAGCCGGTACTGTTTGGGTCAAACACTTATAACGATTTCAC  
 CCAATGGTTCCATTGGGAGGATTCAGTCTTCAGGTATCCGCTACAGAAATGGGTGAAGAAGTTTTCAT  
 CAATCACTCAAGTCAGAGCTGTGAGAATGAAAATCAACCCACCAAACTAA

YOR374W\_homolog 499aa (SEQ ID NO 504)

MFKKALPLVSKLITPKGITYNQPLGLFINNFYVHPKQKQKFFEVISPSTEEKITEVVEALEEDIDTAVEA  
 AQAAHYHNGWAQGPPEQRSKVLPLKADLIBENAEELLAQFTWDNGKSLQNARGDVALTAAYFRSCGGWAD  
 KILGSQINTGNTHFNVTQRPVPCGQIIPWNFPLLMASWKLCPVATGSTTVLKTAESTPLSALYLSQL  
 LVFAGMPKGVLTNVSFGGATAGAAIAKHPKIEKVAFTGSTATGKIIMKLAABSNLKKVITLELGCKSPNI  
 VFNDADLCKTTONLIIVSYNSGEVCCAGSERLLIQSGVYDQVVEKPKFAAESVKVGNPFDEDTFMGAQV  
 SDVQLSKLLKXVBSCKSQGATVVTGGARADGKGYFVKPTIFADVKKMDIVREETFGPVVTLIKFDTVD  
 EAVHILANDSDYGLAAGIHSADVNNKIDVAVRVKACTVWNTYNDPRPMVFFGGFSASGLGREMGFEVLH  
 EYTQVRAVRKKNPFPN

YPL089C\_homoLog 1836bp public: 1.1816 (SEQ ID NO 505)  
ATGGGTTAGAAGAAAGATTGAARATAGAACCATTGACAGACGATAGAAATCGTACAGTGAAGTTTGTGAAG  
CGTAAGCCAGGGTTATTTTAAAAAGCTCATGAATTAGCTGTCGCTCTGTCAAGTGAATTAAACGGTATTT  
ATCGTTGGCAATAATAATAAAGTATATGAATATTCTACTGTTGAGGCAAAATGAGATTTTTTAATGCCTAT  
AATAAAAAACATTTAAAGCTCAGAAAAACATGATACATGAATCGAAGATTTCCGAACTATTATTTCGAAATTTAGA  
AAGAAACGACATTTAAATGAACCACTTAATGAATAAATCAGGTCGTGTAGTTGGCACTAATAACAUATTG  
AACGATGAAGACTATGATCATAATGTTTCATGAAGCGGGCGATGAGGATTCGGAATATGAAAGCCATGAT  
AATCTCTCCACAACCTAAACCGGCACAAAAGATCAGAGTCGGTTAAAAAAGAGCAAAACCCCAAGTGT  
AATAGTACCCCAACCTCCACCACCGCTCCACCACCTCATATATCTTTAAATTAATGTTCCAAACATTTACC  
AACCCCCAAAATTACAAAALACAGATTGATGAGACAATAACACTTCGGCAACCGCCCCCTACTCGGCAC  
AAAAATGAACCAACCGATGCAACCGACCAAGTATTGAGGCTACAAATACCGAATGATGCCAACGCAATACG  
AATAATTTCCCATAGTGGTGTTAATAATAGTAGTGCGAAGCAGCCGAGAGAACAGTGACGGCAGTCGAC  
AATAGTGCAACCAACCAAAACACTCAATCGAGCAATACAAACATCAGGTACAGGGGACTGCTGATACCAAT  
TCATCGCAACTAAATTCRAATGGTAATAGTAATTTAGTGCCCGGAATGTTCCMAATACCAAGATTTTCG  
GGATTTTCATCGTTTCGATCACCAGACTCAGCAAAACCAACATTAACGTTACCTTTGCAAAACCAATCA  
CAAAACGTATCTCCAGCTAGTGTGTGATCACCAGGTTTTACCAATTGACAGGAGGAAGCAATGCAATATTT  
CGAGGAATGCAACCAATCAACCGTGGGTGGTTGCTATGTCATTTATCCAGCCCAAGTATATCAGCAATAT  
CAAGCAATTCCAAAATCACTCAACAACCAAGAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
CAATCTCAGCCGCAGCCATCATCGCAACTGGTTGGAAATCAAAATGCACAAATTGGAATCAGCAGCAGCA  
TCGCGTTCTGGTTTACCGACAGGGACACAATTTAATAATGGTGAACAAACACCAATTTTCAAGATTGCCA  
TCAAGTATACGTTAATGATATGTTCCCTTTCCCATTCCTATCAAACTTTCTTGCACTCAAGATTGGCCA  
TCAGGTATAACCAACCACTACTCATCTACCAAGTATTTGTAATATGCCATTGAGTGAATTTGCACTG  
CAACCACTCCCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA  
CAACA  
CAACAGCAACTGCAAGTACCTGTTATCCCAATACAACAACAACAACAACAACAACAACAACAACAACA  
AATCGCAAAATCAGCTAATCTAATACCAGGGTTTTTACAAAACCAACACAGCCACTGGAAATTCGGCA  
AATGCTTTCCAGCTGAGTGATGCTGGTGTGTTACTAATCCCAACCCACAGCAGGAAGTTCAAGTTTACCA  
GATGTCATTAACCAACAACATGAGACTAATAAAAAATCATATAA

[illegible]

YAL003W\_homolog 693bp public: 1..693 (SEQ ID NO 507)  
 ATGAGTGCACAAAGAAGATTTAAATUTTTATATCTGCACAATAATAGAGTTTATTTCAAATGAGACAATTGCATT  
 TTACAAATTACCGACTACAGGAATAAACAAAAAATATAAACGATATACTAACATGTTTTGATAGTACTACT  
 CCCACTCAAGCTCGATCTCACTCTCTACAAAAGCTTTTCCAAAACCAATTCCCACAATTCCACGAGATGGTTTC  
 AACCACTATTGCTTCACTTCACTGAAGAATTCCGAAGACTGCCAGCCGGTAAAGCCCCGAGCGCTTCTGTGGT  
 TCTGCTGCTGCTCGCTGCTGAAGAAGAAGATGACGAAGATGCTGCAGCTGTGTCGGTTCTGATGATGAAGTT  
 GATGAAGAAGCTGAAAAAATTGABGCAACPAAGATTAGCTGAATACGCTGCTAAGAAGGCTGCTAAAGGT  
 CCAAAACCAAGCTGCCAAATCTATTGTCACTTTGGATGTCAAACCATGGGATGATGAAACTGATTTGCAT  
 GAATTATTGACCAACCTCAAGCTATCGAAATGGAAGGTTTGACTTGGGGTGCTCACC AATGGATTCCA  
 GTTGGTTTTCCCTATTAAAAAATTACAAATTAACTTGGTTGTTGAAGATGCTTTAGTCTCATTGGATGAC  
 TTACAAGCTGCTGTTGAAGAAGATGAAGACCACGTCCAATCTACTGATATGTCTGCTATGCAAAAATTG  
 TAA

YALCQ3W\_homolog 230aa(SEQ ID NO 508)  
MSDKFCDNLISDNNRVISMRLILQLSITGINKKYKRYTNMFDSITATQADVTYVKAPOKEFPQITRW  
NHTASFTEEFENIPACKAPASGSAAAAAEFFCEDVDLPGSDDEVDRARKIKQQRIARYAAKKAAG  
PKPAAKSIVTLDPKWDDETDLDELLTNVKAIEMGLTWGAQHWVPGVFGIKKLQINLVVEDALVSLDD  
LQAAVEEDAEHVVSTDDAAMOKL

YAL060W\_homolog 1185bp public: 1..1185 (SEQ ID NO 509)  
ATGAAGGCAATTGTACACCACGATAGAGGAGATACTAGATACGACCCCAATTTCCCTGATCCACAAATC  
ATTCGACTGGATGATGTCAAAGTCAAAGTTCATTATTGTGGGATTTCGGTACTGATTTAAAGAATAAT  
ACTGATGHHXGGATTTTTTXXXCACCGAAACCTCAATTGAATGAAATTTCCCAATCCCATCAATTCAA

157/251

GTGATGGGTCATGAAATTAGTGGTGAAGTAATTGCTATTGGGGATGATGTAACCAATGTAAAGTGGGT  
 GATAAAGTTGTTGTTGAACGTGACAGGAACCTTGTTPAGATAGACATCGTACCAAGATCCTAAAAATGGC  
 GATCTGCCIAAACCAAAATGTCCAACTTGTGTTTCGGGTAACTATAATGCGTGLGATTATCTTGCTTTA  
 ATTGGTTGTGGATTGCTAATGGTGGATGTGCAGAAATTTAGTTGTTGCTAGTCTGAAAGTTATTGCA  
 TTCGATCAGAAATAAAATCCCTATGGATATTGCGGCATTAATTCAACCAATAGCTGTTAGTTGCCATGCT  
 GTTAAAGTATCAAAATTTTAAACCCGGTTCATATGCATTAATTTAGGTGGTGGCCCCATTGGATTAAACA  
 ACAATTTTGGCTTGAAAGGTAATCAAGTCTCCCAAATTGTTTAAAGTGAACCAAGCATTAGCAAGAAGT  
 CAATTGGCAGAGAAATTAGGAGTTATTACTTATGACCCCTACGGGTAAATCAATCGAACAATGTGTTGAA  
 GACTTAAAAAATTATCCCGGGAGGTTATGGTTATGAATATTTCATATGATTGTTCTCGAGTTAAGGCA  
 ACTTTTGAACCTGGATTGAAACTTTGAAAATTGGTGGATCTGCAACAAATGTTGCCATTGGGCTCAT  
 AAATCAATTCCATATATATCCTATGGAATTTACCTTTTCAGAAAAAATGTTAACTGGATCAATTTGTTT  
 GTTAAAAAGATTTTGAACAAATCAATTAAGCAATTGAAAATGGTTTAAATATCGATTGATGAATTGAAA  
 ATGTTGATTACCTGAAAATTCATTTACAAGATGGAATTGAAAAGGGTTTTCGAATTAAATTAATCAC  
 AAGGAAAAACATATTAATAATTGTTTCTCCGAAAAGTGAATATTTACTATGCAATGGAGTAAATGAT  
 TCCAATAAATAA

YAL060W\_homolog 394aa (SEQ ID NO 510)

MKAIVYHDRGDIRYDPNFFDPQLIRSDDVKIKVHYCCICGTDLKEYSLGPIFFPPKGELENEISQMESTQ  
 VMGHEISGEVIAIGDDVTNVKVGDKVYVKTGTCLDRHYQDPKNGDSPKPNCPSCVSGNYNACDYLAL  
 (GCGFANGGCAEYLVVASSKVIADFQNKIPMDIAALIQPIAVSWHAVKVSNEKPGSNALTLOGGPGLT  
 TIFALKGNQVSOIVLSEPALARRQLAEKLGIVITYDPTGKSIEQCVEDLKLSPGGYGYEYSYDCSCVKR  
 TFETGLKTLKLRGCATNVAIWAIKSIPLYPWEITLSEKMLTGSICFVKKDFEESIKATENGLISIDELK  
 MLITSKIHLQDGIKGFLELINHKEKHILFSPKSKYLLCNGVNDNSK

YBL058W\_homolog 1116bp public: 1..1116 (SEQ ID NO 511)

ATGTCTCAAAATACTCCAGATTCCCAATTGATTGCTGAATTTGTATCTATAACAAATTCCTTCTACATAC  
 CTTGCTGAACAGTATTTACTGAGAAACAGCAATGATTTAGTGGAGCCAGTTGAGGATTTCTATGCCAAC  
 AATGAACCATCTCAAAAATCAGAAACCAAAAAATCTTCTTCTTCTAATGCTAAAGGCTCTGGTGGTTAA  
 ACATTTAGAGACTTGAACGATGAAGATGATGATGAAGAGGATGACAAGACCAATACCAATTTCTTTACT  
 GGAGGAGAGAAATCAGGATTGCAAGTTCAAGATCCCAATAAAGATAACCAATATGACAGATCAATAAATT  
 GATCAAAATTTTCCAAAAGCCAGAGAACAAATGCAACCAACAGATGATAGACCAAGTGCTTCTCAAGAT  
 GATCAACCATCACCAATTAAATTTTTCAGGCAAGCGTTCAAAATTGCGTGAACGGAATGAACCAAGTCAA  
 GTAGTGGAGGATCCTAATGCCAGTGCTAABAAATTCAGACCTAGTAAAGTGACTAGAGAAATTACATTT  
 TCGAACAAGGTTTACAGTAGGTGATGGACCTTTGTCATAGATACCAATGATCCAACAAACGCCAGTGT  
 TTGCAAGAAATTGAACCAAGGAAGAGTTCCAATGTCAATTTTAGATGTTGAAATTTGGCCAACATGTTGA  
 GTTTCTCTATACAGAAACCGACGAAGATTGCGAACCTCCGAAAAGAAAATTGGTGGTTATCACCGT  
 GUAGGTCATAGACTAGGCTCACCCAGTACCTGCGGAGGTACTTGTAAATAATGAAGCATCATCTCAACCT  
 GATATCAAAACCCAAACTGAAATTTCTAAACCAAAAGACGAAGGCGAAGCTGACTCCACACTTCAATA  
 ACATTTGCCAATGGTAAAGAACATCACACAAATTCATTTCTCGGATTTCTATTCTCAAGGTTTATCGAA  
 TTTGTTAAAAATCATGAATATAATTTCTGAACCTACTAGACCATTCACTTTAAAGTCATCCATTCCAGTC  
 AAACCAATAGAACCAAGTAGTGACATTACAATTTCTGATGCTAAATTTGAAAAATGCAGTGATTGTTCAA  
 AGATGGAAATAG

YBL058W\_homolog 371aa (SEQ ID NO 512)

MSINTFDSQLIAEFVSTNNSITYLAEQYLSRNSNDLVRAVEDFYANNEPQKSETKKSSSSNAKSGVK  
 TFRCLNEDDDDEEDUKTNINFTTGGKSGLQVEDPNKDKDNORSIIDQIFQKAREQMQQFEDRPSASCC  
 DQPSPIKFSGKQPKIGDGNFESQVVEDPNASAKKFRPSKVTREITFWKQGFVTGUGFLHRYDDPRNASV  
 IQELNQCRVPMISILDVEFCQDQVDVSVYKCTDEQWTPPKRKIGGYHAGHRLGSPVPGEVLVNNEASSQP  
 DEKTEPEISKPKNEGGDSTVQIRFANGKRTSHKFNSSDSILKVYEFVKNHEYNSEPTRPFTLSHAPPV  
 KPIEESSDITISDAKLKNAVIVQRWK

YBR039W\_homolog 804bp public: 1..804 (SEQ ID NO 513)

ATGGCTCTTAATCCATTAAAAACATTGAAAAATCACAAATACCATGAAGATTGTTGCCTCTACTAGA  
 TNGAGTAAAGCTCAAAAAGCCATGGCTTCATCTCGTGTCTTCAATGAAACTGATAAAGAAATCTTTGTCT  
 AATGCTGAACCAAAACCAATTCAGAAGAAGCTTCTAATCTGATGACAAAACCTTATTGATTGTTGTT  
 TCTTCCGATAAAGGTTTATGTGGTTCTATTCATTCTCAAGTTTCCAAAGCTGAAUAGAAAGAGAACTGAA  
 GAATTAATAGGTAAATGCGATATTTGTTGATTGGTGATAAAGTCAAAGCACAAATTTGAGAACTTAT  
 GCTGACAAAAGTTAAATTCCTATTCAATGGTGTGGTAAACAGAAACUAAATTTCACTGAAGTTGCCTTA  
 ATTGCTGATGAAATTGCTAAATTAGGTAACATGTTGAAATTCCTTACACAAAATTTGTTTCT  
 GGTGTTTTCATTGAACCATCTAAATTTTCCATTTATGCTGCTGATGCCAATTGCTTCCAGGTTTA  
 AGCAAAATATGAATCGAAAAATGAAGAAATCACTTCTGATGTTGCTCAATTCCTTTTATGCTAAACAACTTG  
 TTGACTGCTATGGCTGAAGGTTATCTATCTGAAGTTTCTGCTAGAGAAATGCTATGGACAAATGCCCTCC

158/251

AAGAATGCTGGTATATGATCAACAGTTACTCTATTTTGTATAACAGAACTAGACAAGCCGTCATTACC  
AACGAATTGGTTGATATCATTACTGGTGCTTCCTCATTGGACTAG

YBR039W\_homolog 267aa (SEQ ID NO 514)

MRLKSIKNIEKITNTMKIVASTRLSKAQKAMASSRVFNETDKELLSMAEPKPIEEEASKSDDKTLILIVV  
SSDKGLCCSIHSQVSKAARKKTEELNGNVDLCIGDKVKQILRTYADKVKLAFNGVVGKEEFPNTEVAL  
IADEIAKLGNYENVEILYNKFVSGVSVFEPKFSIYAADAIANSPLSKYLENEEITSDVAQPSIANNL  
LTMAAEGYASEVSARRNAMDNASKNAGDMINSYSILYNRTRQAVITNELVDIITGASSLD

YBR062C\_homolog 450bp public: 1..450 (SEQ ID NO 515)

ATGTTATCTGCATCTAACGAAGAAGCCATAGCATCAGCATTGCGACAATTGAGTGAATCAGAAGGATCA  
ACACTTGCCTCAATCACTCATGATCTGCTTGGTGAACAAAACATCGAAGGGGCTCACTGACGAATAC  
TTGGATACPTTTGGAACGTATTCAGTAAAAACAAATTACTGATAAAGACCGCATCTTGTCCAATTTGTACA  
AATCGATTCAAAGATGATAAGCATCCATTGATTGTTCAGATTTCCTTTCTCGTCACTGAGTCAATCATATT  
TTTGATTGGAATGTGTTGGGCCGTGGTTGCAAAATGAATTCCACTTGTCCAATGTGTGGAACCAATATC  
TTAGAGGTCAGAAGCTAAATAGAAGGAAAATAAATAGATGAAGAAATAAAAAAGGCCUUAAGAAGAAGATTCC  
GAGGAAGAAGAAGAAGGTTGGGATATATATGCAATA

YBR062C\_homolog 149aa (SEQ ID NO 516)

MLSASNEEAIASALRQLSESEGSTLAQSLMDSLGEQKTSKGVDDYLDLFLERIPVKQTTPDKDASCPICU  
NRFKDSKHEPLIVRLPCGHGVNHLFDLECVGPWLQMNSTCPMURTNILEVEANRRKIIDEELKKAQBEIS  
EEEEEGWDIYG

YBR101C\_homolog 855bp public: 1..855 (SEQ ID NO 517)

ATGGAAAATTTATTACATTTGGACATTTGCACAAACATCAGGCGATAAAGCAGCTCTTGAAAAGATTGGA  
GAACCCGATCAAAACCCACTTAATCAATTATTNKTTCCTCCCGATGAAGCCACTTTAATGAAGGAAAGT  
ATAAAAGTGTGTAATCAACCGATGTTCATTTAGAAGATAAAGAGATCGCCTTGGAATAATTTCCAAATG  
TTGATTTGAAAATTTAGATAATGCAATAATATTGGTAATTTGAAATTTATGGAATCCATTGATTGACATT  
TTACCCMAACAAGATACCCCTGTTGAATTGAAAGTACTTATTTGTTGAATAATTGGAACCCGCTGTACAA  
AACAAACCCCAAAATCTCAAGAAGATTTCATTTGAACCTGAAGGATTGAGTGAATTGATAGCAATTAGCACA  
CATCACAAAAATTTGAATTTCAACTGAAGGCATTGTTTGTCTATTTCTTTCATTTATCAGAAATTTTCAA  
CCTGGAATATGCAAGTTTGGMAATTGCAAGCTTTGAAACTCATTAATTTTGATAACAAGAACAACAAG  
TATCAATTGAGAATTTTATCATTAATATCATCCATTTTGAGTAATGGCTTGAAGCATAGCTTTGAAAGCA  
CAATTCANAGAACCAAAATTTACCTCACTATTTAGCCCTCGGTATTGAATGAGGATTCAAAACACTACTTGT  
GTGGCAAAATCTTTAAACAATCTGTTTCTCAATTTGAAATCAATTAACCTATGAGTTTACCTTTACAAGAAAA  
TATGAATAAATAGAGGAATCCAAGTGGTTGAAGCAATTGAGTGAGAACTTAATATTGATGATCTCAAT  
AATCCCAACACAGGCCACATCTCTTAG

YBR101C\_homolog 284aa (SEQ ID NO 518)

MEKLLHWTLAQSGDKAALEKIGEPDQKALNQLFGQPDATLWKESTKVVESTDVSLEDKBIALENFEM  
LIENLDNANNIGNLKLWNPILIDLAKEDTPVELKVLICGTTGTAVQNNPKSQEDFNTEGLSELIELAQ  
DDKKFELQSKALPAISSFIRNPQPGYAKPEKLQGLKLINFUNKNNKYQLRILSLISSILSNGLDDSLKA  
QPKAKLPHYLASVLNEDSNTSLVDKSLNIVSQINQLNYEFSLEEKYBINRGIQWVEGLSEKLNIDDLN  
NAKQATSS

YBR139W\_homolog 1653bp public: 1..1653 (SEQ ID NO 519)

ATGCAATTATCTACATTAGTCACTTGGTTGGCTGCTTTAACTGTGGTGCACAGGCAGTATCATTTCCXHC  
AACAAATTTAAAGATCAGATATATATGGATTCTGAGGAAAGCTCCCCAGATTTATATTTGGAGTCAGCG  
TTCAAAGACTTGGGTTCAATGGCCAGTTGATTTGATTACTGCTTGGGTCAGAAATGCAATCTGAAATTTACA  
CCTGAACAAATTTGCCAAATTAATCAATCAATATGAGTCTAAAAATGAAAAACCAAGAAAAATAAGTCT  
AAATCCAATGTGGAUATTTCTTCAUCAAAGTTCCAAGTTTGAAAAGCTTTCCAATGATATAATTTGCTGGC  
TATTTCAATGCGTGTAAAAGAGAGTTTCCAGAAATTTTGGCTCTTGATACAGGTGAACAAATACACTGGG  
TATTTAGATATTTGACTCATTAGATAAACATCTTTTCTATTTGGTTTTTTTGAAAGTACAAATGATCCAAAG  
AATGATCCATATTAATTTATGGCTTCAATGGGNGTCCAGGTTGCAAGCTCTTCAACCGGATTAATTTTTTGAA  
TTAGGACCATCTCGATCAACAAAACCTTTACACCCAGTTTACAAACCATATTTCTTGGAAATTTCAATGGC  
TGGTPTATTTTCTTATGATCAACCCGTTGGAGTTGCATATTTGATATACAGGAGGAGATGAAGTTAAGAA  
ACTCTCAUTGCTGCTAAAGACGTTTATGTGTTTTTGGAAATTTGTTTTCCAAAAATTTCCACAAATTTCTG  
ACTAATAAGTTTTCACATTGCGGTTGAATCTACGCCGGTCAITTAATACGAGCATTTGCTTCAGAAAC  
ATTAAACATGCCGATAGGTCATTGTAGTTGGCATCTGTGTTGATTTGGTAAACGGTATCACCGATCCAACTG  
ATTCAAGATGGTTTCTATAAAUCAATGGGCTGTGGTGAACGTTGTTTACAAACCTGTTTTGACAACTGAA  
CAGTGTGATCAAAATGGAAGGGATTATCCTAGATGTGCTAAATTAAGTAAATTAATTTTACAGTTTCCAA  
TCTCCCTGACTTTCTCTCCAGCTCAATACTACTGTGATTCCCGTTTATTTCAACCTTAAGCTCAAAACA  
GGATTAATAATCTTATGATATCAGAAAGGATTGTGCGAGGCAAGCTGGTAATTGTATCTAGAAATGGAC

159/251

TACTTGGATGAATACTTGAATCTCGATTATGTGAAAGAGAGCTGTTGGTGCTTCTAATATTGACATTTTT  
 ACITTCATGTGATGACACCGTGTGTTAGAACTTTATTTTATGATGGTGAATGAACCTTTCCAACAA  
 TATGTTGCTGAGTTATTGGACAAATAATGTACCTGATTTGATTTATGCTGGTGACAAAGATTATATTTGT  
 AATTGGTTGGGTAACTTGGCATGGGTAAACGAATTTGGAATATTCAGATAGTGAACATTTTGCACCAAAA  
 CCATTACAATTATGGAAACAAGATGGCAGAGAAAGCTGCTGGCAGAACTCAAGAATCACAAACATTTTACA  
 TTCTTGAGAATTTATGACGCTGGTCACATGGTTCCCTTTGATCAACCAGAAAATGCTCTTAGTATGGTT  
 AATACITGGGTACAGGGAGATTATTTCTTTGGTTTACAGGGGTAATAAATTATCTGAAGCTGATTAA

YER139W\_homolog 55caa (SEQ ID NO 520)

MQLSTLVTLAALTVGAAVSPGNNLKDQIILLDEESSPDLYLESVFKDLGSLPVDLITAWAEMQSELS  
 PEQIAKLTINQVRSKNEKPEKNKFNPMSTFSSPSSKFELSNDKFAGYSMRVKESFPBILGLDTPVKQYTC  
 YLDIDSLDKHLFYWFFBSNDPKNDPIILWLNGGPGCSSSTGLFFELGPSSINKLHPVYNPYSWNSNA  
 SVIFLDQPVGVGYSYTGGDEVKNLTLAARDVYVLELFFQKFPQFLTNKFHIIAGESYAGHYIPAFASEI  
 INNADRSEELASVLINGITDPLIQDGSYKPMGGGGGGYK/VLTTEQCDQMERDYPKCAKLTKLCSYFQ  
 SALTCPVPAQYYCDRLFPYVQTLNPVDTRKDCAPQCCNCPVEMDYLDEYINLCYVVKFVAVGASNIDIF  
 TSCDDTVFERNFILDGDMKPFQYVAELLDNVPVLIYAGDKDYICNWLGNLAWVNELEYSDSEHPAPK  
 PLQLWKQDGGKAAGEVKNIIKHFTFLRIYDAGHMVPPDQPENALSMVNTWVQGDYSFGLGUNKLSEAD

YCL052C\_homolog 1446bp public: 1..1446 (SEQ ID NO 521)

ATGAGACAAAGAACCAACCATTATATATCCTTATCTAGTCATGATGGAATCATACTAATCTTAAATCGA  
 ACAAAATTTCCAAATTATCAAGCATACCTTAATCATTTATTCACAATTGAGAATAAATATACCATCACCACC  
 ACCACCACACAACCTTAACAAATCATCATTTATATCTGGCAATTAAAGAATTAAGAATTCAAACGAAATTC  
 AATAATAATGAATCAGGTATACCAATTTTTTTCATTTTATTATGAACCAGGACTTAATATTTATGCTGTA  
 CCACAAATCTAATGTCGACAAATTAGAATTTTGGCAACAAGTTGAACAATTGATAATGGAATTTATAGGG  
 ATTTAAATTTATCTTTCACAACAATGGATTTGCTAATGTTAATTTCTTTTTATTATCATGATATTCAACCTCAA  
 CCATTTATTGAATTTGAAGAAGGATGGAAATTCAAATTTACATCCTAAATCCAATTATGATTATATATATAT  
 AATCAAGATATAAATTTATTTATTTCCGGAATTTGTTAACAATGTGTTCAGAAACAGAATTTAATCTTGAAGT  
 GGTATTTATAAGAATTTGGTTTGTTTTTAATTGATGAAAAAATCTCAACTAATGATGATTTTGAATTTA  
 AGTGGTATTTAGAGTGATATTAGATGAAGATAGTAAATACTAATAACAAAGAAGATGATACATAGACACA  
 ATGTTTTCATATATAAACCACACATACCGAGTTTTCATGATTCTACCACTACCACTACCACTACCACTACCA  
 CCACAAACCATTAATCCTATTTTGAAGTACTGAAGTTAACAACAACAATCTGTTATTCCAAGTATTTT  
 GATGTTGAAAGAAATTAATAATTTTACTTATTTATTTTGAATTTAAATAAATCATTAATATTTGATCAATTTCAA  
 AACATTCCAATAGGATCCCAATTAATTTATTAATAATGGGAATAAAAAATTTAGAATTACCAGAATATAAA  
 ATTTAAATCAATGGGGTAAATGAAGTTTATTTGAATTTGAATTTGATAATGATAATCATATCCCTCATCAT  
 ATTAATTTTAAAGTTTCAATTCAGATATCAATTTACCTCAAAATAATCATTTCCCATTCCTAAATTAGTAAT  
 GTTTTAAATTCGTTACCAATATTTTATAGGTTCTAATCTCAAACAAGGAAATTTATTAGATAAATCA  
 CCTTTTGTACTATAAAGAGATGTTAAATTTGGTGGTAATTTATGAAATTTATTTTACTGAAGATACAGTT  
 TTTTATCATTTTACAGAAATTCGACAAATTCCTCAATTTCCCGGATTTTCAACACTATTAGAAATTAATATT  
 CCTCATGGGAAACTACATTTGATAGAGTCAATAATATAACTTCACTTGGTTTATTAATTCCTGTATTG  
 ATGATTTTATATAGCCATTTCAATAAGAGTTTTCATGAGTACCCTTCAAAGACGAAAGGGATTAA

YCL052C\_homolog 481aa (SEQ ID NO 522)

MRQRTTIYNPYSSHDGIIITNLRITNFQLSSIPNHLFTIENKYTITTTTTTQPNKSSLYSAIKELRIQTKF  
 NMNESGIPPIPSFIIEPGLNLXAVPQSNVOKLSTWQQVEQLIMELLGIKLSSQOWIANVNSFYVHDIQVQ  
 PLLNLKECWKPKLHPRKSNYDYIYNQDKIITRELETVVSETEFNLEGGIYKEIGLFLIDEKISTNDQLNL  
 SGIRVILDEDSKTNKKKKS LHKCMFKHKPRHRSFDDSTTTTXXII PQGLHPILSTELNMTTIVIPDF  
 DVEECKFYVYLNLNKSLIFDQFPQNIPIGSQLIINNGNKNLELPEYKINQWCMELLFEFEFDNDNDIPHH  
 INLTVHSRYQLPQNNHSHSQISNVLNLSLPIFIGCNVKEGNLLDKSPFDTKRDVKIGGNYETVFTEDTV  
 FYHLQNSDNGSKSGSSTLLEINIPHGKTTFDKVNMTSLGLLLGYLMILYASIRVFMSTTSKTKRD

YCR009C\_homolog 887bp public: 1..882 (SEQ ID NO 523)

ATGTGGAAAAAGAAAAAGAGGGGAATTTTTTTTGTGATTCATTTTITTTTTTTCTTTTATCTCGCACAT  
 TTCTTTCTTTCACTAGACATGCTTTGGGGAGGATTTAAGAAAGCAATCAATCGAGCTGGCGCATCTGTT  
 ATTGTCAAGGATGTTTGACAAAGACTATCGATAAGCACTTTGATGTGGAGGAGAGAGGATACAAGACCTTA  
 AAGACTGACAGGGACGAATTTACAGAAAGCTGCCAAGGGGTATTTGGACAAACATCAAGCCANTCACCAGT  
 TCCCAAGTCACAATTCGCCAGATTAATTTATTAACCTTTPAUGAGGAGTGAAGCAGGACAAATCGCTCTAC  
 TCGAATGCTTGGGACTTATTACATGCCAGAGTGTCAAGGAGTTTGGATGAGGAGACTGTGAACACAGATGAT  
 GGCCCGTATAGGGAGACTGTTTTGGATCCAATTTGAAAGTTTTTCCAAGTACTTTAGTGAGATTGAAGGA  
 GCAATCAAAAAGAGAGCACACAAGAAGATTGACTATGAGCAGTGCAGAGCCAAAGCTTAGACGGTTAGTCT  
 CATTAACCTGCCAAAGATGCGGCCAAGTTCCCAAGCGCCGAGAGGAATTTGTCGATGGCCAAAGAGATT  
 TACGAAGAGTTGAATGACCAAGCTCAAGGCCGAGTTGCCGAGTTGATTGCAATGAGGGCTCCCTTTCTAC  
 GATCCGTCGTTTGAGGGCTTGGTCAAGATCCAGTTTGAAGTTCTCTACTGAGGGGTACTCGAGATTGGCA



160/251

CAGATCCAACAGTACTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTTCCTTGGACGGCAAGATT  
GATGATATGTTGGCACAAATCCCAAGCTTTGAGCTATACTTCCTTTAGGAAAGTAG

YCR009C\_homolog 293aa (SEQ ID NO 524)

MWKKKKREFFPCHSFFFTTYLAHFFLQLDMSWGGFKKAINRAGASVIVKDVKTMDDKDFDVEERRYKTL  
KTAGTNLQKAAGYLDNIRAITNSQVTIAELIYNLYEESKQCGSLYSNVGTYYMQSVKEFDEETVKQID  
GPYRETVLDPFGKFSNYFSEIDEAIKKRAHKKIDYEQCKAKVRRLLVDKPAKDAAKLPRAEKKLSMAKEI  
YDEENDQLKAELPQLIALRVFPYDFSEALVKIQDRPCTEGYSRLAQIQQYVLPASRDEYANGLLDQKI  
DDMLAQMQGLSICSLGK

YCR010C\_homolog 858bp public: 1..858 (SEQ ID NO 525)

ATGTCAGCTGATTTAGAAATCAACAACCACAAGATCATCATCTTATTATTGAAAACAAGGGTCATAAC  
AGTAGCAACCACCACCACCACAACAACATTCACATCATCTTATGATCCTCATCGCAATTACTAAA  
ATTTGAAACTGATGGAGATTTATGTTTACTTTTGGTAAATGAAAGATATTTACGTTTGTGATTTAGTTTGAAGCA  
TTTGGTGGTACTTTAAATCCAGGGTTAGCTCCACCACCTAAAAATGATTTTGGCTAAATCCTGCTCCATTG  
GGATTATCGGCATTTGCTTTTAAACAACATTTCTTTTAAAGTTTAAATTAATTCGTAAGCTAGACGGCTTACT  
ATTCCTAAATATGTTGTTGGATTGGCAATTTTCTATGGTGGTGGCTCCCAATTAGTTGCTGGTATGTTT  
GAATTTGGCCGTGGTAATACTTTTGGTGGTGGTGGCTTTGAGTTTATACGGAGGATTTTGGGGTGGTTGG  
GCTGCTATTCAAGTTGATTCATTTGGTATTAAAGCTGGCTTATGCTAAATAATACGAGAATTACATTAT  
GCTCTGGCATATTTTAAATTCCTTGGTTTATTTTCACATTTTCTTGTATGCTTTTAAACGGTTAAATCT  
ACTGTGGCATTCTTTTAAATATTTTCTTTTAAAGTATTACATTTTATTATTGGCAATTTCTGATTTT  
ACTGGTAAAGTGGCAATTAAGAAAGCCGCTGGACTCTTTGGTTTAAATTAATCTCTTCTGCTTGGTAT  
AATGCTTATGCTGGTATTTGCTAATCTCAAAATAGTTATATTAATCTGTTAAAGCTATTCATTAACAGAT  
TTACAAGATCCAACAAGAAAAAATAATAA

YCR010C\_homolog 285aa (SEQ ID NO 526)

MSADLENQPPQDIHILIIENKGDNSKKIHIIHNNNSTSPYDPIIHPIITKLETDGDYVTFGNERYLRSDLVLA  
FGGTLNPLGLAPPPKNDPANPAPIGLSAPALITFVLSLINCEARGVTIPNIIVGLAFYGGAAQLVAGMF  
ELAVGNTFGGVALSSYGGFWGAANAIIQVDSFGIKAAAYANNTEELHYAVGLIFLIQWFIETFFLMLLTVKS  
TVAFFLIFFFLSITFLLLAISDFTGKVAIKKAGGVFGLITAFVAMYNAYAGIANPQNSYITVKAILPLPD  
LQDPTRKNK

YCR021C\_homolog 1029bp public: 1..1029 (SEQ ID NO 527)

ATGTCCGCTGCTGTTTCAACTTTATCCGATATCATCAAACGTAATGATGCTGTTAAGCTGAACCCACCA  
AACCCAAATTATTGATTTACATATCACTGAACATGGTAGTGATTTGGCTTTGGGCTGTTTTTTCAGTTTTC  
GCATTATTTGCAATTGTGCATGGATTCAATTTACAGTTTTTACGAGTTAGAAAAATCTGGTTTGAAGAGA  
GCTTTATTGACTATCCCATTTTAAATAGTGCTGTTTTTGCCTTTGCTTACTATACTTATGCTTCTAAC  
TTGGGCTATACTTGGATTTTGACAGAAATCAACCATGCTGCTACTGGTTTATAGACAAATCTTTTATGCA  
AAATTTGTTGCTTGGTTCTTGGGTTGGCCATTAGTGTTGGCTATTTTCCAAATTAACCAATACCAAGC  
TTTACTACTACTGAAGATGACTCTGATTGCTTAAAGAAATTCATTTCTTTGTTTGAAGCTTTGTTTACT  
AGAGTTTGGCAATTTGAAGTTTTCGCTTTGGGTTTATTGATTGGTGCTTTAAATTTGAATCTACTTTACAA  
TCCGCTTATTTCACTTTTCTCTCTGCTGTTCCAAATTCCTTGGCTATTTATTTAGTCATTAATGATGTGGTT  
GTTTCATTTGGTTCACTTCTCTCAATCAGTCTTTGGCAATGCTCTTATCCTTGGCTTTTGTATTGTTTGG  
ATTTTGTACCCAGTTGCTTGGGTTTGGAGTGAAGGTGGTAATGTTATTTCAACCAGATTCAGAAGCAGTC  
TCTATGGTATTTTGGATTTGATCAGTTTGGTGTATTTCCAATTATCTTGAATTTGGATTGGCATTAA  
AACGTTGATGAAGAATTCTTCACCAAAATATGGCATTTCUATTTGAAACCAGAAAAATGAACATGCTCCA  
ACTGCTACTGAAGATGTTGAAAAGCAGTTGGTGAAACCCCAAGACATTCTGGTGATACTGCTGTTGCT  
CCATCAGCTCTTCCAGACACTGCTCTTGGCTCAAGCACAAAGCCCAAGCTCAAGAACCTATTTAA

YCR021C\_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSIIKRNDVNVNPPNPFIIDHITHEGSDNLWAVFSVFALFAIVHGFYISFTDVRKSLKLR  
ALLTIPLFNSAVFAPAYYTYASNLGYTWILTEFNHAGCTGFRQIFYAKFVAVFLGWFLVLAIFQIITWTS  
FTTTIDESDLLAKPISLFEALFTRVLALIEFVLGLLIGALIESTYKNGYFTFAVVFQLFAIYLVINDV  
VSFGSSSSHSVFGNAITLAFVTVWILYPVAVGLSFGGNVTQPDSEAVFYGLIDILITFGVTPETLFWTAIN  
NVDEEFFTKIWHFHLKPENEHAPTATEDVEKAVGETPRHSGDTAVAPSGVPDGTGAQAQABAEERI

YDR178W\_homolog 510bp public: 1..510 (SEQ ID NO 529)

ATCATTTCAACTTATTACCTATTGCTTTAACCACCTTTAACTAAATCATCATCATCATCATTTAACT  
ACTACTGTTAGACCAATTATTATTGGCCAATTTTACTAGAGGAATTAAACTATTCTCAACCACCAGCT  
TATATTGTTGGTACAGTTAATGATGCTTATGTACCACCACCACCACATAAATTAGAAGGTTTCATTACAT  
TCGACTAGTGAANGGATTGTTGCTAATGGTATGTTACCATTAGTTTTACCACCATTATTACTGGTGGT  
GGTGGCTTCGACTTTAATTGATTCCACCATGTCAGCATTATTAATTATTTCAATTTGTCATACTGGTTTCCAA  
AGTTTGTATTATAGATGATATTCCTAAAAGAGTTTATGGATCTTATCATTAATTTAGCCATGTATTTATTC

161/251

ACTTTTGGTACTGGTATTGCTGGTTATGGTATTTATCAAATTGAAACTAAAGAAAGGTGGTGGTTTCCAAT  
ATTATTTCAAACCTTTGGAAAGCTTAA

YDR178W\_homolog 169aa (SEQ ID NO 530)

MISTYSRIGLTTTLTKSSSSSSSLTFTVRPLILANETRGIKTIPTQPPGYIVGTVNDAYVFTPPHKLEGLII  
WTSERIVAIGMLPLVLAPFITGGGASTLIDSTMSALLLFHCINTGFQSCIIDDIPKRVYGGYHMYAMYLC  
TFGTGIAGYGIYQIETKEGGVSNIIISKLMKA

YDR202C\_homolog 387bp CDS: 1..387 public: 1..387 (SEQ ID NO 531)

ATGACAGCAAATATCTTGAATAATAAAACATTTCATAGATACTGTATTATCAATACAACTCAAAAT  
GATAAAGAATTACATTGGTATATATAAATATAATTTTACCCGATTTACCTCAAAATCATAGAGACTTTA  
CAGATTTGTTCAAATTTGTTGAAGTACAATTCACCACAAGAACCTGATTCCAAACAAATGTATTGAAAAA  
GGTCCATCTATCAAGCTACCTTTGTCTTTAACCAATCAACAAGATTCTGTCAATGGCATAATAACCCGA  
GATGGACCATATATCACAGATCTTAATTTGACGGTTAAGAAATCATTATTTCAACAAGCATTTCCATAAG  
TTGCGCTTAATAAAGCCAATGGTTTATAGAACAACCTGTTAAT

YDR202C\_homolog 129aa (SEQ ID NO 532)

MTANILNMKTFIDTVLSIQSTQNDKELHWYIINIILPDLPIIETLQICSNLLMYSNPQEPDSKQCI EK  
GPSIKLPLSLTNQQDSVNGIITREGPYITDLNLTVKNHYFNKHPHKLRLIKPMVLEQIVN

YDR256C\_homolog 1458bp public: 1..1458 (SEQ ID NO 533)

ATGGCTCCAACATTTACGAATTCACCGGTCAACCAATTCACAGAACCAATTTGCCACTCAAAAGACTTGGT  
CAACACGGTCCATTGTTGTTACAAGATTTCAACTTGATTGATTCAATGGGCCATTTCCGATAGAGAAAGA  
ATCCCAGAAAGAGTTGTCCACGCTAAAGGTTCCGGTGCCTATGGTGTTTGTGAAGTCACGACGATATC  
ACTGATATTTGTCTGCCAAATTCCTTCCACACTCTTGGTAAGAAAACTAGAAATCTTCAACCAGATTTCTCT  
ACTGTTGGTGGTGAATTAGGTTCTGCTGATACTGCTAGAGATCCAAGAGGTTTGTCTACCAAAATTTTAC  
ACTGAAGAAGGTAACCTGGATTTGGTTTACAACAACACTCCAGTGTTTTTCATTAGAGACCCATCTAAA  
TTCCACATTTTCATCCACACCCAAAAGAGAAACCCAGAAACTCACTTGAAGGATGCTAACATGTTTGGG  
GATTACTTGACTAGCAATGAAGAATCCATTCAAGTTATGGTTTTATTTCTCCGACAGACCTACTCCA  
GCTTCTTACAGAGAAATGAATGGTTACTCTGGTTCACACTTATAAATGGTCCAAACAAAAGGTGAATGG  
TTTTACGTTCAAGTTCATTTCACTCAGTGACCAAGGTATTAAGACTTTGACCAACCAAGAGCTGGTGCT  
TTAGCTGGATCTAACCCAGATTACGCCCAAGAAGATTTGTTCAAGAACATGCTGCTGGTAACTACCCA  
TCATGGACTGCTTACATTCAAACCATGACTGAAGCCGAAGCTAAAGAAAGCTGAATTTTCTGTGTTTGAAT  
TTGACCAAACTTTGCCCACACAAGAAATACCCATTGAGAAGATTTGGTAAGTTCACTTTGAATGAAGAA  
CCAAAGAACTACTTTGCTGAAGTTGAACAAGCTGCTTTTCTCTUCAGCCCACTACTGTTCTTTACATGCSAA  
CCATCTGCTGATCCAGTCTTGCAATCAAGATGTTCTCTCTATGCTGATACACACAGACACAGATTTGGGT  
ACCACTATACCAAATCCAGTGAAGTGTCTGTCTACCCGTTGCTGTTTTCAACCCACATATGAGAGAT  
GGTGCTATGACTGTTAATGGTAACCTGGGTAGCCATCCAAACTACTTGGCCAGTGATTAAGCCAGTTGAA  
TTCAAACAATTTTCTCTTCAAGAAGACCAAGAAGTTTGGAAATGGTGGTGGCACTCCATTCCTACTGGAA  
GCCACCCAGCTCAATTTCAAACAAGCTCAAGAATTTGGGAAAGTGTGTTGAAGAGATATCCAAACCAACAA  
GAACATTTGGCCCAACAACATTTGCTGTACATCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
GCATACITTTGGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGGAAATTAATCTCCA  
AGAAATAA

YDR256C\_homolog 485aa (SEQ ID NO 534)

MAPTFTNSNGQPIPEPFATQRVGQHGPLLLQDFNLIDSLAHFDRERIPERVVAHAKGSGAYGVFEVTD  
DDIINICAAKFLDTYGGKTRIFTRFSTVGGELGSAOTAREPRGFATKFYTEEGNLDLVYNTPVFFIROP  
SKFPHFIHTQKRNPEPHLKDANNFWDYLTNEESIHOVMVLFSDRGTPASYREMNCYSCIITYKWSNKKGEW  
FYVQVHFISDQGIKTLTNEEAGALAGSNPDYAQEDLFKNIAAGNYPSWTAVIQTMTRFAAKEAEFSVFD  
LTKVWPHKKYPLRRFGKFTLNENPKNYFAEVEQAAPSPAHTVPYMEFSADPVLQSRIFSADTHRHRLG  
INYTQIPVNCPTVGAVFNPHMRDXGAMTVNGNLGSHPNYLASIKPVEFKQFSLQEDQEVWNGAATPFHWK  
ATPADFKQAQELMKVTKRYPNQRELAHNIIVHAAGADAATQDRVFAYFGKVSQDLADAIKKEVLELSP  
RK

YER103W\_homolog 1971bp public: 1..1971 (SEQ ID NO 535)

ATGTCTAAAGCTGTTGGTATTGATTTAGGTACAACCTATTCTGTGTTGCTCATTTTGCCANTGATAGA  
CTTGAAGATTGCTAATGATCAAGGTAATAGAACAACCTACCCCTTCATTGTTGCTTCACTGATACTGAA  
AGATTGACTCGTGATGCTGCCAAGAATCAAGCTGCTATGAACCCAGCAAACACTGTTTTCGATGCTIAAA  
CGTTTTAATTGGGAGAAAAATTTGATGATCCAGAAGTTATAAATGATGCTAAACATTTCCCATTTTAAAGTC  
ATTGATAAAGCAGGTAACCCACTGATTCAACTTCAATATAAAGGTGAAACTTAAACATTTTCAACAGAA  
GAAATTTCTTCAATGGTTTAAACAAAAATGAAGAATTTGCTGAAGGTTATTTGGGTTCTACTGTTAAA  
CATGCCGTTGTTACCGTTCCAGCTTATTTCAATCATTECTCAAACACAAGCCACCAAGATGCTGGTACT

ATTGCTCGTTTGAAATGTTTTTAAGAAATCATTAAATGAACCTACTGCTGCTGCCATTGCTTTATGCTTTAGAT  
AAAAAAGGTTCAGAGGTGAACATAACGTTTAAATTTCGATTTCGGGTGGTGGTACTTTTGTATGTTTCA  
TTATTAGCCATGATGAAGGTATTTTCGAAGTTAAAGCCACTGCTGGTGAATACTCATTTCGGGTGGTGA  
GATTTTGATAACAGATTAGTCAACTTCCTTTATTCAAGAAATCAAGAGAAAGAACCAAGATAATTTCC  
ACCAACCAAGAGCTTTAAGAAGATTAAACAATGCTTTGTGAAGAGCAAGCAAGAACTTTGTCTTCTCTCT  
GCTCAACACTCAAAATGAAATTTGATTCCTTATATGAAGGTAAATGACTTCTACACTTCAATCACCAGAGCC  
AGATTGGAAGAAATTGTGTGCTGACTGGTTTCAGATCCACTTTAGATCCAGTTGGTAAAGTTTTAGCTGAT  
GCCAAGATTGATAAATCTCAAGTTGAAGAAATTCTCTTGCTTGGTGGCTCCACCAGAATTCCAAAGATT  
CAAAAAATTTGGTTTCTGATTTCTTTAATGGTAAAGAAATGAATAAATCTAACAACCTGATGAAGCTGTT  
GCTTATGGTGGTCTGCTTTCAAGCTCCCACTTTTAAGCTGGTGAATACTTCTTCCAGACTCAAGATAATTTTG  
TTATTCGATTTGCTTCATTGTCAATAGGTATTGAAACTGCTGTGTGATATGACCAAAATTCATTTCCA  
AGAAATCTACTATTCCAACTAAGAAATCAGAAACTTTCTCCACITATGCCGATAACCAACCAGGTGTT  
TTGATTCAGGTGTTTGAAGGTGAAGAGCTTAAACTAAGATAAACAACITGTTGGGTAAATTTGAATTA  
TCTGTATTTCCACCAGCTCCAAGAGGGCTCCCTCAAAATGAAGTTACTTTTCGATATTGATGCTAATGGT  
ATCTTGAAATGTTTCTGCTTTAGAAAAAGGTACTGGTAAACTCAAAAGATTACTATTACCAACAGATAAA  
GCTAGATTATCCAAAGAAAGAAATGATAAAATGGTTAGTGAAGCTGAAAAAATCAAAGAGAGAAGATGAA  
AAGGAAGCTGCTAGAGTCCAAGGCCAAGAAATCAATTTGGAATCTTAAGCTTATTTCATTGAAAAACACAATC  
AATGATGGTGAATGAAGAGATAAGACTGGTGCAGATGATAAAGAAAAATTAACATAAGCCATTGATGAA  
ACTATTCTTGGTTAGATGCATCTCAAGCTGCTTCTACTGAAGAATACGAAGATAAACCTAAAGAATTA  
GAATCAGTTGCTAATTCGATCATTAAGTGGTGCTTATGCTGCTGCTGCCGGTGGCGCTCCAGGTGCTGCAAGC  
CGATTCACCAAGTGGTGGTGGCTTCCACAGGTGGTGGCCCAAGCTGCCGGTGGTTCAGGTGGTGGTACTGGT  
GGTGAATCAAGTGGTGAACCACTGTTGAAGAAGTTGATTAA

YER103W\_homolog 556aa(SEQ ID NO 536)  
MSKAVGIDLGTTYSCVAHFANDRVEIILANDQGNRTTSPSFVAFDTDERLIGDAAKNQAAMNPANTVFDK  
RLIGRKFDPEVINDAKHFFPKVIDKAGKPVIOVEYKGETTFSPEEISSMVLTKMKEIAEGYLGSTVK  
DAVVTVPAYFNPDSQRQATKBDAGTIAGLNLVRLITNEPTAAATAYGLDKKGSRCHEHNVLTPLDGGGTFDVS  
LLAIDEGIFPEVKATAGTTHLGGEDFDRNLVNVFFIQEFKRAAKYD1STNQALRKLRTACERAKRTLLSS  
AQTSIEDISLYEGIDFYTSTIRAEFEELCADLFRSTLDFVKGKVLADAKIDKQSQVEEIVLVGGSTRIPKI  
QKLVSDFFNCKEINKSINPDRAVAYGAAVQAATLTGDTSSKTQNTLILQWAPLSIGTETAGCINTKLIPI  
RNSTIPYKKSETFSTYADNQPGVLIQVFEGERAHTKDNLLGKFEISGIPPAFPGVFPQIEVTFDIDANG  
TIANVSAIFPKGTGKTQKITITNDKGRLSKEEIDKQVSEAEKFKEEDEKEAARVQAYNQLESYAYS1KNTI  
NDGEMKDKIGADDKEKLTKAIDETISWLDASQAASSTESYEDKRKELESVANPIISCAVCAAGGAPGGAG  
GPGGAGGPGCAAGCAAGGPGCATGCGESSGPTVEVD

YGR086C\_homolog 954bp public: 1..954 (SEQ ID NO 537)  
ATGCATAGAACTTATTCTTTAAGATCCACATAGAGCTCCAACTGCAATCTCAATTTACAAGTCCACCTCCA  
CCACCATCATCTACCAAATCCAAATTTTTTGGTAAAGGTTCCGATTAGTCATACTTTCCGTAAACAAGCT  
GCTGGTGGCTTTAGGTCCAGAAATTTGTCGAGAAAAATGGCCATTTTAATTAATAATGGAAAAAATTTTAATC  
AGATCAATTTGAAATCACTTCTCGTGAAGAAAAAGATTTGCTTAAACAATTAATCTTTATGGGGTGAAGCT  
AATGAAGATCATATTAGTCTATATCACTGATAAATTTGGCGCTTTTAATCTATGAAGTTGGTGAATTGGA  
GATCAATTTATTGATAGATATGATCAATATAGAATCACCTTGAATCTATTAGAGATATTGAAGGTTCA  
GTTCAACCAAGTAGAGAAAGAAAAACAAAAATTACTGATCAATTTGCTTATTTTGAAATATAAAGATCTCT  
CAATCACCAAAAAATTAATGTTTGTAGAAAAAGAAATTTGGTTAGAGCTGAAGCTGAATCTTTAGTTGCTGAA  
GCTCAATTCGAGTAATATTACTAGAGAAAAAATGAAAACTGCTTTTAATATCAATTTGATCTATTAGA  
CAACACGCTGAAAAAATTTCTPITAATTTGCTGGTTATGCTAAAGCTTTATTTAGAATTATTTAGATGAAAGT  
CCAGTCACTCTAAGCTGAAACATAGACCAGCTTATGACGGTTATTTGAAGCTTCTAAACAAATTATTATTGAT  
GCTGAAAAAGCTTTAGCTTTTGGCACTTTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
CATGATGAAGAAGCAAGCAAGAAGATTTTGAAGGTTGCTTATGAGATGATGAATTTGGCTAATCAAGCTGAA  
AATTTAAGAATTGCTGAAAAAGATTTTGTATGAAGTTGAAGCTTAAATTTGCTGCTTAA

YGR086C\_homolog\_317aa(SEQ ID NO 538)  
MHRYSLSRSTRAPTASQLQADPPPPSSSTKSRFFPGKGSISHTFRKQAGALGPELSRKLAAILIKMEKMLM  
RSTETTSREARKDVAQLSLNGEANEDDISDITDKLGLVIYEVGELEDQFIDRYDQYRITLKSIRDIFGS  
VQPSRERKQKITDQIAYLKYPKDFQSPKINVLEQELVRAEAEESLVAAEQLSNITREKLKTAFNYPQDSIR  
EHAKTAITAGYKALLELLDESPVTPGTETRPAYDQVEASKQIIDAENALASWTFUSAVVRPTLSLAA  
LDEFAEEDLGGAYEDELLEDAEAFMLRIAEKDEDEVEAKIAA

YGK197C homolog 1536bp public: U1536 (SEQ ID NO 539)  
ATGTCCTCATGATGATTCAAATCTGAATTCAAACCCCAGCTCAAATCCAACCTCCAATCCCTGCTCAAAG  
CCGTCCTGATATGSGGATGATCAAGCAACGACAGTGGGCTCCGACCATCAATACAACATTTTACGTTTACCC  
CCACCTCGAACCACAAGCCGATGAAGAGGAGATGCGAATTCGGGTGAGCCCATATCACGACAATCAACCTCTC  
CTTGACAGATCAACAATCTCGATATTTCATTTTTCCACGAGATTCGGAGCTCAAGAAGAAAGGAATTGTC

163/251

ACGAAATATCTTAAAAATTTATCTAGTCATGCCCATTTGGTTGCTTAGGAGTGTTCCTATATATTGCGGT  
 TCAATGTATCAGAGAGAAACCCGAATTAAAAACTTGAAATGTTGGTAGITTTAGAGATGAAGAAATTT  
 AATGGCAICCCCTCCACTTTTTTGGCAATCAGCTTCGTGATTTATTGGCCACCCCAACGGCTAGAACACTC  
 GCGGATTGGAAATATATAACACTAGCGAATTTGAACTATTGCATCAAAACACAAACACAAATAAAT  
 GAAGAGCTCATTGCTCAAATTCATCATCAAAATTTATCGGCTCGACATATGTCAAGCAAAATTCATCT  
 TATAACATATACAATGCATTAGCCAAATGGCAATCAGTACAATGTCAGTGACATCTGTGATTGTTACTAT  
 CAAACAGGAGACACCTAAGTAGTGTTGGCCCATATGTGGTGGCATCTATAGATGCCATTCAAACATCTG  
 TGGTTGGATCAAACCTGGTGATGAGGGACATTTGTGAGAATTGCTAATATAACTCTTGACAATGCAAAAC  
 TCGGTTGCTGTCGCCACTACCGCCCTTGGCAATCCAAATAAATTGATATGAGACCATCTACTAGTGGAGTT  
 TTAGTTGCAGCTTTACAAATTTGGTCTTCTTTATCTTGTCTATTGTTAGCTTTTTTCAGTTTCAATTTTTTT  
 GTGATATACACCGATCAGTGGCATTAATGGTGAAGCAAAAGAACTTTTACTTTTATCCAGTTTCTTGA  
 TCAATCATATCGTATTTTGTATCAGTTTAAATGTTTGGTTTGGTTACTTTAGCGTTTCAAGTTGATTTT  
 GCTGTTACATTTGCTAAATCTGGCTTCTTACTTTTACTGGATGGTAACATTTTAACAATGTGGAGTTT  
 GGATTGGCTAACGAATTCGCCGCTATGCTCATACTTACTATCTATCCACCAATGTTTGGGTTTTGGT  
 ATCTTCTGGGTAATTTATAAATATCACACCCACATTCACACCAATTGCTTTGTTACCTCAATTTTATCGG  
 TATGGTTACGCTATGCCAATGCATAATGCTTTTGAATTTTATTCTGTTACTTTTTCAACACGTATAAG  
 GGATTAATAGGAAGAGCATTTGGAATCATAATTCATGGGTGGTATTTTAACATTAATGGCACCAATA  
 GTGGTGGTTTTACTTTGGTAGCACTATGAGTAAAAAGCTGCTGCTCCCGCTGCTGCTGCAAAAAAGGAA  
 AAGGAAAAGTCAAAGTAA

YGR197C\_homolog 511aa (SEQ ID NO 540)

MSHDDSNNSNPNPSNPPTSNPVSKPSDMGRSSNDSSGSEPSIQHFTLAPLEPQGDDEEDMEMGEPISRQSTF  
 LERVQSRVSPFHENLRQQRKELSMKYKTYVVMATGCIQVFSTYWGSMYQRFETRIKNLKNLVLVLEDEEL  
 NGIPPLFGNQLRDLLEPTARTLGDWKIYNTSEFETIASKHNNTLINEEVLRIQHQNRYAIVYKQNSS  
 YNLYNALANGNCTNVSDSVYCYEYETGRHLTSVGPYVVASIDAIQTMWLDQNSVMRDIVRIGNITLDNAN  
 EVAVATTALAFQIIDMRPSTSGVLVAALQIGLLYLIVIVSFFSFNPFVDIHRVSVALMVKQRNELLRYVFA  
 SIISYFVVISLMEGLVTLAPQVDFAVTFCKSGCLVYVMVTFELTMNSVGLANELAAMLILTIVPPMVGFWL  
 IFWVLIINTFPTFTPIALLPEFYRYGYAMPLHNAFELYSVLFFNTYKGLIGRSIGIIIAWVVFELTLMAPI  
 VVVYFGSTMSKKAAPAAAAKXEXKXSK

YGR250C\_homolog 1890bp public: 1..1890 (SEQ ID NO 541)

ATGTCCTGCTGCTGAAACTAATCAACTTCAAGAAATCTATGGAAAAGTTGAACATTGGTTCAACTACTGAA  
 GAACAATCAGCTGCTGCTGCTACTTACCAGCTGCTGATCAATCAGCTGAAGAACAAGCAGAAATCATCTGGT  
 GTTGCCGAGAAATTCCTGCCCTCCTTGTACGTTGCTGCAATTTGAACCCCTCTGTTAATGAAGCTACCTTGTTC  
 GAAATCTTTTCTCCAAATCGGTCAAGTTTCCCTCTATCAGACTTTCTCCTGATGCTGCTCTAATAAATCT  
 TTAGGTTATGCTTACGTCACCTACCACAAGTACCAGAATGCTGAAAAGCCTATTCAAGAATTTGAACCTAC  
 AACCCGATCGAAGGTGCTCCATGTCGTATCATGTCCTCTCAAGAGACCCCAATCTGTAGAAGATCTGGT  
 CATGCTAATATTTTCATCAAGAATTTGCATCCAGCCATCGATAACAAAGCTTTGCTATGACACCTCTTCT  
 GCTTTTGGTAAATTTTGTCTTGTAAAGTTTCCCAACCGATGAATTTGGTCAATCAAGTGTTTTGGT  
 GTCCACTATGAAGCTGCTGAAGCTGCTGAAGCTGCCATTGAAATGTCAATGGATGTTATTTGAAGCAT  
 CCTGAACCTTTTCTTCTGCTAAGCACATTTCTAAAAAAGACCCCTGAATCTAAGTTTGAAGAAATGAAAGCC  
 AACTTCACCTAACATTTATGTTAAAAACATTTGACTTGAACCTATTCAAGAAGAAAGCTTTGAAAAATTTCTTT  
 TCTCCATTGGTTAAGATTTACTTTCCATTTACTTTGAAAAAGACCAAGATGGGAAATCTAAAGGTTTGGT  
 TTTGTTAATTTTGAAGATCATGAATCTGCTGTTAAGGCTGTTGAAGAATTGAACGATAAAGAAATCAAC  
 GGTCAAAAGATCTACGTTTGTAGAGCACAAAAGAAAAGAGAAAGATTGGAGAATTGAAGAAAACAATAC  
 GAAGCTGTTAGATTAGAAAATTTGCCAAATACCAAGCTGTCAACTCTTTCTTGAAGAAATTTGGATGAC  
 ACTATTGATTCTGAAAAATTAGAACAAAGAAATTCMAACCATTTGGTACCATTACATCTGCCAAGGTTATG  
 GTTGATGAAGCTGGTAAATCAAAAGGTTTTTGGTTTTGTTTTGCTTTCACAACCCAGAGAAGGCCACCAAG  
 GCTATCAGTGAATGAACACCAGAATGATTAAAGGCAACCCATTTGATGTTGCTTTGGCTCAACGTAAG  
 GATGTTAGACGCTCTCAATTTAGAACAAACAATTCAGGCCAGAAACCAATGAGAATGCAAAATGCTGCT  
 CCTGGTGGTTTTACCTGGTCAATTCATTCCACCAATGTTCTACGCTCAACAAGGCTTTTTTCCACCAAT  
 GGCAGAGGTAAGGCTCCATACCCAGGCTCTAATCCACAAAATGATGATGAGAGGTTAGAGGTTCAACCATTC  
 CCAGAACATTCGCCAAGACCAGCTCCAAATGGCCAACCAAGTTCTGCTACGGTATTCCACCTCAATTT  
 CAACAAGACTTTAAGGTTCAAAACATGAGACCTCAGCAACAACAACAACAACAACAACAACCAACCTGGATAC  
 TATCCAAACCGTAACCAACCAAGCAAGAGAGACTTGGCTGCTATCATTTCTAGGTTCCACAAGATCAA  
 CAAAAGAGAAATTTGGGTGAAGAAATTTGATCCAAAGATTGTTGCTACCGGTAAGGCTCAAGAAACAGAA  
 CCTGCTGGTAAATCACTGGTATGATCTTAGGTTTGAATAACCAAGAAATTTTGGATTTGTTAGATGAT  
 GATGAATGTTTCAATAACCATTTGGAAGATGCTTTGACTGCTTTTGAAGAGTACAAGAAGCTCTCAACCT  
 CCGGTAATGCTGAAGAGCAAGCTTAA

YGR250C\_homolog 629aa(SEQ ID NO 542)  
MSAAETNQLQESKEKLNIGSTTEEQSAAATTTADQSAEESQGESGVAENSASLYVGELNPSYNEATLTF  
ETPSPIGQVSSIRVCRDAVSEKSLGYAYVNYHKYEDCEKAIEELNYNPIEGRPCRIMWSQRDPSARRSG  
DGNIFIKNLHPAIDNKKALHDTSFSAFGKILSKCVATDEFGQSKCFGVVHYETAEEAAAIENVGMLLND  
RVNPFVGHISAKKDKRESKPEEMKANFTNIYVKNLDLNYSEESFKFLSFPGFKITSIYLEKDDQCKSKGFG  
FVNFEDHESAVKAVEELNDKEINGQXTIYVGRAQKKRERLEELKKQYEAVRLEKLAKYQGVNLFVKNLDD  
TIDSEKLEEBFKPFGTITSAKVMVDEAGKSEKGFVCFVCTTPEEATKAITENMTRMTNGKPLYVALAQRK  
DVRRSQLEBQQIQARNQMRMQNAAAGGLPGQFIPPKFYGQQGFFPPNGRGNAPYPGPNPQMMRGRGQPF  
PEQWPRPGPNQGFVPVYGI PPQFQQDFNGQNMRPCCCCQQQPRGGYYPNRNQTSKRDLAALIISVFPQDQ  
QKRILCEBLYPKIVATCKAQEPEAAACKITGMMLCLENQFILDLLDDDELFNHNPEDALTAEEYKKSRA  
AGNARWQA

YKL117W\_homology\_221aa (SEQ ID NO 544)  
MSSTTTQTPTVLNAQRSSDDAAKNI FYLTIQISDFIDLKIDLKSDHLIIDS KSNDSVYSSIDYHLQID  
FTKSIDPDQSKINTENGSHIFMILRKKDQEEYWFRLTKEKLKYHYIKTDFDKWVDEDEQDEVKDDPND  
PCGGGGPCGAMDFSQMTSGMGGLGGTGGSGGGPGGVLSALASQLGQAGGAGGAAGLDGEEGEEGDEEAK  
KADREKSNATATEKE

YKR075C\_homolog 3042bp public: 1..3042(SEQ ID NO 545)  
ATGTCGTTATCAGGAGAAGTGTTTTTCAGGAGGAGCAACCACCTTCTCAACATATCGAGGCACAAGAIGAT  
GACCATTFTTGAAATACAACTTTAAATTGAAAAGAACTAGATCCATGGGTTTTATTAGATCAATTTATC  
CCCTGATAAAACAAAAGAACAAGATGGTAATAATTACAGAGCAAAATTCATCAACACACAGCTGCATCAACA  
ACCACTTCAAGAAACTTTGGCAGCTATGGCAGCTATACGATCAACAAACAAATTCGTCAATGTTAAACGAA  
ACTCCAAAGCAGTCAACATCATGAACTTACAGATCCATCATCTAATAAATCCGATGGCGATGTAACCCAT  
TCATCAGATGTAGCGCCATCATCTACATCACCTGTCATTCACCTTCACCAACTTCTCTACCCAGCATTTA  
GATTTAAAATCTCCAGAAATTGTTGGCTCATGATGATACAGATTTAGCTGTTGAACTTCACGTCATGTT  
CATTTATTTATCCCAACCAATGGGACGTTTCTGATATTTGGAAGTCCTGGGATACGTTAATTTCCAAAAGA  
AAGATGTTTGCTAATGCTGCAAGATTGGAATATGCTTCCACGAACTTCCCTCCCAACAGCGCTCTAAT  
TTCAGACTATAAGTCCAGAAGTGGTGAAATTTGGTCCGAAGATATGATGTTTACTTTGGCTTTATGGACCA  
ATATTTAAAAGATGATGACCATGTGAATAATGAAATCACGACTCTGATGCTATTGAACTACTGCTACT  
AGTTCTGTTGGCGGGGATATATCTATTTCCCAAAAATGTTCCASTAAGAATGGACCTAAACCAATATTTG  
AAAAAGAGAACAATGGAACAACCTGATGATAAGTCTAATTTCAATTTAATAAAATTACAATTTGGCAACCAA  
ATACATCAAAAGCAAAAGACAACAATAATGGACACACAGAAGAATTGAAAAGACACACATCAATTTGAAT  
CATCCCGATGAATATTTTGATCCCGAAGCCCTTCTGACAAATTAACACAGTCAATATAAGAAATACAGCT  
CCCTACTCATAACTAGTGTGGCCAAATTACAAAGCTTGTGTAAGAACTCCCAATTTCTTCATCTTCTGCT  
AGTTTGAAGATTTGATGAAAGATGAAGCCGTTGTTGTGCTTCTCTCAGAAACAAATCAGTCACGATCAA  
AACCAGAAGATGGTAATGTTTTTCGGGACGTTCAATCCAAAGGTGAAAGACACATACATTTTTAAAGAC  
GAAGTGATGCAATGTATGCCATTGATGTGTTATTCAGATGATGACCAACGATATAATTTCTGATGAAGAA  
GATTATGATTTCTGATGATGACGATGATGATTTATTTATGATCAATTAAGCAATCTAATGACAGTCTAGCT  
CAAGTCACTATATGAAGGAGACGATGAATCCATTGAGCAAGCCCATCAACAGGTAGAGGATGATGAA  
GATGGATCTGAAGATGAAGAAGACGATGAAGGGGGATTCTTTTTAAATGTGAAATCCAATTTCCAAATCCC  
CCAATAATTTTGGGCCAGCATTTCAAGTGCATCAACTTCTACTCCAGTGGCACCATCTTTAAGTCGTCAC  
ACAGATATTACTCTGATACAGCATCAATATCTATCCACCAACAGATGAAGTCTTATTAATAACAATTCATATT  
TTACCTTCAACATCTATTAATTAATGTTTCTGATGAATCTAGTGAGGCAAACTTTATACCTCGAGT  
CTTTCTCATAATGTCAATAATGATATTTAGTAGAGGTTATGATATTATTATTAATGATTACAACACTGTATAC  
ACAATGTAATCCAAACAATTCAGTGTATGCACCTTATCAAAGTCCAGATGTAAGTTGATGTTTCCAGAAAA  
CTTGATAGGGATCCAAATTTTGATTATCAATTTATTGAAAATAACGATAGTATCCCTGTAGTAGATACA  
ACATTTGAGAATAATAGTACCATTAAATAATATGCCAATTCGATAGTCTTCCTGTCATCACCTTTTATCA  
GTTGCTACTTTCCGGTGGAGGTAAAATTTCTGGTGTCACTGTAAATTTCCCAAAATTTCCCATAGTTTAC  
GTCAACCTTAACCCACAAACAACAACAACAATCAACAACCAACCAAGCCAAAGACAAAGGCATCTCC

165/251

TTCCANTTGAGTQATTTCAGAACATCACTCAAAATAGTGATTCCGATGATGATGGTATTTCAGGAATTATCA  
 ATAGGTACAAGAAGATCTAGTCAAGCTTTAGCTCAACTCGGTATTTCAATCATCATTTGACAAGTTCTACA  
 CAAGAAACAGCACCACAACATTTCCCGGATGCTAAAGAGATTGAACCGGTTGCTGAACATGTTTGGAGT  
 ATTAACCCACCATATTTCTCGACTTCGATTTCTAAGCAACCTACAAGTTCAAGTTCACTTTACACAACCTG  
 TTTTTCGGAGGTGCTGGTGGGTTAAGTAGTACTGATAAAGAGTTCTCGAAACCTGTTTTAGGAGGATCA  
 ACGTCAGCATCAACATCAACATCGCATGATGAGAAGACTACTACTATTGATTCTTCAAGTACTCOGTTT  
 TTCCAAGTACCAAAATAGAGATTATACTCCTTCTCCAGATAATAATACCTTTGACTCGTACATTATCTAAT  
 ACATCCAAGAAATCTTCAACCATTAACCACCACAACAACCTTCAGAGAATGCATTTCAGAGGTTGATGGACAA  
 CAATCACATCACAATCACAATCACAATCACAGTTGCCACTGCCAACACAACCTGCAACCACGACGCGGA  
 TTATTATTTTGATGAAGAAGATTCTGAAGATCTCGAAGATGAAGGAATGGTTATTGGTGGTAAAAGAGAA  
 GAAAGAAATACATGCACAAGCATATAATGCATTAAAGTCAAGTTGCAGGTAGAAATGGTATCCATAGT  
 CCAAGTCCACAATTTGGTAATGCTAGTGCACATCTCAACATCAAGATCAAGGTCATGAAGATGAACAT  
 GAACATGAACATGAAGAAATCATAAGAATCTTGTGGTCAAGCTAGAGGTTTAGTTAAACACTTTCTTT  
 GGATAA

YKR075C\_homolog 1013aa (SEQ ID NO 546)

MSLSGEVTFSGGATTSQHIEAQDDHIFENTTFXLRKTRSMGLLEDFIPDKLKEQDGNNSSEANSSTTAAST  
 TSSRNLAAMAAIASQINSSVNETPSSQHHTIESLSNNEDGVDTHSSDVAPSSSTSPVNSPSPSTSSPAL  
 DLKSPPELLPHDUTDLAVEFSRHVDYLSHQWDVSDIKSWRYVISKRKDVANAARLENA,SWRTWAQRRSN  
 LKTIISPEVVMWSKDSOVTVLYGPILKDDHVMNENEDSDAIEITATSSVAGIIISIAKKCSSKNGPKPII,  
 KKRTMRFQSMISHSNLLKLQLATQIHQKKREQKLKQCEELKRQHQLNHPDEYFDPEALSNKLNSQYKNTA  
 PTHNTSVAKLQSLKTFNSSSSASLKDLMKDEAVVVPSSSEQISHDQNQFDGNVSGDVESKGERHIFND  
 EVMQCIADIVYSDDEQRYSNDEEDYDSDDDDDDYDQYEPNSDSLAQSHLYEGDDDESIEEADDEVEDDE  
 DCSDEEDDEGGFFLNKXSNAPETLGQHSASSTSTPVAPSLSRITDITDDTASISTTNSKSYRTIQI  
 LPSISINYGSDSSDEANFYTTSSLSHVMNDISRGYDYDYDNTVYTKNPNNSVYASVQSPDVPDVPEN  
 LDMGSNFDYEFIEENDSIPVVDTTFENNSTINMFIYSSEPSPLSVALSGGKNSGVTVNSPNFPPIVN  
 VNSNPQQQQSQAKPKPKTKASPFQLSDSEDDENEDSDDFGISGLSIGTRRSSQALAESVFOSSLTSSST  
 QETAPQHFFPDAKBIBPVAHVSSINPRYSSTSISKQPTSSSSLSQSFQGGAGGLSSTDKELSKSFLGGS  
 TSASTSTSHDEKTTTIDSSSTGFFQVFNRDYTFPLNNITLRTLNTSKKSSPLPPQTTSENAFRGDQ  
 QSQSQSQSLSQLPSQQSQPRRGLLFDEEDSEDSEDEGMVIGKREEKKLHGQGYNALSQVAGRNGIHS  
 PSPQFGNASAHLDQDQCHENEHEHEHEENHNKLVGQARGLAKHFFG

YLR216C\_homolog 1221bp public: 1..1221 (SEQ ID NO 547)

ATGCTGTAAGTGGTGAGTGTGTTTUGAGAACATTCACCAGTATTTTTCCAAATTTATATAAAATGAG  
 ATAAAAATTTTGGTTTCTGGTATTTTCTTTTCCACCAACTCATGACTGCCACACCTGTTTATTMTGAT  
 ATTTTCATGCAACGGCAAAACCAAGGSCCGTGTCTTTTCAAACCTCTACGATGATGTTGTTCTCTAAACA  
 GCGAGCTAATTTCCGTTCTTATGTACTGGTGACAAAGCTATATCACCAAATCTGGTAAACCACTTTCC  
 TATAAAGACTCAATTTTCCACAGACTGATCAAGACATTTATGTGCCAAGGTGGTGACTTTACCGCTCCT  
 TCCGACCATTTGGGAACCTGGTGGTGAGTCCATTTACCGAGAAAGTTTCAAGATGAAAACCTTTAAGTTG  
 AACCATAAACAAACCATTTTGTGTGCAATGGCTAACTTCGGACCAACACCACTGCTCAATTTTCT  
 ATTCACAACAGTTTCCACACACCACTTGGACGCTAAACACGTTGTGTGTTTGGAGAAGTCAATTGAAGGGA  
 TCAATTGTACGTCAATTAGAGAGAGCGGAAAACCTGCCAATCACAGACCAGTAGAAGATTGGAAAAAT  
 GCTGATTGTGGTGAGCTTCCAGCCAACATGAGCCGGTTGCACCTGGGTGCCCATGATCCAACTGGTGTAT  
 AGGTACGAAGAGATTTTAACCGACAACGAUATATCGACATCAACAACCCGCAATCTGTTTTCCGGGCT  
 GTEACCAAAATCAACCATATTGGTACCAAACTTTTGAAGAAGGGAATTAGAAAAATCATACGAAAG  
 TATACCAAGGCCAATAGCTACTTGAAAGATTACTTTCCCGAAGGTTTGTCTCCAGAAGACTTATCAACA  
 TTGCATGGCTCAAAATTATCGTGTACTTTGAACGCTGCGTTAGTGGCAATTGAAATTGAAACACGGCAAA  
 CATGCAATTGCTGCTGCAACAATGCATTAGAAGTAGAGCAATCGACGACAAATCCAAAACCAAGCA  
 TTATACAGAAAAGGTATGGGCTATATCCTAGTCAAGAGCGAAGAACAGGCTCAAAACATTTCTGAAGAA  
 GCTCTCGAANTAGAACCTAACGATGCTGCTATCAAAAAGGATTACAAGAAGCTAAACACAACATCAAG  
 TTGGCTGCTGACAAACAAAAGAAGGCAATGGCCAAGTTCTTCTCATAA

YLR216C\_homolog 406aa (SEQ ID NO 548)

MCKVVSVFENIPVFFPNLYKNEIKFSFVFPPPHQIMTATPVYFDISCMGKPKGRVVPKLYDDVVPKT  
 AANFRSLCTGDKGISPKSKPLSYKDSIFHRVIKDFMCCQCDFTAPSDHLCTGGESTYGRKFFDENFKL  
 HNKKPFLLSMANSQPMNINGSQFFITTVPTPHLDXKHVVFGEVIEGKSTVRQLERSEKGANDRPVEDWKI  
 ADGELPANYEPVASSAGTGTGDTYFEETDNDTIDNNFQSVTAAVSKLKLIGTKLKEGKLEKSYEX  
 YTKANSYLNLYFPEGLSPEDLSTLHGLKLSCYLNALVALKLKHGKDATAAANNALVEQIDDKSKKA  
 LYRKGMGYITVKBDECAOKILEEALALEPNDAAIQKGLQBAKHNIKLRREKQKKMAAKFFS

YMR009W\_homolog 537bp public: 1..537 (SEQ ID NO 549)

ATGCTCGAATTTTATTTTCATGATAACAAACATACACTTCGAAATTTTACTGAAGATCACAATTCAGGA  
 GAACCAGTTAGTTTGATCAACTAGCTGAAATTTGGTGTATTTACAAGTACATTACTACCCAGGAAGAA

166/251

TTAGACGCATTTGGCTACTGAAAGAGAATACAAGAATAGAGATGTTGTTACTTTAAACTTACCAGCCTTC  
 AATAATGATFATTGATGCTTATANTCCCAATCCAACTTTTACAAAGAACATTATCATGAAGATGAG  
 GAAATTAGATATATTGCTGAAGGTCGAAGGTTATTTTGATGTTAGAGATAAACAAGATCGTTGGATTAGA  
 GCTAAATTTATCCCTTACGATTTGTTGATTTTACCAGCAGGAATTTATCATCGTTTTACATTGACTAAT  
 GCTGCAAAACAGCTCAAGGCAGTTAGATTATTTAAACATGAACCTAAATGGGAAGCTATCATATAGAGAC  
 ACAGGAATAAATACCGAAGCTCGTGAACTCTATGCTAAGACTATTGCACTATAG

YMR009W\_homolog 178aa (SEQ ID NO 550)

MVBPYPHDNKDTLENFTEDHNSCEPVSEFDQLAEIGVLYKYICTQEELDALATEREYKVRDVVTLNLPAP  
 NKDLIDAYNAKMQQFYKEHYHDEEIRYLAEGEGYFDVDRDKQDRWIRAKLSFYDLLILPAGIYHRTI/TN  
 AAKFVKAVR/LFKDEPKWEAINRDTGKNTARELYAKTIAV

YMR11W\_homolog 1641bp public: 1..1641 (SEQ ID NO 551)

ATGCTTCAAGACAACGCTTCATCAACATCTACAGCTGAGGCTGTAAATAATGAPATCAAAGTCAAAGAT  
 GAATTTCCACAAGAAGAACAAAGCTTCATCTAGTTTAGAAGATAAACTGTGAGTGCATACATTGGTATC  
 ATTCAATTATGTTGTTCTTATTGCTCTTTGGTGGTTTCGTTTTCGGTTTCGATACTGCTACTATTTCCGRT  
 TTCATTAATATGTTGACTTTTTAGAAGATTCCGTTGCTACTAAAGCTGACGGTACTCTTTACTTTTCC  
 AATGTCACAACCTCGCTTAATGAATGCTTTCGTTCAACGCTGGTTGTGCCATTGGTGCAATTATCTTGTC  
 AAAAGTCGGTGAATATGATGGTAGAAGAGTTGGTATCATGACTGCTATGATTGTCTATATTGTTGGTATT  
 ATTGTTCAAATTGCTCTCAACATGCTTGGTATCAAGTCACTGATTGGTAGAATTAATCACTGGTCTTCCC  
 GTTGGTATGTTATCAGTTTATGTCCTTTGTTTCATTTCCGAGGTTTCTCCAAAACATTTGAGAGGTACT  
 TTGGTGTGCTGTTTCCAATTGATGATTACCTTGGGTATCTCTTGGGTATTGTTACTACCTATGCTACT  
 AAGATTPACTCAGACTCTTACAAATGGAGAATTCCATTAGGTTTATGTTTTGCTTGGGCTTTATGTTTG  
 GTTCTGCTATGTTTGAATGCCAGAATCTCCACGTTACCTTGTCCGGTAAAGACAGAAATTCAGATGCT  
 AAAATGTCACCTTGTAAAACTAACAAAGTTTCCCCAGAGGACCCAGCCTTATACCGTGAACCTTCAATTA  
 ATTCAAGCTGGTGTGAAAGAGAAAGATTAGCCGGTAAGGCATCTTCCGGTACTTTATTCATGGTAA  
 CCAAGAAATTTTGAAGGGTTGTTGTTGGTGTCTATGTTACAAGCCTTACAACAATTGACTGGTGATAAC  
 TATTTCTTCTACTACAGTACCCTATTTTCAACTCCCTTGGTATGAATGATTCTTTCCAACTTCTATC  
 ATTATTTGGTGTATTAACCTTTCGTCCTCACTTTTGGTTGCTACTTATGCTATTGAAGAATGGGTAGAGA  
 CTCTGTTTGTAACTCCTTCCCTTCCCATGCTCTGTCTGTTTCTTAATCTATTCTCTGGTTGGTACTCAA  
 CATCTTTATATTGACAAACCAGGTGGTGGCTAGTAGAAAACCAGATGGTGATGCCATGATCTTTATGACT  
 TCACCTTATATGTTTCTTCTTGTCTTACATGGGCTGGTGGTGGTTTACTCCATTATTTCTGAACCTTTAT  
 CCATTCAGAACTPAGAAGTAAGGCTATGGGTTTAGCTAATGCTTCCRAATTGGACCTGGGCTTTCTTAATT  
 TCTTCTTCTTACTTCAATTTATTACTGATGCTATCCACTTCTACTACGGTTTCGTTCTTTATGGGATGTTTA  
 GTTTCTTCCATTTCTTTGCTTACTTTTATGGTTTACGAAAATTAAGGTCTTACCTTGGAAAGAAATTGAT  
 GAATTGTACTCCACCAAGTCTTCCATGCAAAATCAGCTGGTTGGGTGCCACCTTCCGAAGAAGAAATG  
 GCAACCTCTACGGGATATGCTGGTGATGCCAAAACCAGAAGAGGAACACGTTTAA

YMR11W\_homolog 546aa (SEQ ID NO 552)

MSQLNVSETSPALAVNNEIKVKDEFQRQEEQAHTSLEDKPVSAIYIGIIMCFLIAFGGFVFGFDTGTISG  
 FINMSDFLERFPGGKADQTHVFSNVRTGLMIGLFLNAGCAIGALFLSKVGDVNGRVRVGIMTAMIVYIVGI  
 IVQIASQNAWYQVMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTAVCCFQIMTTIGIFLGYCTTYGT  
 KSYSESRQWRIPLGLCFAWALCLVAGMVRMPESPRLVVGKDRIEDAKMSLAKTNKVSPEDPALYRELQL  
 IQAGVERERLAGKASWGLFNQKPRIFERVVVGVMQLALQQLTGDVNYFFYYSTTIKFSVGMNDSFQTSI  
 LICVINFASTFVCIYAIERMGRRLCLLTGSVAMSVCFLLIYSLVGTQHLYIDKPGGASRKPDGDAMIFMT  
 SLYVFFFASTWAGGVYSIISELYPLKVRSKAMGLANASNWTWGFELISFFTSEITDAIHFYVGFVFMCLL  
 VFSIFVYVFMVYFKGLTLEEIDELYSTKVLFPKWSAGWVPPSEEMATSTGYAGDAKPEBEHV

YMR11OC\_homolog 1986bp public: 1..1986 (SEQ ID NO 553)

ATGAGTAAACCATCTTCCATCAAAAACCTCAAGGCATCTGCTATTAAACCCCTCGGCTAATTCAAAATCA  
 AAAACCCCAAAAATTGAGACCCCAAAAATGCAACAAGTTGAAACACGATTAGAAGCCGAAGTTCCAACA  
 ACTAAAAGTTTCAATTAAGAGAAACAGTATTACTACTGAATCTCTTAAGGCTTCAGAAGATAAGTCTACT  
 CCACAAAAGCACTAACACCCCTGCTGCTGCTGTAGCAAAAGTCTAATCCAAATACCAATGAGAGCCAGCT  
 AAAATTCCAAACGAAAACCTCTTAAAAACAGAATCAACCACTGAGTCAAAAACAAAACGGTGCAACAACA  
 ACAAAAGGAAAAATCTGATGTTCTGTTGGAGACAAAATCGACCTCATCACTACTGTCAGCAACAATAAC  
 TCGGTCTTACAATAACUGAGTTGTGGAGATTCCTATTGGTCTTGAAGAATTACTAAGGCCTTCCAT  
 ACTCCCAAAACACACTCTTTACAGTTTATGATTGAACAATACGAAACTTGTACTTTACATGAAGAC  
 AACCAGGAAGCTTTTGTGTGACGCTTTTCAAAAGCACTTTTCAACCTCTTCTTCCGAAACAGAAACTAT  
 GAATTTGCCACTGGATTGAATGAGCTAGTGTATTATATGTACAGCTCCACAATGGAGCAAAACCAACA  
 CCTGTTGACAGAGTCCCATTCATTTTCTTTGAAATCCAGTTTACATTGAGAGAAATTCCTTTGGGAACA  
 ATTTTATGCTATTGCTGCTTTCAATTATCCGTTTTTTGCTCTCCATCTCACCAATAGTTGGTGTCAATAACA  
 AGTGGCAACACAGTTCACCTCAAGCCTCTGAGTTAAACACCCCGTTTTTCCAAGCTTTTTACTGACTTG  
 TTGTCAAAAGCATTTGGACCCAGAGATATTTTGTGTGTCAATGGGCCATTCTGAAACACATGCTTTG

167/251

TTGGAACAAAAATTTGACAAAAATGTTTATACTGGTAGCGGTTTGGTAGGTACATAATTTGCGAAAAAG  
 GCTGCGGAAACCTTGACACCCAGGTATTTTGGAGTTGGGAGGAAAGTCACCTGCTTTTGTTTTGGATGAC  
 ATTTCTGACAACGACTTCCCAACTGTTCTCCGAAGAATTCCTTGGGCTAGATTTGTAAATGCTGGTCAA  
 ACATGTATCGGTGTTGACATATGTTATTTGGTGGCAAAGTCCCAAGCACGACAAATTTATCCTGGCCTTGCAA  
 GAGGTAAATGAAAAAGATTTTTCAGACGTTGACAAGACGAGAAAACTTTACCCATATGATCCATGAC  
 CGGGCATTITGAGAAAAATGGAGAGTATACTCAACACTACTTCTGGTAATGTGATAATTTGGAGGCAAGCTT  
 GATCATGGCACAAACATATGTTGGGACCTACCGTGATTGATAACCTAACCTGGACAGATTCTCTATGAAA  
 GACGAGATTTCGGGTCCAATTTTACCAATTTTAACTACACTGATCTTGAANAATCCTGCTGTAATAAT  
 ATTGCTAACCCAGGATACCTCCCTTGGCACAATATATCTTTACAAGTGGACCTACATCTAGACAGTATAAT  
 TCCCAAAATTAACACTACTACCACTTTGCTTAGATCTCGCGCATTCCTTATCAATGACCTTTTGATGCAAT  
 ATTGCTTTGACAAATGCTCCGTTTGGTGGTGTGGAACTTCGGGAAAACGGTGCTATCATGGACAGTTTC  
 TCATACAGAGCTTTTACACATGAGAGGACCGTCTCGAACAACATTTGTGGAATGATTGGGTACTCAAA  
 TCAAGATATCCCCCATATGCCAATAAAAAAGACAAATTTGATCCCGAGCTCCCAACAAAAGTACGGTGGT  
 AGACTTTCCTTCAATACACAAGGGAATCTGAGAATTCGAGGTCCACCCCTCTTGTTTTCTGCTTGGAAAC  
 AATGCTCTTGGGGTAGCTGAATTAGTACGTGATTTTATTGGAGCTGGTTTGTGA

YMR110C\_homolog 661aa (SEQ ID NO 554)

MSKPSSIKKSKASAIKPSANSKSKTPKIFTPKIQVETRLGEGVPTTKVSIKRNSTTTESVKASEDKST  
 PQSTNTPAAAVAKSNPNTNAEPKIPNEKSLKTESPSSQKONGATTTKKESDVSLETKSTSSITVSMNN  
 SVLQYTELSEIPIGVERITKAPHSGKTHISLQPRKQLRNLVFTMKONQZALCDALQKDPHRLPSETRNY  
 EFATCLNELVFIMSQLHKWSKPQVDELPLNLSLNPVYTERIPLGTTLVTAAFNYFFVSTSPITVGAIA  
 SGNITVALKPSSELTPRFSKLFTDLLSKALDPEIFPVVNGAIPEITCLLEQKFDKIVYTGSGLVGTIIAKK  
 AAETLTPVILELGKSPAFVLDDISDKDLATVARRLAWGRFVNAGQTCLOVDYVLVAKSKHDKFISALQ  
 EVIEKEFFQDVKTRNFTMHITHDRAFERMESILNITSGNVIIGGKLDHGTRYVGTVIDNVTWTDSSMK  
 DELFGPILFILCTYTDLEKSCRELANEDTPLAQYIFTSGPTSRQYNSQINTITTLVRSCGLVINDVMMH  
 LALHNAPFGGVGTSGNGAYHGBFSYRAPTHERTVLEQHLWNDWVLKSRYPFYANKKDKLIASSQQKYGG  
 RVWFNREGNVRIGGPPLLFSAWNALGVAELVRDPFAGL

YNL031C\_homolog 411bp public: 1..411 (SEQ ID NO 555)

ATGGCTAGAACAAAACAAACAGCAAGAAAATCTACTGGTGGTAAAGCCCCAAGAAAACAATTAGCTTCC  
 AAAGCTGCTAGAAAATCTGCTCCATCTACTGGTGGTGTCAAGAAACCCACAGATATAAGCCAGGTACT  
 GTTGCTTTGAGAGAAATCAGAAGATTCCAAAAATCTACTGAATTAATTGATTAGAAAATTCACCAATCCAA  
 AGATTAGTCAGAGAAATTCGTCAGATTTCAAAACCTGATTTAAGATTCCAATCTTCTGCTATTGGTGTCT  
 TTACAAGAAGCGTTGAAGCTTACTTGGTTGGTTTATTTCGAAGATACTAACTTGTGCTATTCCATGCT  
 AAGAGAGTTACCATTCAAAAGAAAGATATGCAATTAGCTAGAAAGATTGAGAGCTGAAAAGATCTTAG

YNL031C\_homolog 136aa (SEQ ID NO 556)

MERTKQTARKSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKPGTVALREIRRFOKSTELLIRKLRFQ  
 RI.VREIAQDFKTDURFQSSATGALQEAVEAYLVGLFEDTNLCIHAKRVTIQKXNQQLRRRLRGERS

YNL134C\_homolog 1086bp public: 1..1086 (SEQ ID NO 557)

ATCAAAGCAGCTATCATTTCTGGATCTTTTGAACCTTATCAATTAGCGGAAATTAAGATATTCCTCAA  
 CAAAAATAAAAGAAAATGAAATATTAATCAAAGCAGTAGCTTTTGCATATAAACCCCACTGATTGGAAG  
 CACATTGTTTATCAATGGGCAGCCAGGTGATGTTGTTGGTTGGATGTTAGTGGGATCATTCAGAA  
 GTGGGTCTCTCAAGTAAGTGGGTTTGCAAAAGGTGACACTGTAAGTCTTTTATAACTGCTAATAGATCA  
 CCTCCACCTGGAGCTTTTGCAGAAATATGTAGCTGTTGATCCTGCTACTTCGATAAAGTACAATAAGAAT  
 TTTGAACATTTGACTAATTTACAAGTATCTGAAATCCACTCATTTGAAGGGCAGCAAGTATTAATTTA  
 GGTITGGTTACCGTTGGGCTTTTCATTTCTCATTTACTTACGAATTGACAAACAAAAGCAACCTGGGGAT  
 AGTATTTGACTTGGGGAGGAGCAACTGCAACTGGAGTTCTAGCCATTCAGGTTGCCAACTACTGTAT  
 AATCTCAAAGTAATCACCACAGCATCACCCAAAAACCACACCCCTCTTGAACCAATTAGGGGCAAGTAT  
 CTTTTCGATTAATCCAGACCGCTGATCTTGTCAATTAANTTAAGCAATATTCGCCAAATTAATTTGCTCTT  
 GATAUGATTTGAAACACCAGAAACCTTTCAAAAAGTTTACGACTCAACAGAGGGGTCTCAAGAAATATTT  
 ATTGATTCCTTAGCAGGTTTAGACTATCGATCAATTTGCTGCCAATGATGCTAGAGGAGATCAAGTACAT  
 TGGGGCACACCATTCCTTGTTTTGGCATCTTTAAAAGAGAAAACCTGTGTTTAAATGAAAATTAATGTTCAA  
 ACACCTGAATGTTAGATGATTTTACTCAGTGGTGGCAAAGGTGGTCCCTCAAAATTAATGATCCTATT  
 AAACATACAAAATTTAAAGTTAATTAAGAGGATTAAGACTCCGTAAAGTGAAGGTTAGAAATGTCTAGA  
 AATAATAAACCTCTGCTGAAAAGGTTGTATTTAGAGTTCTGGATCTGTA



168/251

YNL134C\_homolog 361aa (SEQ ID NO 558)  
 MKAATISGSPFYQIAETKDIQQKIKENEILAKAVAFAINPTDVKHIVYQLGSPGDDVVGCDVSGIIEE  
 VGSQVTGFAKGDVSAFITGNRSPTGAFABEYVAVDPATSIKYNKNFEHLTNLQVSEIHSFEGAASTKL  
 GLWTVGLSPSHYLRIIDNKKQPGDSILLWGGATATGVLAALQVAKLVYNLKVITTAPEKNHTLLKQLGADY  
 VPDYGDADVYVVKIKNIGQIKFALDTIATPETFQKVYDSTEGSQEVFIDSLAGLDYRSIAANDARGDQVH  
 WGHITACLASLKEKTVFNENYVQTPPELLDDFTQWVQKVVPQIIDRIKHINLKLNLNEGLDSVSKGLELESE  
 NNKLSAEKVVFRVSDS

YNR002C\_homolog 798bp public: 1..798 (SEQ ID NO 559)  
 ATGACGCTCTTCATCTTCTCAAAAATCTGTTGGATCTTCAATCATAGATGCAAACCAAGGACCAATATAAA  
 AAAGTTCGAAATTCGTCGGAGAGGGTGGTGAATTTGTTATTATCAATCGTCACAGTACTACAGACATGAC  
 TTGATGGCTGCGCTTCGGGGGTACTTTAAACCCAGGTGCTTCTCCTTGGCCAAAGATCAATATCAACCT  
 GCTCCCTCGGGTTATGTGGGTTTGGCAATGACCACTTTCTCTTATCTCTTTACAATGCCCCAAGCTATG  
 GGTATCAAAGTTCCAAATGTGGTAGTTTTCATTGCATGTTTCTACGGTGGTGCAGCTCAATTTTTTGTCT  
 GGACGTTTGTAGTTTGTGACTGGAAATACATTTGGTATGACTGCATTGACATCTTACGGTGCCTTCTGG  
 TTCAGTTATTTCAGCAATCTTGGTTCATAGTTTGGTATCGCTECAGCTACGAAGCTTCTGAAGAAACA  
 GCTTCACAGTTACCAANTGCCATTCCATTTTCTTACTTCTTGGGGTATCTTACATTTATGTTGTGCT  
 TTGAACACTTTAAAATCTACAGTTACTTTTCAGTTCTCTGTTTCTTCTTATTGTTTGTAACTTCCTTTG  
 TTACTTGTCTGCTCAATTTAGTGGAAAGAGTCGGTGTCTACTAGAGCTGGTGGTGTCTTTTGGTGTATCACA  
 GCCATTGTTGCTTCGGTGAATGCCTTAGCCGCTACTGCTACTCCAACCACTCTTACTTCCAACCTCTT  
 TCTATTCCATTGCCAGGTAACGTTGTTTTCAAGAAATAG

YNR002C\_homolog 265aa (SEQ ID NO 560)  
 MTSSSSQKSVCSILLIDANQGFLKKVELAGEGGGFVILNRKKYYRHDLMAAFGGTLNPGASFWPKININP  
 APLGTCGFAMTTFTVLSIYNQAQMGTKVFNVVSLACFYGGAAQFFAGCFEEVNTGNTFGMTALTSYGAFW  
 LSYSAILLVDSFGIAAAYEASEETASQLENAIGFFLLAWGIFTFMLWLNLTILKSTVIFSSLFPLLFWTPLL  
 LAQGHFSGRGVTFRAGGVFGVITAIWAWNIALAGTATPTNSYFQPVSIPLPGNVVFKK

YOL139C\_homolog 630bp public: 1..630 (SEQ ID NO 561)  
 ATGCTCTGAAGAATTAGCTCAAAAAAAGTGAAGAATTGTCATATAGATTCCAAGACTGTTTCTTGATTCCAAA  
 GAAGAATTTANTGCATACCATTCATTGAACAGTAGATGGACATTTATGGTACACTAAACCACAAACCCAC  
 AAGAGTCAAAAACTGGCATGATTTATTAAAGCCAGTTATAACTTCTCATCTGTTGAAGAATTTTGGGGA  
 ATTTACAACTCGATTCCACCAGCAAAATCAATTACCTTTGAAATCAGATTATCATTGTTCAAAGAAGGA  
 ATTAGACCGGAATGGGAAGATGAGGCTAACTCAAAAGGTGCTAAATGCCAATTTCTCCTTCAACAAAAA  
 CTGGAAAGTCAATCCAATCATAAATGATTTGTGGTTAAGAGGTTCTGTTGGCAGTTATTGGTGAACCTATT  
 GAGGATGAAGAAACGAAGTCAATGGGATTGTGTTGAATATCAAAAGCAAGCTTACAGAGTCGGTATT  
 TGGACCAAGAGATTGTGATGAATCCAANTTAAGACTGTCGGTGCAGAGATTCAAGAAAGTCTTGCAATTA  
 AACGATGAACAAAAAGTTGAATTCATGTCGCATGATGCTTCCAACACTAGAGGGCGCTGAACCTCAANTT  
 GTTTTCTAA

YOL139C\_homolog 209aa (SEQ ID NO 562)  
 MSFELAQFTEETSLDSKTVFDKSEEFNAKHPLNSRWTLWYTKPQTNKSENWHDLLKPVITTFSSVEEFPWC  
 IYKSLPPANQLPLKSDYHLFKGIRPEWEDEANSKCKWQFSENKKSEVNPTIINDLWIRGLLAVIGETL  
 EDEBENEVNGIVLNIRKQAYRVGTWTKDCDESKLKTVGERLKKVLQLNDEQKVEFMSHDASNTRCAEPQI  
 VL

YOR120W\_homolog 888bp public: 1..888 (SEQ ID NO 563)  
 ATGCCAGCTCAATTGCAAGTTAACACTGATTATTTTCACTTTAAACAATCGAAACAAAATCCCAAGCTGTT  
 GGATTAGGTACTTGGCAACCAACCAATGAAGACCAAGCTTACAGAGCGCTCTTAGCAGCTCTTAAGAAC  
 GGATACAGCACATTGATACCGCTGCAATTTATGGAAATGAAGAACAAGTCGGTAAAGCCATCAACCCAC  
 TCTGGAGTTCCAAGAGAAGAATTGTTTGTACTACCAAAATTCGGAATGCTGACCATAAAAATATTGAA  
 GAAACCTTACAGACTTCATTGAAAAAATTCGGTCTTAACTATGTTGACTTGTACTTGATCCATTGGCCA  
 GCCTCAATTCAGAGTCAACTAATAAACCATATACTGATTTTGATTATGTTGATACTTATAGACGTTTA  
 CAAAAAGTTTATAAGAACAGCAAGAAAAATCAGAGCAATTCGGTCTTCTAAATTTCAUAAAAAGAAATTG  
 CAAGAGTTATCTCTTCGGAAACCTGTCCATGTTCTTCTCTGCTGTCAACCAAAATTGAAGCTCACCATTG  
 TTCACTCAGCCTGAATTTGATGATTATTTGAAGAAAAAGGTATCGTTTTTGCAGCTTATTCACCATTC  
 GTTCTACAAACTCTCCATTATTCAGAAACGAAACUATCGTTAAATCGCTGAAAAGAAATGGTGTGAA  
 CCAGCTCAAGTTTGTGTTATCTTGGCAATTCAGAAAGAGACTGTGGTTTTTGCCATAATCCGTCAACGAA  
 TCAAGAGTTATTTCTAACTTGAAACATTCACCTTACCTTCAAGAGATTTCCAAACATTCGAACAAATTC  
 TCTGAAAAAGATGGTCTTGTGAGAACTTGTAACCCAGCTTTTCAACAACCTTTGATGATTAA

169/251

YOR120W\_homolog 295aa (SEQ ID NO 564)

MPAQLQVNTDYFTLNNCNKIPAVGLCTWQATNEDBAYRAVLAALKNGYKHTDTAATYGNEEQVGKAIKD  
SGVPREELFVTTKLWNADHKNIIEEALETSLKKLGLNYVDLYLIHWPASIDKSTNKPYPDFOYVDTRYGI  
QKVYKNSKKTIAICVSNFTKKKLERLLSSEGVDVVPVAVNQIEAHPLLQPELYDYLKEXGLVLEAYSPL  
GSTNSPLFKNETIVKIAEKNGVEPAQVLVSWAIQRKTIVLPKSVTESRVISNKTFTLPSEDPETLNKL  
SEKDGVVVRTCNPAFNNFDD

YOR122C\_homolog 381bp public: 1..381 (SEQ ID NO 565)

ATGCTTTGGCAAGCCTACACTGATAACTTAATTGCTAACGGTAAAGTCGATAAAGCAGCCTTATATTCA  
AGA3CCG3TGACGCATTATGGGCCCCAATCGGGATCATTCGAATTACAACAACCAGAAATCACTGAAATT  
GCCAAAGSTTTCGATAGTGCCTGAAGGTTTGCAAACCAGCGGTTTACACGTTTCAAGGCCAAAGTACTTT  
TTGTTAAGAGCTGACGACAGATCAATTTATGGTAAACACCAAGCCGAGGGTGTATTTGTGTTAGAACCT  
AAACAAACTATTTTGATCGCCCATCTATCCAAGTGGTGTTCAAACCAGGTGAAGCTACCACTCTTTGTTGAA  
AAATTAGCCGATTACTTGATCAATGTCCGTTATTAG

YOR122C\_homolog 126aa (SEQ ID NO 566)

MSWQAYTDNLIANGKVDKAALYSRAGDALWAQSGSFELQCFEITEIAKGFDSAEGLQTSGLHVQGGQKYF  
LLRADDRSIYGKHEAEGVICVHFKQTILIAHYPSGVQPGEAATTLVBKLADYLINVGY

YOR261C\_homolog 993bp public: 1..993 (SEQ ID NO 567)

ATGTCAACAACCTGCAACTAGCACAAATGAATTGGCCCTTTCTGGATAAGTCAGTAGTAGTTTCTCCCTTG  
GTTTTACTATCTGTGGTGGACCATTATAATAGAGTTGCCAAAGATTCCTAAGANGAGAGTTGTTGGGGTA  
ATATTAGGATAAATCTACTGACACAATCAAGTTACAACTCGTACGCAATTCTTTTGAAGAAGAC  
CAGAAGAACCCTGGAGTATGGTTTTTGGACCACAATTTTATAGATTCAATGGGAGAAATGTTTAAAAAA  
ATTAATGCCAAAGAGAAATTGATTGGCTGGTACCATTTCAGGACCTTAAATTGAAACCATCAGATTTGAAA  
ATTAATGAGGTTTTTCAGAAGATACACCGACAACCCATTGTTCGTTAATTGTTGACCTTCACCAACAGAGAA  
GTTGGTATTTCCAACAGATGCATATTTTGGCCGTTGATGATATTAATAACGATGGCTCTGCTGCTGAAAG  
ACATTTATTCATGTCCCTTCCTCGATTGAAGCACAAGAAGCTGAAGAAATTGGAGTTGAACATTTGTTA  
AGACACATCAGAGACCAAGCTGCTGGTAACTTGTCTTAAAGCTTTCTCAACACATCAATCATTATTG  
CCTTTACATCAGAAGCTTGGAGAAATTGCAATTTATTTGGATAAGGTTTACCAAAAGAAATTAACCTATG  
AATCATACTATTTTGGGGAAATTACAGAATGTTTTTAATTTCTTGCCAACTTCATGCACCAACTGGGG  
AGTGATCTCGATGGTGGTTTCAGACTCGTCTCATGCAATTAGCCACTGCATTTACTGTCAGACAAATGAC  
CAATTCATCATCATATACATTAGTACATTAGTTCCGAGCTATTATTGCATTCCTATGATTTGATCGAAAAAC  
AAGTTAGAAAAATAAAAGTTGAACGAAAAATAAAGCACAAAGCTTCCGTGGCTGAACCTGCTATTAAATAGC  
GAAAGAAAGATTCTATAGAAGATTAA

YOR261C\_homolog 330aa (SEQ ID NO 568)

METTATSTINELALLDKSVVVSPLVLLSVVDHYNRVAKDSKKRVVGVILGDNSTDTIRVTNSYAI PFRED  
EKNPGVWFLDHNFIIDSMGEMFKKINAKEKSLICVYHSGPKLPKPSDLKINPVFRRYTDNPTLLIVDVQPRE  
VGLPTUAYFAVDDIKNDGSAAEKTFIHVPSLIEAEEAEFIGVEHILRDRDQAAGNLSRVSETHQSUL  
GLHQKLGFTANYLDKVVYQKKLPMNHITLQKLQNVNLLPNLKKXSGSDLDGSSDSSHALATAPTVRKTD  
ELMIYISTLVRAIIAFHDLIENKLENKKLNPKAKASVAESSLNSEKKDSIED

YPR035W\_homolog 1122bp public: 1..1122 (SEQ ID NO 569)

ATGACTACTTCCCTTACACAACAACTGCTATTTTGGCCAAATATTTGGAATTGTCTCAAAATGGTAAA  
ATCTTAGCTGAATACGTTCTGGATGATGCTGAAGGTAACACTAGATCCAAATGTAGAACTTTATCCAAA  
AAACCAACTAGTGTGATGATTTACCTGAAAGGAATTTATGAAGGTTCACTACTGGTCAAGCTCCAGGC  
CATGATTCTGATGIGTATTTAAGACCACTTGCTTTTATCCTGATCCATTTAGAAAAGGTGACAAATATC  
ATTGTTTTTAATGAATGTTGGAACAATGATGGTACITCCAAACAAATTTAATCATCCTCAAGAAATGTGCT  
AATTGATGAAGGCTCATGCTAGTGAAGAAGTTTGGTTTGGTTTGAACAAGAATATACTTTATTTGAT  
CAATATCATTATCCTTATGGTTGGCCAAAAGGTGCAATCCAGCTCCTCAAGGTCCTATCTACTGTGGG  
GTTGGTACTGGTAAAGTTGTTGCTAGAGATGTCAITGAAGCTCATTTATCGTGCTTGTCTTTATGCTGGT  
ATCAACATTTCTGGTATTAATGCCGAAGTTATGCCATCTCAATGGGAATTCCAAGTTGGTTCATGTGAA  
GGTATTGAAATCGGTCATCAATCATGGATTGCTCGTTATTTATTACAAAGAGTTGCTGAAGAAATTTGCC  
GTCAAGATTTCCCTCCATCCAAAACCTTTGAAGCGTGATTCGAATCGTGTGGTGTCTACTAATGCTT  
TCTACCAAAATCTATGAGAGTTGCTTGGTGGTATGAAGTTATTGAATCTGCTTTGAGTAAATTCGCCAAA  
AGACACNAGGAACATATGTTATGATGGTGCCGATAATGATCAAAAGATTAACTGGTGGTGCATGAAACCT  
GGTCAATATGGATACTTTTTCATCAGGTGTTGCTAACAGAGGTGCATCTATCAGAAATTCAGACAAAGCT  
GCTAAGAAAGGAATATGGTTATTCGAAGATAGAAGACCAGCTTCTAACATTTCATCCATACTTGGTCACCT  
CGTATCATGCTGACACAATCTCTGGTTCTATTCCAGATGCTGATATGGCTAAAGAAATCCTTTAGAGAA  
AGCAGTGATGATAACTAA

170/251

YPR035W\_homolog 373aa (SEQ ID NO 570)

MTTSLTEQTAILAKY<sub>1</sub>ELSQNGKILAEYVWIDAECHTRSKCR<sub>11</sub>LSKKP<sub>21</sub>TSVDDLPFWNYDGSSTGQAPG  
 HDSDVYL<sub>31</sub>RPVAFY<sub>41</sub>PD<sub>51</sub>FRKGDNI<sub>61</sub>JVLNECHNINDG<sub>71</sub>FPN<sub>81</sub>KFNHRH<sub>91</sub>EC<sub>101</sub>AKLMKAHASEEVW<sub>111</sub>FGLE<sub>121</sub>QKEY<sub>131</sub>ULE<sub>141</sub>D  
 QYDYPY<sub>151</sub>GWPKGG<sub>161</sub>FAP<sub>171</sub>QCP<sub>181</sub>FFYCGVGT<sub>191</sub>GKVVAR<sub>201</sub>DVIEAHYRACLYAGINISG<sub>211</sub>INAEV<sub>221</sub>MPSQWR<sub>231</sub>PQVGPCE  
 GIEMGDQL<sub>241</sub>WIARY<sub>251</sub>LLQ<sub>261</sub>RVAEEF<sub>271</sub>AVKIS<sub>281</sub>FHPKPLKGDWNGASCH<sub>291</sub>TWVSTK<sub>301</sub>SMRVPGGMKV<sub>311</sub>BSALS<sub>321</sub>KLAK  
 RHKEHMLLYGADNDQ<sub>331</sub>RL<sub>341</sub>GRHET<sub>351</sub>GHMD<sub>361</sub>TFSSGVANRGASIR<sub>371</sub>IPRQVAKBGVGY<sub>381</sub>FPEDRRPASNID<sub>391</sub>PLYVT  
 GIMVETICGSI<sub>401</sub>PDADMAKEFLRESSDDN

YMR099C\_homolog 900bp public: 1.900 (SEQ ID NO 571)

ATGCCAGTTGAAGAGCTTGAAGACCGTGTATCATCTACTGATCCAAATGACTCAACTAACAGAGCCACC  
 ATTTTCMAATTTTGGTGGTACTGCTAGTTTCTTGGCAAAAACAAATAATCAAGAAAAATTTGGTTATCAGAA  
 GGTGCTCATTTAGATGGAAGTAAAGCCGTTAGAGGTGGTATCCCATTTAGTTTTCGCCAGTTTTCGGTAA  
 CAAAAAGATTCAAATCAACCAACTTTCAAATTAACCTCAACATGGATTTGCTCGTAATTCAACTTGGGAA  
 TTCTTGGGACAAACTCAAGAAAGTCCATTACGGTTCATTTGGATTAGGTCCAGAAAATGTTGATCCA  
 GAAACTTTGAAATTATGGAATTATGATTTCACTTTTCATTTTAACTGTTAGTTTGACTAAAGATAAAATTC  
 GTTACTTCAATTGACGTGGAAAAACACCTGGTAAAGAAAGCATTTGAATTTAATTGGTTGTTCCATACATAT  
 TATAGAATCCATGACATCAACCGATACACTAGTTTACCAATTTAATTGACCAACAATGTTACGATCAATTG  
 ATTGGTGAATCATATATCGAAAGGCCACCGTTATCAGTTTCCATGAACAATTTGATAGAAATTTAATTC  
 AAAGTCAGTTTGGAAAAATCCATTCAAGTCGTTGATAAAGGTCAGTTCTTTTCAATCTTCAATACAAAA  
 AACTTGCCTGATTCGGTGTGATGGAATCCATGGACTAAGAAAGCTGAAGGTATGGCTGATTTCCAAACCA  
 AATTCAGGGTTTCATCAAAATGGTCTGTGTTGAGCCAGGTCAATGTTAACTCAATGCTCTCTTTACCAGCT  
 GGTGGGAAATGGTCAGGTGGTCAAGAAATCACTATTGGCGGTGAGATTAAAGTTCAAGCTAAATATTAT  
 TAG

YMR099C\_homolog 299aa (SEQ ID NO 572)

MPVEELED<sub>1</sub>RVII<sub>2</sub>TD<sub>3</sub>PND<sub>4</sub>STN<sub>5</sub>RATIL<sub>6</sub>KFGAT<sub>7</sub>VVS<sub>8</sub>WQ<sub>9</sub>NQ<sub>10</sub>EKLWL<sub>11</sub>SEGAHLDG<sub>12</sub>SKAVRGGI<sub>13</sub>PLV<sub>14</sub>FPV<sub>15</sub>FGK  
 QKDSNH<sub>16</sub>PTFKL<sub>17</sub>PQHCFARN<sub>18</sub>STWE<sub>19</sub>FLG<sub>20</sub>GIQ<sub>21</sub>QES<sub>22</sub>PI<sub>23</sub>TVQ<sub>24</sub>FLG<sub>25</sub>PPENV<sub>26</sub>DP<sub>27</sub>ETL<sub>28</sub>KL<sub>29</sub>WNY<sub>30</sub>DF<sub>31</sub>TL<sub>32</sub>IL<sub>33</sub>TV<sub>34</sub>SL<sub>35</sub>TK<sub>36</sub>DKL  
 VTSIDVENTGKEAFEFN<sub>37</sub>WLF<sub>38</sub>HTY<sub>39</sub>YR<sub>40</sub>IHD<sub>41</sub>ITD<sub>42</sub>TLV<sub>43</sub>NL<sub>44</sub>ID<sub>45</sub>QCY<sub>46</sub>Q<sub>47</sub>LIGESYIEKAPVIS<sub>48</sub>PHBE<sub>49</sub>FD<sub>50</sub>RIYS  
 KVSLEKSIQVVDKGV<sub>51</sub>LF<sub>52</sub>N<sub>53</sub>HRK<sub>54</sub>NLPDSV<sub>55</sub>VWNP<sub>56</sub>W<sub>57</sub>WKAEGMAD<sub>58</sub>FOPKSG<sub>59</sub>PHOM<sub>60</sub>VC<sub>61</sub>VE<sub>62</sub>GHIV<sub>63</sub>NS<sub>64</sub>MV<sub>65</sub>SL<sub>66</sub>PA  
 G<sub>67</sub>GKWSGGQ<sub>68</sub>EITIGGEIKVQANIY

YR1085W\_homolog 3519bp public: 1.3519 (SEQ ID NO 573)

ATGGATGGTGGCGATACCTATATATGTATAAAACAAATTTAATGCCAGATTAGGCCGATGAATTGACTCTT  
 AAAATTTGGCGACAAAATCCAACTATTTGGCTGACGATAGAGAAATATAATGATGGTTGGTTACATGGGCAAA  
 AACTTCTTGACTGGAGAAGCAGGCTTATATCCAAAAACATTTACTCAATTAATAACCAACCAATGATAGT  
 AAAACACTTCTTAGATCGAGGTCAAGAAGAATGATGGCACTTAAAGTTCCGACCAAGAAACACACCA  
 AAGCACACCACTACTCCCGTGGTGTGAGTAATCTCAATCCCAACACTCCTCCAAATTAACCTCCAAACA  
 TTGTCTACTTCAACAGAACCTTCCCATTTAGCTGAACCAATGTCTCACTTAAATTTAAATTAAGAAITCT  
 CAATCTTCTCAATATACTGGGTCTCATTGGAACGCCAAATTTGATAGAGCAATTACAAGAACTTCAAGGG  
 TCTAATGCCGACTTGACCAATTTGGCAATAGTTTAAATGAGCACAGAAACCAACCACTACAAATACCAAC  
 ACTAATATAATAATAATAATAATAATAATAATGCTGCTACTAGTAATAATTACAACCAACCAACAGTTAAATG  
 TCGAAGAAATCAAAATGATAGTCTTTCTAGTCAATATCAATATCAATCACAAATCCCAACCAACCAAAACAT  
 TTGAGTGGAGATAAAATCTGACAAATCTTAACTGAAGATTTGGACCCCTTTGAAAGCAAAATACTTGGACA  
 CCAAGCAAGTTTCTTCTTATTTTGCCTTGGTGTTAGGGTTTGATATGGATGTGGCTGGGAATTTGCT  
 CAACACAAAATCACTGGAGAAATCTTGTGTTGAATTCGAATTTAAATCTTTTGAAAGAAATGGATATTGAT  
 TCATTTGGTACCAGATTCAAATTAATAATAAGAAATTTGGGAAATTAAGGAATTTGAATACTGAAGGAGTT  
 AAAGATAAACAATTGAGAACAGATTCTCTGTGACTGGATCAACTGGTAAAAATGACACTACCTCATCA  
 GCATTAATTTCTCCACCAACTGCTTCCACAACCTTTACACGATGCGGTGCTCATATCGATGAATGAATTAAT  
 ATGTTAAATAATAC<sub>1</sub>TGGCABAACAACAACAACAACTAATGCCATCAGCCGTTT<sub>2</sub>TGASCAACACTTCTGAC  
 TACAA<sub>3</sub>TAAATAATAGTCAACAACAAGTGGTTCTCAACATCATCAGAGGAAAAGG<sub>4</sub>TCAT<sub>5</sub>TGTCGGTGGAT  
 GTTGGCCCCACAACAATACTTGGCTTCTGATTCTACATTTATCTCGCCTAGAAGAGCTCTCTCAACCCACA  
 TCTGGTGGAGGCCCAATTGATACAAGTTATAAATTTGGTGGTGGAAAGCGAATACGATAGACCACCTTCA  
 CACTATGGCATGTACATGACACGTACTAACGCTTCAAGTCATGCTTGGGAAGTTCAATCACCAGGAATC  
 AACTCAGGACCAGCTTCAATTAATGATCTGTTTCCAAATCATAATAGAAATGGATCATCAACTTCA  
 AAACAACACCAAGAGAAATTCATCAGTAACCAACATAACAATAACAATAACCGGTAACAGCAACCCAC  
 AAGCATCATCAGACGTCATTCTTCGGTATTCTCATACCTTTGCTCTCGGTAAATGATGATTCTGGCAAAA  
 CCAACACCAAAATTAATTCAGTAGTAAGTTCCAAAGTAACAATTTGTACAGCGTGGTGAATGATGATCA  
 GGAGATTTCACTTCTTCAAGCAATAACAACABAATAACAGTAACCTTAGTGTGGCCAGCCACATCAG  
 AGAGAAACCACTAGTGGTCAATCGTCTCTTCATGAATCAGGATCCAAATCGAAAGGAAATCAACAATTT  
 TTTGATTTATCCAATTCACCAGTTGATATTGATENTGCCAAGCTTTCTCCAAAAAAACTGAATTTCCGTA  
 TCAGTTGGCACCAGTCAATGGATGCAATTTGGTGGTAAATGGAGACGATAGACGTCTTGGCTAGTGAATCT  
 ACAGGATTGAGTCAATCAAAACCTAATAATTCATCAAGACTTAAGGCATTCTGTCACCTCAACUCAA

171/251

AGTTTCCGAAGTTTAAACAGGGTUGAAGAACTGAAAACATCAGUATTTCAAGAAGGTATACGTGAGATT  
 ACTCCTGATGAAGCCATTAAAACTGCCAGTCATAGTGGTTATATGTCCTAAACGTTCAAATAACAAATTTA  
 GCGTGGGAGACAAGATATTTCCACATTACACGGTACCAGATTATCATATTTCCAATCTTTTGAAAGATAAA  
 AAGGAAAAAGGTTTTGATTGATATTACTGCTCATAAAGTGATACCTATTGATAGTGTAGTGATGATACCT  
 GATAAAGCTGATAGATATGCTGCGATGTATGCCCTCGACAACATTTCCTGGTAATTATTTGTTTTAAATTG  
 GTTCCACCGGCTCCAGGGTTTAAAAAGGGGTTAACGTTTACGCAACCGAAAACCTCATTATTTTGGCTGT  
 GAAAACAGAAGAAGAAATGAGAGCTTGGGTCAAAGCATTAAATGCAAGCCACTATTGATATTTGATGATTCT  
 GTTCCTGTTGTGAGTAGTTGTTCTACCCCACTGTCAGTTTGAATAAAGCTCAAGAATTGTTAGCTAAA  
 GCCAGAGAAGAAACCAAATTACGAGATGAACAACCTAAAAGCTAATGGCTACATTAGAAGCTTAGAAGAT  
 ATCAATGATACTTCATTTCTGGCATCTTTGGATTATCCTGATATGACTCGAGATATTGCTTTTGGTAGT  
 ACTTCTCCAGTAGCAGCAACTTCAGCACCTAAATTGACTCTTGATACTAAATTTAATAGGAAAAGTTCT  
 GGAACATTGGGAACAACGGGGACAATAGGTACTCCAGGAACAACAGGTGGTACGGTAUCCAACAACACCA  
 CAAATACCAAGATCATCAAGTCAAAGTGGTGGTTTGGCTTACCTTATTATTAGCTTCTGGGTTTAA  
 TCACCCAAATCAGGAGGTGGTGCCGGTCCAGGAGCAATTGTATCATCGTCTTCTCCAAATTAATGAAAAT  
 GGACUTTTAAGAAATTCAACTTCAAATTGAGAATATTTTGGTGATATTACTTATAAAAGTTTAAAAACA  
 CCATCTCGACAAAATTCCCAATATGCAAGTATCACTAGTGGTGGTGGUAGTAATGGGTTTGGGATATGGT  
 TCCACCAATAGTGGCTAGGTGGACACAGCAACAGCAATTGGAGGAGGAGGAGGAGGAGTATTATCATCA  
 TCCATTCATATTTCTACTGGTTCTGGATCAACAGCAAGTTCAATGAATTATAAATAATATAACAACAAC  
 AACACACAACAACAATTCTGTTAATAGTCCGATTAAATGAATTTAGATCTTCAAGGGAATTGAAATCATCA  
 TCGTCACCAACGACAACAACAGGTACATCTTCAACATCAGGGGAAAAAACCCCAATCAGGTAGAACATCA  
 GATAAATGTTGGGATTTTCAAGTGATGCTTCAGGTAGTCACTACTTTTGTATTAAACCGAAAAAAATAA

Y9L085W\_homolog 1172aa (SEQ ID NO 574)

MEGGDITYICLIKQFNARLGDLSLKIGDKIQVLADREYNDGWYMGKNLLTGEGLYPKTFTQLITNDNS  
 KTTCSRSPRRMMAPKSSDQETTPKDTTTPVSSNLNPNTPPNYPPTLSSSTEPShLAEPMSQLNLNKDS  
 QSSQYTGSHLNSQIDRALQELQCSNADLTNSGNSFNEHRNHHYNNNTNNNNNNNNNAATSNYKQPQLM  
 SKKSNDELSSQYQYQSQSQQPKHLSGDKSRQSLTEDLLDFLKANTWTPKQVSSYFALVLGFMDVAGKFA  
 QHKITGEILLFELDLNLLKELDIDSPGTRFKLYKEIKLKELNTEGVKDKQLRTDSSSTGSGTKNDYTS  
 ALNSPPTASTTLHDAVPHIDNNMLNNTGKQQTQLMPSAVLTNTSDYNNNSQQQSGSQIHQRKRSSSDV  
 VAPQQYLASDSEFMSPRRAPQPPSGESPLDTSYKFGAGSEYDRPPSHYGMXTRTNWASSHALGSSSPCI  
 NSRPASSIYDSFSNHNRRNGSSSTSKQHHRNRSVTVNNNNNNNGNENHKHHHRHSSVPSYLSGNDDSAK  
 PTPKLLSSKFQSNLYKGGDDGHGDFTSNNNNNNNSKLVSPAQIKRETTSGQSSLHESGSKSKGKSQI  
 FDLNSPVDIDDAKFSFKKSNVSVRTKSMDAIGENGDRRVAJDSITGLSQSKFPNNSRLXGIRATSTQ  
 SPSISLGSKKSKTSFAQEGIREITPDEAIKTASHGCGYMSKRNNNLAWRTTRYFTLHGTRLSYTQSLDK  
 KEKGLIDITAHKVIPIIDSDYTDKADRYAAMYASITPAGNYCFKLVPPAPGFKDGLTITQPKTHYFAV  
 ETEEHMRAWVKALMQATIDIDDSVPVSSCSPTPVSNLKAQELLAKAREETKLRRBQLKANGYIRSIED  
 INDTSFSASLDYPMGSDIGFGSTSPVAATSAFKLTLDTNFRKSSSGTMGTGTGTGTGTGTGTGTGTGTGT  
 QIPRSSSSQSGGFASPYLLASGLLSFKSGGGAGGPGGIVSSSSPINENGPLRNSTSNSEYFGCTTYKSLKP  
 PSRQNSQVASTDSGGGSIQFGYGSNNSCUGGPAITAIGGGGGVLSSSTPYSTGSGSTASSMNYNNNNNN  
 NNNNSVNSPINEFRSSRLKSSSSPTTTCTSTSGKKPQSRRTSDKMLGFSSDASGHTPTVKPKK

YBR019C\_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

ATGTCAAACCAATATATTTCTTGGTACTGGTGGTGCAGGTTACATTGGTTCTCATACAGTTATTTGAATTA  
 ATCAGTAATGGATATAAAGTAGTCATTGTTGAATATTTAAGTAATTTCTTCTCATGATGCAGTTGCTAGA  
 ATTGAATTCATCTGTCAAACAACATGTTCCATTTCTATGATGTTGATATCAGAAATATGAGCAATTGAAAT  
 AAAGTTTCCAAGATTATAAGATCTCTGGACTCATTCATTTGCTGCTTTGAAAGCTGTTGCTGAAATCA  
 ACAAAATCCCCCTTAGCATACTATGATAATAATGTAATCAGGTACTGTCAACTTATTGAACTATGTAAAG  
 GCCAATGATGGAAGACAATCTTTTTCAGTTCTTCAGCTACTGTCTATGGTGATGTTACTTAGATTGCT  
 GATAATTCAATGATTCCTTATCCCTGAACAATGTCCAATGGATCCAAACAATCCATATGGAAGAACAAAA  
 TTCATTATTGAGTCGATTTTAAAAGATATTTATAATAGTGATGATGCTTGGAAAGTAGCAATTTTGAGA  
 TATTTTCAACCCCAATTGGTGGTTCATCATCTGTTTATTAGGTGAAGATCCATTTGGGATCCCAATAAC  
 TTATTACCTTATTTGGCTCAAGTTGCTATAGGTAGACGTGAAAAATTGTCTATTTTTCCGAAATCAATAT  
 AATAGTGGTGATGGTACCCCTATTAGAGACTATATTCATGTGGTTCATTTGCCAAGCGTCACATTTGCT  
 GCATTGGCGCTATTGAAAAACTTGCATCTAAAGGCTTTGATCGTGAATGGAATTTAGGTACTGGTAAA  
 GGATCCACTCTTTTGAAGCTTATCATGCATTTAGTAAAGTTGTTGGTAGAGAAATGCCCAATGAAGTT  
 GTTGAAGACGGTCTGGGGATGCTTGGATTGACTGCTAAGCCAGACAGAGCAAAACAAGGAATTGCA  
 TGGAAAACTGAACCTTACCAATTGATGATGCTTGTAAAGATTATGGAAATGGACTACTGAGAACCCCTTT  
 GGATTCAACAATGAGAATTATTTGGGAAGAAATTTGATGGGTTCAATAACCGTTTGCACAGTTTGTGT  
 CCTCGTGACTTCAAGTTAACTTAGCGAATCTGCTGCTGCTATGATCCAGCTATCACGTTGAAGGAATTC  
 AATATGGTCAAAGCTTATAATAACGCTGAAGATTTCAAATCTGAACTAACCCATTTTCTCGTACACCT  
 GTTGGTAGAATATGCCAATAGAAATTTCAATGGAGAATTTAAATTGAATGGAAAAATGTACAAAATTAAC  
 AAAATGAAGGACCAACCACTTGCATGGTGGTCCAAATGGATTTCGATAAACCAAGATTTCTTTGGTCCA  
 GTTGTGAAAAATCTGATGGAAGCTTTTCTGTTGATTTCTTCTTGGTTGATAAAGATGCTAATGATGGG

172/251

TTUCCAGGTGAGCTTGAAGCTATCGTACATTACACAAATTGATGACTCCTCAGTGGAAATTGAATATGAA  
TGTCAATTATTATCTGGTGAAGCAACAATTGTCAATATGACTAACCATAGTTATTTCAATGTTTCCAACT  
TCAGACACTATTGAAGGAACCGAGGTAAATTTGATTACTGATAAAATGTTAGAAGCTGCATTCCACAATTA  
TTACCAACTGGTAAATTTATTGAAAATGAAAAAGCTGCTAGCCCAATTGTGTTAAATGAGAATGACGTA  
TTTGAUAAATTGTTTATTGTTGATGAAGAATGTGGTATAGATACTCGTGATAAACCTTTGAAACCAAGTC  
TTTGAAGCAACTAGTTTTGTCCACAAACAACAATTGAAGATATCCACCCTGAACCAGCTTTCCCAATTT  
TACACTGGTACAGCTGTTAATACATAAGGTTTTTGGGAAAAGATGTGGTTTCTGCGTGGAAACCAAGTAGA  
TTTATTAAATGCAATCAATCACAAGAATGGTCTAATCAAGTCATCTTGAAAAAAGGTGATGTTTATCGA  
AGTAAATTAATATGAATTTCAATAG

YBR019C\_homolog 675aa (SEQ ID NO 576)

MSNEYILVTGGAGYIGSHTVIELISNGYKVIVVDNLNSSSYDAVARIEFIVKQHVFFYDVBIRNYEQLN  
KVFQDYKISGVIHFAALKAUGESTKIPLAYVDNNVSGTVNLEVCANDVKTIIVPSSSATVYGDVTRHG  
DNSMIPPIPEHCPMDPTNPYGRTKFIIIESILKDIYNSDDAWKVAILRYFNPICAHPSGILGRDPLGTPNN  
LLPYLAQVAIGRREKLSIFGNDYNSRDGTPIRDYIHVVDLAKGHIAALAYLKNLQSKGLYREWNLTGCK  
GSTVFEVYHAFSKVVGRELPHEVVGRRAGDVLDLTAKPKRANKELQWKTELTLDACKDLWKWTTEHPF  
GFNIENYSWKEFDGFFNNRLHSFVAGDLKVNLANRCALIQAITLKDSNMVKAYNNAEDFKSE7NPFPGTT  
VGRYANRISNGEFLNGKVYKLTKEGANNLECGANGFQKQDFPGPVVKS RDGKFFVDFLLVDRDGNDC  
FPGYLEALVHYTLDSSVEILEYECQLLSGEATFVNMTHSYFNVSNSDTLEGTEVKLITENKMLEVDSQL  
LPTGKFLIENKAASPIVLNENDVFDNCFIVDEECGIDTRDKPLKQVFEATSEVTNNKLIKISTTEPAFQF  
YTGDGVNTKGFGRGFCVEPSRFINAINHEKWSNQVILKKGDVYGSKIKYSEFQ

YCR005C\_homolog 1194bp public: 1..1194 (SEQ ID NO 577)

ATGAGAGGTATCAAAGGTTTAGTTTGGGAAGGTTCTGTTTGGACCCAATTGAAGGTATCCGTTTCAGA  
GGAAGAACCATCCAGACATTCAAAGAAGATTGCCAAAAGCACCAGGTGGTGAAGAAACCATTACCAGAA  
GCTCTTTTCTGGTTGTTGTTGACTGGTGAAGTTCCAACCTGACGCCCAACTAAGGCTTTATCCGAAGAA  
TTTGCTGCTAGATCAGCATTACCAAAGCACGTTGAAGAATTGATCGACAGATCTCCATCTCACTTCCAC  
CCAATGGCTCAATTTCCATTGCGGTTACTGCTTTTGAATCTGAATCCCAATTTGCCCAAGCTTTAIGCT  
AAAGGTGCCAACAAATCCGAATACTGGAAATACACTTACGAAGATTCCATCGATTGTTTAGCTAAATTG  
CCAACCATTGCTGCTAAGATTTACAGAAAACGTTTTCCACGATGGTAAATTTGCCAGCTGCCATTGACTCC  
AAATTGGATTACGGTGGCTAACTTTGCCAGTTTGTTAGGTTTGTGCTGACAAACAAGGAATTTGTTGAATTA  
ATGAGATTGTACCTTACCATCCACTCTGACCACGAAGGTGGTAACGTCCTCTGCACACACCACCCACTTG  
GTTGGTTCCGCTTTTATCTTCCCCATTCTTGTCAATTAGCTGCTGGTTTGAATGGTTTAGCTGGTCCATT  
CACGGTAGAGCTAACCAAGAAGTTTTTGGATGGTTGTTCAAAATTAAGACAAGAAATTAACCGGTGACTAC  
TCCAAGGAAGCCATTGAAAATACTTGTCCGAACCTTGAACCTCCGCTAGACTTTTCCAGGTTACGGT  
CACGCTGTCTTTAGAAAGACCGATCCAAGATACACTGCTCAAAGAGAAATTTGCTCTTAAACATATGCCA  
GACTACGAATTTGTTCAAATTTGGTTTCAACATTTACGAAGTCCGCTCCAGGTGTTTGAACCAACACGGT  
AAGACCAAGAACCCTATGCCCAATGTGCACCTCCCACTCTGCTCTCTTCTTACAACTACTACGTTTGGCT  
GAACAATCTTTCTACACTGCTCTTGTTCGGTGTPTCCAGAGCCTTTGGTGTCTTGCACAAATTCATCTTG  
GACCGTGGTATCGGTATGCCAATIGAAGACCAAAATCTTTCTCCACTGAAAAATACATTGAATTTGGTTC  
AAAAACATCAACAAAGCTTAA

YCR005C\_homolog 397aa (SEQ ID NO 578)

MRGIKGLVWEGSVLDPIEGIRFRGRTIPDIQKELPKAPGGEEPLFEALFWLLLTGEVPTDAQTKALSEE  
FAARSALPKHVEELIDRSPSHLHPMAQFSIAVTALESESQFAQAYAKGANKSEYWKYTYEDSIDLLAKL  
PTLAAKIYRNVFHDGKLFAAIDSKLDYGANLASLLGFGDNKEFVELMRLYLTIIISDHGCGNVSAHPTHL  
VGSALSSPFLSLAAGLNLGAGPLHGRANQEVLEWLFKLREELNGDYSKEALEKYLNETLNSGRVVPGYG  
HAYLRKTDPRYTAQREFALKHMPDYELFKLVSNIEYVAPGVLTKEHSTKNPNPNVDNHSISGVLLQYYGLT  
EQSFYTVLFGVSRAPGVLPQLILDRGIGMPIERPKEFSTKEYIBLVKNINKA

YCR345C\_homolog 1653bp public: 1..1653 (SEQ ID NO 579)

ATGTCATTAGATAATTCAACAGAAAACCGTGATTTGGAAGAAAAGGAAGAAATTCCAAAGAACGAACAT  
AACCAACAAGGCCAACCAAAACGACAAACAATGACCATATACCTACTTTGGAAGATAAACCATTTGAAGGAA  
TATATTGGTATTAGTATTTTGTGTTTCTTATTGCCCTTTGGTGGTTTCGTTTTCGGTTTCGATACTGGT  
ACCATTTCTGGTTTCATTAACATGACTGACTTTTTAGAAAAGATTTGGTGGTACTAAAGCTGACGGTACT  
CTTTACTTTTTCCAAAGTTAGAACTGGTTTATTGATTGGTTTGTTCATGTGTCGTTGTCGCATTGGTGCA  
TTATTCTTTGTCTAAAGTCGGTGATATGTATGGTGAAGAGTTGGTATCATGACTGCTAIGATCATTTAT  
ATTGTTGGTATTATTGTTCAAATTTGCTTCAACATGCTTGGTATCAAATCATGATTGGTAGAAATTATC  
ACTGGTCTTGCTGTGGTATGTTATCAGTTTGTGTGTCATATTATATCTCAGAGGTTTCTCCCAACAT  
TCGAAGACTACATTACTTTACTCTTTCCCAATTGATGATTACCTTTGGGTATTTTCTTGGGTTACTGTACC  
AGTTACGGTACTAAGAAATACTCTGACTCCAGACAATGGAGAAATCCATTGSGTTTATGCTTTTGCTTGG  
GCCTTGTGTTTGTCTTGGTGGTATGGTAAGAATGCCAGAACTCCACGTTACCTTTGTCGGTAAAGATAGA  
ACTGACGATGCTAAGATTTCACTTCCCAAACTAACAACGTTTCTCCAGAGGACCCCGCATTTATACCGT

173/251

GAACCTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAAGATTGGCCCGTAAGGCCATCTTGGGGTGTCTTTA  
 ATCACCTCGTAAACCAAGAAATCCTTCAAAGAGTTATTGTTGGAGGTATGTTGCAATCATTGCAACAATTTG  
 ACTGGTGATAACTATTCTTCTACTACAGTACCACCAATTTCAAGTCTGTGGTTTAAATGATTCCCTTC  
 GAAACATCTATTATCCTTGGTGTGCATCAACTTTTGTCTCCACTTTTTGTGGTATTTATGCCATTGAAAGA  
 TTGGGTAGAAGACTCTGTTTATTAACTGGTTCCGTTGCCATGTCCATTTGTTTCTTAATTTACTCATTTG  
 ATTGGTACTCAACATCTTTACATTGATCAACCAAGGTGGTCCAAACCAGAAAACCAGATGGTAACGCATG  
 ATTTTCATTACTGCACCTTTATGTTTTCTTCTTCCGTTCTACATGGGCTGGTGGTGTCTACTCCATTGTT  
 TTTGAACCTTTATCCATTAAAAGTCAGAAGTAAGGCTATGGGTTTTGCTAAATGCATGTAACTGGTGTGG  
 GGTTTCTTGATTTCCTTCTTCACTTCATTTATCACTGATGCTATCCACTTCTATTATGGTTTTGTGTTTT  
 ATGGCGTGTTTAGTGTTTTTCCATTCTCTTTGTTTACTTTATGATTTACGAAACTTAAAGGTCTTACTTTTA  
 GAGGAAATTGATGAATTATACCTTACCAAGGTTGTTCATCGAAATCAGGCGGTTGGGTTCCACCTTCT  
 GACCAACAAATCGCTTCGTGCCAAAAGCTATACCTGGTGATATCCACGAGATGAAGAGCAAGTTTAA

YDR345C\_homolog 550aa (SEQ ID NO 580)

MSIHNSTNNRDLERKEEIPKNEHNFQGFQNNENNEHIPTELEDKPLKEYIGISILCFLLIAPGGFVFGFDTG  
 TISGFINMTDFLERFGGTKADCTLYFSNVRTGLLIGLFPNVGCAIGALFLSKVGEIMYGRVVGIMTAMLIY  
 IVGLIVQLASQHAWYQIMIGRIITGLAVGMLSVLCPLFISEVSPKHLRGTLVYCFQLMITLGIFLGYCT  
 SYGTKKYSISRSQWRIPGLGCFAMALCLLGGMVMPESPRLVVGKDRIDDAKISLAKTNKVSPEDPALYR  
 ELQLIQAGVERERLAGKASWGALITGKPRILERVIVCCMLQSLQQLTGDNVFFVYSTTIFKSVGLNDSF  
 ETSIILGVINFASTFVGIIAIERLGRRLCLLTGVSAMSICFLIYSLIGTQHLIYIDQPGCPTRKPDGNAM  
 IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGLISFETSEITDAIHFYVGFVF  
 MGCLVFSIFFVYFMIYETKGLTLEEIDELYSTKVVPWKSAGWVPPSDEEMVRAXGYTGDIHADEEQV

YDR545W\_homolog 1194bp public: 1..1194 (SEQ ID NO 581)

ATGGCATCCGAAGGTATTACTGAAATCGACTCTGCTTTAAATTGAAACCAATTAACGATAACGTCGCTCTAC  
 AAGTTCGACGACTTAAACTTGAAACCAAAACATTCGTTAGAGGTATTCTTGGTTACGGGTATGAAACTCCA  
 TCCGCTATTTCAACAAAGAGCCATCTTGGCCAAATCACTGAAGGTAGAGATGTTTTGGGTCAGCTCAATCC  
 GGTACTGGTAAAACCGCTACCTTTTACCATTCTCGCATTTACAAAGAATCAATGAAATGAAAAAGCCACT  
 CAAGCTTTAACTCTTGGCCCCCAACCAGAGAAATTCGTTTGGCAAATCAAGAATGTTTATCACTGCTATTGGT  
 TTGTACTTCAAGCTTACTGTCCATGCTTCTATTTGGTTGGTTACCTCAATGAAGTGACGAATTTGAAGCTTTT  
 ACATCTGGTGTCAAATTTGTGCTTGGTACTCCAGGTAGAGTCTTAGACATGATTTGAAAGAAGATATTTT  
 AAAACCGATAAAGTCAAGATGTTCAATTTTGGATGAAGCTGATGAAATGTTATCAAGTGGATTTAAAGAA  
 CAAATTTACAACATTTTTCAGATTATTACCAGAAACCACCCAAATTTCTCTTATTATCTGCCACCATGCCA  
 CAAGAAGGTTTTGGAAGTCACCACCAAAATTCATGAACAACCCAGTCAGAAATCTTACTCAAAAAGATGAA  
 TTGACTTTTGAAGGTATCAAAACAATTCATATTAAATGTTGAATTAGAAGATTACAAATTCGAATTCGTTTC  
 TGTGATTTGTACCAATTCATTTCTGTCAACCAAGCCGTCATTTTCTGTAACTACATCCAAAGGTTGAA  
 TTTTAAACCAACAAATTTGAGAGAACAAACATTTTACTGTCTCTGCCATCCACGCTGATTTGCCACAAGCC  
 GAAACAGACACCATTAAGAAAGAAATTCAGATCTGTTCTTCAAGAAATCTTGATCTCTACTGATTTGTTA  
 GCTAGAGGTATTGATGTCCACAAAGTTTCTTTAGTTATTAACATACGATTTGCCAGCCAAACAAAGGAAAC  
 TACATTCATAGAATTGGTAGAGGTGGTCTGTTTCGTTAGAAAGGGGGTTGCCATCACTTTCTCACTGAC  
 AGAGATGTTGGTATGATGAGAGAAATGAAAAAATCTACTCTACTCAAATCGAAGAAATGCCAGCTGAT  
 ATTGGTGTCTTATTTGCCTAG

YDR545W\_homolog 397aa (SEQ ID NO 582)

MASECITEIDSGLIETNYENWVYKFDIINLKNIVRGIFGYGYETPSAIQQRALFPITEGRDVLAQAQS  
 GTGKTATFTSALQRINFNEKATQALILAPTRELALQIKNVITAIGLVLKVTVHASICCTSMSDDIEAF  
 RSGVQIVVGTGPRVLDMERRYFKTDKVKMFIIDEADEMLSSGFKEQIYNIFRLLPETTQIVVLSATMP  
 QDVLEVTTKFMNPNVRILVXKDELTLGKIQFYINVELEDYKFDCLCDLYDSISVTVQAVIPCNVRSKVE  
 FLTNKLEQHFTVSALHADLPQAERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLFANKEN  
 YIIRICRCGRFCRAGVALNFVTDSDVGMRELEKFYSTQIEEMPADIGALFA

YIL057C\_homolog 606bp public: 1..606 (SEQ ID NO 583)

ATGGCGGGGAAGAAAAAGTCTAAGTCTGAAGCTTTTACCATTAGATTTAGACAATATTAAACCAATGGAT  
 CATTTTACAACCAGTCCCTAAAACAAGATCATCATCAATTACCTCAATGAAAGTGCTGATGAACCAAGCT  
 ACTATGAACAAGTGTGTTTACCACCTACATCAAGAATTTGACGAAATTCGAACAATTTGAATCATTT  
 GTTCGTGAAGAAACTTXXGATAATGATTTTGATTATTTUCATGGTAGATTACATTTATATCCACCAATTT  
 GTTATCAAGAGTTGTCAAAATAATCTTGAAAAAATCAAGCCTACCATGAAATGAAAACTUCAAGAAATTT  
 AGACCTGALTTACAACATCATATTCAAAAACNTTTAATTAAGATTGAAAAATGTTGTGTTTACGAG  
 TTGAATTTTGGTAAAGGAGAAGTTGTGAGACTGATTAAGAGTTACTTCGAAATTTAAAGACCAAACT  
 GATCATGGCTTTAGTAAAGAAGAAGATATGTATGATAGACATTGGAGATTGGAACTGGAGTTGATGTTCT  
 TGTACAAATGAATCAGCTATGGTTGATGTTGAATATAAATCCATTTCCAAATGTA

174/251

YLL057C\_homolog 201aa (SEQ ID NO 584)

MAGKKKSKSEALFLDLNFKPMOHLQVPKTRSSSITGIESADFTGTNRQVLI/PPTIKPDELEQPFSSF  
VRDETWDNDFDYFHGRLHYFFVFNKSCQNLKIKFTMNKNSKKPRDLQHHIQKHLIKULEKCCGYE  
LNFGRGSEVVDNKTVMKFKDETDFHGFSSKEEDMYDRHWRLDLVSCTNESAMVDVEYKSI PM

YKR097W\_homolog 1662bp public: 1..1662 (SEQ ID NO 585)

ATCGCTCCCTACTCTCTGTTGAATCTTCAAACAATTTCCGAGGTACCCCAACTATCAAATCCACTCAA  
GACCCATTGGTCCAAAAGTTGCTCTCTTAATACGACACTGTGATCAGACACAAATGCTCCAGCTTCCAACC  
TTATACGAAGATGGTTTATTAGAAAAAGGTACTACTATCTCATCTACTGGTGTCTTAATGGCTTACTCT  
GGTAACAAAACCGGTACATCTCTTAAGACAAGAGAATTGTCCACGAATCCAGCTCATGCCATAACATT  
TGCTGGGGTCCAGTGAATAAACAAGTTGACGAATTAACCTTGAAGATTCTTAGATCAAGAGCTTTGGAT  
TACTTGAGAACTAGAGAAAAGTTGTTTGTGTTGTTGACGCTTATGCTGGTTGGGATCCAGATACAGAAATC  
AAGGTCAGAAATTATCTGTGCTAGAGCTTACCATGCTTTGTTTCATGACCANTATGTTGATCAGACCAACT  
GAAGAAGAATTAAAAAACTTTGCTGACCCAGATTTCACCATCTACAATGCTGGTCAATTCCCAGCCAAC  
ATCCACACTAAAGGTATGACTTCTGCCACTTCTGTTGAAAACAACCTTTAAAGATATGGAATGGTTATC  
TTGGGTACTGAATATGCTGGTGAAGAAAGAAAGGTATCTTTACTGTTATGTTCTACTTGAATGCCAATC  
AAACACAAAGGTTTGAATTTCCACTCTCATGTAAACCAAGGGTTGAAAAGGTGATGTCACCTTTGTTCT  
TTTGGTCTTTCTGGTACTGGTAAGACCACTTTGTTCTGCTGATCCACAAAGAAAGTTGATTGGTGTGAC  
GAACATTGTTGGTCCGACAATGGTGTGTTCAACATTGAAGGTGGTGTGTTACGCCAAATGTTTGGACTTG  
TCTGCTGAAAAGAACCCAGAAATTTTCAACTCCATCAAGTTTCTGCTATTTTGAAGAAATGTTGTCTAC  
CAACCAATCAACCAAGGTTGTTGACTACGAAGATTCAATCACTGAAAACACTAGATGTGCATACCCCA  
ATTGATTTCAATCCATCTGCCAAGATTCCATGTTTGGCCGACACCCATCCAACCAATATTATCTTGTTA  
ACATGTAAGCTTCCGGTGTGTTGCCACCAAGTCTCAAAATTGACTAATGCTCAAGTTATGTATCATTTC  
ATTTCTGGTTACACCTCCAAGATGGCAGGTACTGAAGAAGGTGTTACTGAACCAACAAGCTACATTTCTCC  
GCATGTTTGGTCAACCAATTCTTGGTGTGTCACCCCAATGAATATGCTCAACAATTGTTCTGACAAGATT  
TCCGAACACAATGCCAAGGCTTGGTTGTTGAACACTGGTGGGTTGCTTCTTCTGTTGCTCAAGGTGGT  
AAGAGATGTCCATTGAATACACCAGAGCTATCTTGGATGCTATCCACTCTGGTGAATTGTCTAAAGTC  
GAATACGAAAAAGTTCCAGTTTTCAACUTTAATGTTCCAACTTCTTGTCTCTGGTGTCCAAAGTGAAT  
TTGAACCCCACTAAAGCTTGGACCCCAAGGTACTGATTCAATCAACAAGGAATCAATCTCTTGTCTACC  
AAGTTTGTGAAAACCTCAAGACATACGCTGATCAAGCTACTGCTGAAGTTAAAGCTGCTGGTCCAGAA  
GCATAA

YKR097W\_homolog 553aa (SEQ ID NO 586)

MAPPTAVESSINFCCHPTIKSTODPLVQKLSLNTDVERHNAPPPTLYEDCLLEKGTITISSTCALMAYS  
GNKTRGRSPDKRIVDESTSSHNWCPVNVKQVDEIWKTSRSLADYLRTRREKLFVVDDAYAGWDPRYRI  
KVRTTCARAYHALFMTNMLIRPTEEELENFGEPDFTIYNAGQFFANLHTKGMTSATSVIEINFKDMEMVI  
LGTEYAGEMKKSIPTVMFYLMPIKHKVLTLLHSSCNQGVKEGDTVTLFFGLSGTGKTTLSADPQRKLTGED  
EHCWSDNGVFNIEGGCYAKCLDLSAEKEPEIFNSIKFAGILENVVYDFITKVVDYEDSSITENTRCAYP  
IDFIPSAKIPCLADTHPTNIIILLTCDASGVLPFVSKLTNAQVMYHIFISGYTSKMAGTLEGVTEPQATFS  
ACFQGFYLVLLHPMKYAOQLSDKISEHNANAWLLNTGFWGSSVAQCGKRCPLKYTRAILDAIHSCELSKV  
EYKVPVFENLNVPTSCPGVPSEILLNPTKAWTQGTDSFNKRIKSLATKFAENFKTYADQATAEYKAAAGFE  
A

YOL126C\_homolog 1014bp public: 1..1014 (SEQ ID NO 587)

ATGCTCAAAGTCCCTATTTTATAGAGCTGCTGGTGGTATGGTCAACCAATTATCTTTATTGACCAATTA  
AACCCAAATGTGATCAATTTGGCATTATTTGATGTCGTCAATGTTCCAGCAGTTGGTGCTGATTTATCT  
CATATCAATTTCTGATTTCTCAAACTCAATCTATTTACCAAAAAGATAAAGAAGATAAAACTGCATTAGCT  
CCTGCATTAAAAGGTCTTGATTAGTCAATATCCAGCTGGTGTCCAAAGAAAACCAAGGTATGACACAGA  
GATGATTTATTCATATTAATTCATCAATTCGTTCAAGGTTTATGCTGAAGGTATTGCTGCCAATTCTCCA  
AAAGCTTTTGCTTGGTGATTTCTAATCCAGTCAATTTCTACTCTACCAATTCTTGCCGAACTTTACAA  
GCTAAAGGTGTTTATGATCCACCTAGATTTTGGTGTGTTACTACTTTGCGATATTGTTAGAGCCCAATACT  
TTTATTTCTCAATTAATTCCTAGATCAAACTAAACCATCTGATTTCAATATTAATGTTGTTGGTGCCCAT  
TCTGGTGAAACCAATTGTTCCATTATATTCAATTAGGTAACCTCTAAACANTATTATGATATATTATCTCAA  
GAACAAAACAACGAATTAATCAAAAGAGTTCAATTTGGTGGCGATGAAGTTGTTCAAGUUAAGAATGGT  
GCTGGTTCGCCCACTTTATCCACGGCTTATGCCGGTATAGATTAAGCCGAATCAATTTTAGCTGCTGT  
AAGGTTAAAACCTGATATTGTTGAATGTACTTTCTTGAACCTTGGATTCTTCAATTAAGGTYCTTCTGAA  
GCTAGAAAATTTGGTAAACATTTAGATTTCTTTTCAATACCAGTTCAATTAGGTAAGGTAAGGTAAGGTAAGG  
CAAGTAAATATGATATCTTAAATCAAAATTTCTGATGATCAAAAAGAAATTTGTAAGGTTGCCATTGAA  
CAATTACAAAAGAAATATTGAAAAAGGTTGTTTCAATTTGCTAAGAAATAA

175/251

YOL126C\_homolog 337aa (SEQ ID NO 588)  
 MVKVAI LG AAGGIGQPLSLITKLNPNVDELALFDVNVNPGVGADLSHINSDSKTQSYLPKDKEDKTALA  
 AALKGS D LVII PAGVPRKPGMTRDDLFNINASTVQCLAEGIAANS PKAFVLVISNPNVNSTVPIVAETLQ  
 AKGVYDPA R LFGVTTL DIVRANFFI SQLFLDQTKPSDFNINNVGCHSGETIVFLYSLGNSKQYYDILSE  
 EQKKELIKRVQFGDEVVQAKNGAGSATLSMAYAGYRLAESILA AVNGKTDIV ECTFLNLDSSIKGASE  
 ARKLVKDLDFPSLPVQLGKNGITEVKYDILNQISDDEKKLLEVAIEQLQKNIEKGVSPFAK

YBL072C\_homolog 621bp public: 1..621 (SEQ ID NO 589)  
 ATGGGTATTTCTAGAGATTCACGTCACAAAAGATCCGCCACTGGTGCCAAAAGAGGCCCAATTCAGAAAG  
 AACAGAAAGTTTGAATTACCTAGACAACCTAGCCAACACCAAGATTCCTCCAAAAGAATTCACCTCTGTC  
 AGAACCCAGAGGIRKGTAAACCAAAAATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTTCTTTGGCCTTCC  
 GAAGGTGTTTCCAGAAAAACCAGAATTGCTGCTGCTGTTTACCATCCATCTAATAACGAATTGGTTAGA  
 ACCAACACCTTGACCAAAATCTGCTGTTGTTCAAACCTGATGCTACTCCATTCAGACAATGGTACGAAAAAC  
 CACTACGCTGCTACTTTAGGTAAAAAGAAACCGTCTGCTCATCTCTCCTCAGGCTGCTGAAGTTGCCGAT  
 GCCAAGAGATCAAGAAAAGTCCGAAAGAAAATTGGCTGCTAGATCTGGTCTGCTGCCATTGAATCCGCT  
 GTTCACCTCTCAATTCGGTTCCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGA  
 TGTCATGCTTACATCTTCCAAGCTGAACAATTAGCCTTCTACTTCAGAAGCTTAACCTGCTAAGAAATAA

YBL072C\_homolog 206aa (SEQ ID NO 590)  
 MGI SRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFSWGS  
 EGVSRKTRIAGVVYHP SNNBLVRTNTLTSAVVQIDATPFROWYENHYGATLGKKKGGAHAHAHA AEVAD  
 AKRSRKVERKLAARSGAAATESAVDSQFGSGRLYAVLSSRPGQSGRCDCYILEGEELAFYLRRLTAKK

YBR009C\_homolog 318bp public: 1..318 (SEQ ID NO 591)  
 ATGTCACGTPACCGTAGAGGAAAAGGTGGTAAAGCTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA  
 ATTTTAAGAGATAACATTCAGGTATTACAAAACAGCTATCAGAAGATTGGCCAGAAGAGGTGGTGTT  
 AAACGTATTTCTGCTTTGATTTATGAAGAASTCAGAGTTGTCTTGAAACAATTTTCCAAAACCTTATC  
 AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT  
 TTGAAGAGACAAGGTAGAACCTTGTATGGTTTCGGTGGTTAA

YBR009C\_homolog 105aa (SEQ ID NO 592)  
 MSCTGRGKGKGLCKGGAKRHRKILRDNIQGITEPAIRRLARRGGVKRTSALIYEEVRVVLKQFLENVI  
 RDAVITYPEHA KRKTVTSLDVVYALKRQGRITLYGFGG

YBR189W\_homolog 489bp public: 1..489 (SEQ ID NO 593)  
 ATGGCCCGGTGAATACCGGTTTAAAAAACAAGGGGGGAATCTACAGAATTGGGGTTCCAAATCTCCTAAA  
 ATCAGAAGAGCTGCTCGTGAAATTGTAAACAGAGGTGAANAAGGCCCCCAAAAAGATTATTCGGAAGGTA  
 ATGCCTTTGATCAGAACATTAATCAGATTCCCTTTCTTGCTCTGAGCACAAAATGAAATTGGATTATGTC  
 TTGGCTTTGGAACCCAGAAATTTCTTGAACAGAGATTCCAACCCCAAGTTTTTCAAATTAGGTTTAGCT  
 AGATCTATCCCCCAAGCCAGAGTTTTSATCACCCAAAGCCACATTGCTGTTGGTAAACAAATTGTTAAC  
 ATCCCATCATTTACTGTCAGATTGGACTCTCAAAAACACATTGACTTTCCCCACAACTCTCCCATACGGT  
 GGTGGTAGAGCGCGGTAGAGTTAAGAGAAAAGAACCAAGGTAAAGGTGGTGAAGAAGGTGCCGAAGAAGAA  
 GATAA

YBR189W\_homolog 162aa (SEQ ID NO 594)  
 MACEYRFYKQGGNLQNWGSKCPKIRRAAREFVTRGEKGPKKIRKVMALIRLVRFGFLSEDKMKLDYV  
 LAWNPVFLNRRFQPOVFKLGLARSIPHARVLTQSHIAVGKQIVTIPSFTVRLLSQKHIDFAHNSPYG  
 GGRAGHVRKKNQGGKGGEGAESEE

YBR191W\_homolog 330bp public: 1..330 (SEQ ID NO 595)  
 ATGCCACACAAATACTACCACGTAAGACTGGTATTGTTTACAACGTTACCAAATCCTCCGTTGCTGTT  
 ATCATTAACAAAGTTGTTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGAGTTGAACATGTTAAA  
 CACTCTGCTTGTCTGTCAGAAATCTTGAACACAGTTAANTCTAACCTCTCTAAAGAAGAGAGAAGCTAAA  
 GCTAACCGGTGAAACUGTTTACTTGAAGACACAAGCTGCCAAGCCAAGAGGTTCAAGAATTATCTCCACT  
 GAGGTAACATTCTCTAAACTTTGGCTCCAGTCTGCTTACGAAACTTTTCAATTAA

YBR191W\_homolog 109aa (SEQ ID NO 596)  
 MPRKZYIIGKIGLVNVPKSSVGVLIINKVVGNNRYIEKRVMLRVEHVKHSACRQEFLNRVKSNAAKKREAK  
 ANGETVYIKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YCL035C\_homolog 384bp public: 1..384 (SEQ ID NO 597)  
 ATGATAGACAAAATGCTGCTGATTCTTGCTGGGGATTCAATTTGTGGTATCAACCACCTCCACCTACT  
 GCACAAACTCAGAAAGAAATCGAACACACTATTAACCTCTCACAAGATTGTTATTTATCTAAACCTTAT



176/251

TGTCOCATTTTGTGACCAAACCAACATCTATTAAATGAACAATATCCACAAGAATCGTACGAAGTCATA  
AACTTTGAATATTCTCGATGACGGATTGACTATTGAGAAATCAATTGTATGCTAATCTGGTCAATATATG  
GTGCCCATATCTTCATAAACGGACAACACGTTGGAGGAAATTCAGAAGTTCAGCAATTGCACACCAAT  
GGGAAATTGCAAGAATTATTGAATCTCAGAAATATTGA

YCL035C\_homolog 127aa (SEQ ID NO 598)

MIDKMSSILANGFNLMYQPPPTTAQTEKBIHTINSHKIVLYSKTYCPFDQTKHLINLQYYPQESYEVI  
NLNILDDELTIQNQLYANTGQYMPVPIIFINGQHVGCNSEVQQLHTNGKLQELLNPQKY

YDL004W\_homolog 486bp public: 1..486 (SEQ ID NO 599)

ATGTTTCAGACAAGTTTTCGGTCAAGTTACCAAAACATCAATTCACGTGGGTTAAGAGAACCTTATGCCACC  
GAGGCCCGCGTGTCTACAGATGCTTTGAAATTATUCTTGGCAATTGCCACACCAACCTTATACACACGAC  
TCCGAAGTCCCAACAAGTAAACTTGCCATCTGTCAACGGTGATTTGGGTATTTTGGCCCAACCACATTCGA  
ATTGTGCAACAATTGACACCAGGATTGTTAGAAATCATTTCCAAAAACGGAGACTCTGACCAATACTTT  
GTCAGCGGCGGTATCGCCATGGTCCAACCAGGAACAAGTTGACTATTTCCGCCATCGAAGCATTCAAC  
ACCGAUCAAATTGATCTTCTGCGGTCAAAAACCTTGATTGCCGATGCCUAAAAGAGAGCTGAATCTAGT  
GATGAAAAGGTGCTGCTGAAGCCAACATCGAATTGGAAGTGTAGATGCTTTACAACATTTTACTAAG  
TAA

YDL004W\_homolog 161aa (SEQ ID NO 600)

MFRQVFRQVTKQSFTGVKRTYATEAAVSTDALKLSLALPHQTLYNDSEVQQVNLPSVNGDLGILANHIF  
IVEQLRPULLELIISKNGDSUQYFVSGGLAMVQPGNKLTISALEAPKTDQILD SAYKNLIADAQKRAESS  
DEKVAAREANTELEVIDALQHFTK

YDR099W\_homolog 795bp public: 1..795 (SEQ ID NO 601)

ATGCCAGCCTCCCGTGAAGATTCCGTTTACCTTGCTAAATTAGCCGAACAAGCAGAACGTTATGAGAA  
ATGGTTGAAACATGAAAGCCGTTTGCCTCTGGCCACCAATTGTCTCTTGAGAGAACGTAATTTATTA  
CTGTGTTGCTTACAAGAAATGTCAATGGTGCTGCTCGTCTCTTCGAGAGAAATGTTTCAATCAATTGAACAA  
AAAGAAGAAGCCAAAGGAAATGAGAGCCAGTTGCTTTGATCAGAGATTACCGTGCCAAGATTGAAGCT  
GAATTGCTTAAAATTTGTGAAGATATTCTCTCTGTGTTGAGCGACCAATTTAATTACATTTGCCCCAACT  
GGTGAATCAAAAATATTTTACTACAGATGAAAGGTGATTAACCAAGATACTTTGGCTGAATTTGCTATC  
GCTGAAAAACGTAAGGAAGCTGCTGATTTATCATTAGAGGCTTATAAAGCTGCTTCTGACGTTGCTGAG  
ACCGAGTTGGCCACCAACCCATCCAATCAGATTAGGTTTAGCATTGAACCTCTCTGTTTTCTACTATGAA  
ATTTTGAACCTCCCCAGATAGAGCTTGTCATTTAGCTAAACAAGCTTTCGATGATGCTGTTTCCCTGATTA  
GAAACCTTATCTGAAGATTTCATACAAGCATTCMACTTTGATTATGCAATTATTGAGAGATAACTTGACT  
TTATGGAACGATTTATCTGAAGCCCCAGCTGCCACTGAAGAACAAACAACANTCCAGTCAACCTCCAGCT  
GCTCAACCAACAGAAGGTAAGGCTGATCAAGAATAG

YDR099W\_homolog 264aa (SEQ ID NO 602)

MPSAREDSVYLAKLAEOAERYEEMVENMKAVASSGQELSVEERNLLSVAYKNVIGARRASWRIVSSIEQ  
KEEAKSNESQVALIRDYRAKLEELSKICEDILSVLSDHLITSAQTGESKVFYVKMGDYHRYLAEPAL  
AEKRKEAADLSLEAYKAASDVAVTELEPPTHPIRLGLALNFSVFYVEILNSPDRACHLAKQAFDDAVADL  
ETLSEDSYKDDSTLIMQLLRDNLTLWTDLSEAPAATEEQQQSSQAPAAQPTGKADQE

YDR099W\_homolog 642bp public: 1..642 (SEQ ID NO 603)

ATGCTCTGAATCTGAGAAAAATGTACATTTTCGTACAATAATATACACCAGTTATGTCAAGAAATAGCCCT  
AAGATCAAAGAATTTAAGCCTGACTTTGATCATTTGCTATTGGTGGCGCTGCTTTTATTCCAGCTAGAAATG  
TTGCGTTTCCTTCTTGAAGAAGAACAGGTCAACCAACGTTAGAAATTATGCTATCATATTGTCTTTATAC  
GAAGAGATTGAGACTGAAAACGGTATTGAAAAGCCAGCTACCCAAGTTCTGCGGTACTCAATGGATTAT  
TATCATCAATCTAAAATTGACTTGCTTGCTAAAAATGTGTTAATTATTGATGAGGTTGATGATACCA  
ACCACTTTGCATTACCCAGTCAGTGAATTGAAAAAGATGTGGAAGAGCANTCAAAGCCAAAGCTGCA  
GATCCTAAAGATACCAAGTTTGGTATTTTGTGTTTGCACGACAAGCAAAAGCAAAAGCAAGCAAGT  
CCAGATGATATTTATCAACACTGCTAATTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
CCATGGGAGTCTACTGACATTGTTTATCATCAATGAAAGCTGAAGAACAAGGAACCATGTGTTCTCT  
CCTTCATCCACTTTAGAGTAA

YDR099W\_homolog 213aa (SEQ ID NO 604)

MSESEKMYLSYNNIHQLCQELAPKIKEFKPDLLIAIGGGGFIPARMLRSFLKEPGCPNVRIMAILLSLY  
ELIESENGIEKPGTQVVRTONIDYHQS KIDLVGKLVLIIDEVLDTRITPLHYAVSELAKDVEEQSKAKGA  
DPKDTKFGIFVLHDKQKQKKAELPDDIMKTCNYFAARSVPDSWIAYVWFSTDLVYHQMKAHEQGNDFL  
PSSTLE

YDR418W\_homolog\_498bp\_public: 1..498(SEQ ID NO 605)  
ATGCCTCCAAAATTTGATCCAAATGAAGTTAAATTCCCTTTACTTAAAGACCTGTTGGTGGTGAAAGTTGGT  
GTTTCATCTGCTTTAGCTCCAAAGATTGGTCCATTAGGTTTATCCCCAAAGAAAGTTGGTGAAGATATT  
GCCAAAGCCACCAAGAATACAAAGGTATTAAAGTTACTGTTCAATTGAGAATTCAAAACAGACAAGCT  
ACFGCTTCTGTTGTTCATCCGCTTCAATCTTTAGTCATCAACGCTTTTGAAAGAACCCAGTCAGAGACAGA  
AAGAAGGAAGAAAGACGTCAAACACTCTGGTAACATTCCAATTGATGAAATCTTTGAAATTGCCAGAAA  
ATGCAACACAAATCATTCGGTAAGCAATTTGGUATCTGTCTCCAAGCAAAATCTTGGGTACTGCTCAATCT  
GTTGGTTCGAGAGATTGATGGTAAGAACCCTCATGACATATTGACGCCATCAACGCTGGTGAATTTGAT  
GTTCCAGAAAACCTAG

YJR418W\_homolog\_165aa(SEQ ID NO 606)  
 NPPKFDTPNEVKFPIYLRAVGGEGVASSALAPKICPLGLSPKKVGEDIAKATKEYKGIKVTVQLRIQNRQA  
 TASVFPDSASLVITALKEPVRDRKKEKNVKHSGNIFLDEIFETARKMQHKSFQGNLASVSKELGTAQS  
 VGGPVDGKGNPHDIIDAINAGEIDVPEN

YDR513W\_homolog 360bp public: 1..360(SEQ ID NO 607)  
ATGTTTCGTACATTATTAACCAAAAGACTATTCAATACATCAACAATGGTTTCATCTCAAGTTAAGAAC  
AAGTGCGAACAATTGATCAAAACCAAAACCAAGTTTTCATTGCCTCCAAATCCTATTGTCCATACTGTAAG  
CTTACCAAAAGCACAAATTGAAGCTATAACAAGGATGCTTACATTCCTTGAATTACACCAAGTTCCACGAC  
GGTGCTGAAAATCCAAGAGCATTTAATGGGAAATCACATGGTCAAGAAACCGTTTCCAAATGTCTTTATTGGT  
GGTCAACATATTGGTGCCAATTCGGATGTGCAAGCTTTGAAGTCTAGTGACAAATTAGATGACAAATC  
AAAGCTCGCTTTATAA

YDR513W\_homolog\_119aa(SEQ ID NO 603)  
 NPRTLLTKRLPMTSTMGASSQVKNKVFQLTKTKPVPLASKSYCPYCKATKSTIEAITKDAYTLELDFVDD  
 GAEIQRALLLETTYGKETVENVFEGGHHIGGNSDVAALKSSQSLDDKIKAAAL

[illegible]

YEL009C\_homolog\_323aa(SEQ ID NO 610)  
MPATTPIIYEDSLFESQDLFASPVKQCHQKVDTVATKNEIGLE<sup>1</sup>NLGLPEMQKASETVSTPFGTHSSVL  
ESGFSTNLGVDNDIDHTPMFDEL<sup>2</sup>DLINCGAKVNSS<sup>3</sup>EDWVALFGDDNDGVAIAGATSKEPMLSINEDNE  
NNDDADDA<sup>4</sup>AD<sup>5</sup>DDDALVPRRDTTEAL<sup>6</sup>ILPSPNR<sup>7</sup>ITSAATS<sup>8</sup>SSLSN<sup>9</sup>SP<sup>10</sup>ESTIATTVTAGGEVVVASK  
KQFQLVTPNPSS<sup>11</sup>TLTP<sup>12</sup>LLDSKNSKKRVKVDHLGCVTYSKKHRSQ<sup>13</sup>FLQPIVVD<sup>14</sup>IKDAALKRAKNT<sup>15</sup>EA  
ARRSRARKMERMSGLEDKVNL<sup>16</sup>ENL<sup>17</sup>EKALCD<sup>18</sup>VERLOEL<sup>19</sup>RVNGIO<sup>20</sup>

YGL123W\_homolog\_750bp\_public: 1..750 (SEQ ID NO 611)  
 ATGTCAGCTGAAGCCCCAAAGACAAATTGGTGATAGAAGAAGAGGTGGTGAAGAGGTTGGTAGAAGA  
 GATGGTGAAGAAAAAGCTTGGACTCCAGTCACCAAGTTAGGTAGATTAGTCAAAGCTGGTAAAAATCAU  
 AGCTTTGAACAAATCTACTTCCACTCTTTCCAGATCAAGGAATACCAAAATCATGATTTGTTATTGCTA  
 GACCTTGAAGATGATGCTCATGAAGATCATAGTCTGTGCCAAACAAACAGAGCTGGTCAAAGAAACCAGA  
 AAGAAGGTTGTGTGCTGTCATTGGTGACTCTAAGCGGTACGTTTGGTTTGGGTATCAAGACCGCTAAGAA  
 GTTGGCTTTGCCATTAAAGCTGCTATTGTATTGGCAAATTATCCATCATCCCCAATCAAGAGAGGTTAC  
 TGGGGTTCTAACTTTGGGTCAACCACTCTTTGCCATGTAAAGTCACCTGGTAAATTTGGTTCCTTGGC  
 GTTAGATTAAATCCCGCCCCAAGAGGTAAGGTATTGTTGCTTCTCCAGTTGTCAAGAGATTAAATGCAA  
 TTGGCTGCTCTTGAAGACGTCTATATCT  
 GCTGCTTTCTGCTGCTATCGGTAACTTACAGTTTCTTGACTTCCAACTTTGGTGGGCTGAAGACTCCATT  
 GCTGCTTTCTGCTGCTATCGGTAACTTACAGTTTCTTGACTTCCAACTTTGGTGGGCTGAAGACTCCATT

178/251

YGL123W\_homolog 249aa (SEQ ID NO 512)  
 MSAPAPKKRQFGDRRRGGRGGRRDGEKGGWTFVTKLGRVLKAGKJTSVEQIYLHSLPVKEYOIIDLLLP  
 DLKDDVMKIRSVQKQTRAGQRTMRKAVVVICDSNGHVGGLGIKTAKEVASAIKAAIVIAKLSIIPIRRGY  
 WGSNLQQPHSLPCKVTKXCGSVAVRLIPAPRGKGVASPVVKRLMLQACGVEDVVTSSSGSTRTTENTLK  
 AAFAAIGNTYSFLLTPNLWAETPLAASPLEVYABEAAAGKKRY

YGR209C\_homolog 312bp public: 1..312 (SEQ ID NO 613)  
 ATGGTTCACGTTGTCACTGAAGTTAACGAAATCCAAACCCCTTTTAAAGGAAAACAACCTTAGTTATTGTT  
 GACTTTTTTTGCCACTTGGTGCGTCCATGTAAAATGATTGCTCCATTATTAGAAAAATTCCTAAAATGAA  
 TATTCTAATATTAAATTTTTGAAAATTGATGTTGATCAATTCGGTTCTTTAGCACACAAGATATAATGTT  
 AGTTCTATGCCAACTTTGATTTTATTCAAAAATGGTGAAGAAGTCAATCGTGTCTATTGGTGCTAACCCN  
 GCTGCTAATAAACAAGCTTTGGCTTCTCTTGGCTTAA

YGR209C\_homolog 103aa (SEQ ID NO 614)  
 MVHVVEVNEFQTLLENLIVVDFATWCGPCKMIAPLLEKFQNEYSNIKFLKIDVDQLGSLAQEYIV  
 SSMFTLTLFKNGEEVNRVIGANPAATKQALASIA

YHR039C-B\_homolog 342bp public: 1..342 (SEQ ID NO 615)  
 ATGTCATCTGGTATCCAATCATTATTGAAAACCGAAAAAGAAGCTCCAGAAATTGTAATGAAGCTAGA  
 AAATATAGAAACCACACGTTTGAACCTCCCAACAACATGCTCAAGCTGAAATTGATAACTATAAAAAG  
 CAAAAGGAAGAAGAATTAAAAAATTTTGAAGAAAGAACACGAGGGTTAAATGAAAGATCGATAAAGAA  
 CCTGATGCTGAAGTTGAAAAGGAAATTGACCACTTCAAAATCCACTTTTGAAAAGAAAAAGAGTGCAGTT  
 GTTAAATTGTTAGTTGACGCTACTGTCAAGCCAACCACTTTACACATAAATCCATCTCAATAA

YHR039C-B\_homolog 113aa (SEQ ID NO 616)  
 MSSGIQSLKTEKEAAEIVNEARKYRTTRLRSAKQDAQAEIDNYKKQKEEELKNPKEHHEGUNEKIDKE  
 ADAEVEKELTSIKSTFEKKKSAVVKLLVDATVKFTFTLHINASQ

YJL138C\_homolog 1194bp public: 1..1194 (SEQ ID NO 617)  
 ATGGCATCCGAAGGTATTACTGAAATCGACTCTGGTTTAAITGAACCAATTACGATAACGTCGTCTAC  
 AAGTTCGACGATTTAAACTTGAAACCAACATTGTTAGAGGTATTTTGGTTACCGGTATGAAACCTCCA  
 TCCGCTATTCAACAAAGAGCCATCTTGCCAATCAGCTGAAGGTAGAGATCTTTTCGCTCAAGCTCAATCC  
 GGTACTGGTAAACCGCTACCTTTACCATTTCTGCATTACAAAGAATCAAAAGAAATGAAAAGUCCACT  
 CAAGCTTTAATCTTGGCCCCAACACAGACAAATTCGCTTTGCAAAATCAAGAATGTTATCACTGCTATTGGT  
 TTGTACTTGAAGGTTACTGTCCATGCTTCTATTGGTGGTACCTCAATGAGTGACGATATTGAAGCTTTC  
 AGATCTGGTGTTCAAATTGTGCTTGGTACTCCAGGTAGAGTCTTAGACATGATTGAAAGAAGATATTTC  
 AAAACCCGATAAAGTCAAGATGTTCACTTTGGATGAAGCTGATGAATGTTATCAAGTGGATTAAAGAA  
 CAAATTTACAAACATTTTCAGATTATACACAGAAACUCAAATTTGCTTTATTATCTGCCACCATTGCCA  
 CAAGACGTTTGGGAAGTCACCAACAAATTCATGAACCAACCCAGTCAGAAATCTTAGTCAAAAAGATGAA  
 TTGACTTTGGAAGCTATCAACAAATCTATATTAAATGTTGAATTAGAAGATTACAAATTCGATTGTTTG  
 TGTGATTGTACGATTCTATTTCTGTCAACCAAGCCGTCATTTCTGTAACTAGATCCAAGGTTGAA  
 TTTTTAACCAACAAATTCAGAGAACAAACATTTACTGTCTCTGGCATCCAGCTGATTTCGCACAAGCC  
 GAAACAGACACCATTTATGAAGAATTGAGATCTGGTCTCTCAAGAATCTTGATCTCTACATGATTTGTTA  
 GCTAGAGGTATTGATGTCCAACAAGTTTCTTTAGTTATCAACTACGATTTGCCAGCCNACAACGAAAC  
 TACATTCATAGAATTGGTAGAGGTGGTCTGTTTCGGTAGAAAGGGGGTGGCCATCAACTTTGTCACCTGAC  
 AGAGATGTTGGTATGATGAGAGAAATTGAAAATTTCTACTCTACTCAAAATCGAAGAAATGCCAGCTGAT  
 ATTGGTGCTTTATTTGCTTAG

YJL138C\_homolog 397aa (SEQ ID NO 618)  
 MASEGITETDSGLIETNYDNNVYKFDDLNLKPNIVRGIFGYGYETPSAIQQRALIPPTKGRDVLAAQAS  
 GTGKTATFTI3ALQRINENEKATQALILAPTRELALQIKNVLTALGLYLKVTVHASIGGTSMSDDIEAF  
 RSGVQIVVGTGRVLDNIERRYFKTDKVKMFTLDRADRMSSSGFKEQIYNIFRLLPETTQIVLLSATMP  
 QDVLEVTTKFMNPNVRILVKKDELTLLEGIKQFYINVELEDYKFDCLCDLYDSISVTQAVTFCNTRSKVE  
 FLTNKLRREQHTVSATIAHAPLQAERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKEN  
 YIHRIGRGRFRGRKGVAINFVTDKRVGMREIEKFYSTQTEEMPADIGALFA

YKL060C\_homolog 1080bp public: 1..1080 (SEQ ID NO 619)  
 ATGGCTCCTCCAGCAGTTTTAAGTAAATCCGGTGTTATCTACGGTAAGACGTCAAAGACTTGTGTTGAC  
 TATGCTCAAGAAAAAGGTTTTGCCATTCCAGCTATCAATGTCACCTTCATCTCAACTGTTGTGCTGCT  
 TTAGAAAGCTGCCAGAGACAAACAAGGCTCCAATCATCTTGCAAACTTCTCAAGGTGGTGCTGCCTACTTT  
 GCGGTAAGGTGTCCACAACAAAGATCAAGCTGCTTCCATTGCTGGTTCATTTCAATTTGCTGCCCTCACTAC  
 ATTACAGCCATTGCTCCAACTTATGCTATCCAGTTGTTTACACACTGATCACTGTGCCAAAAAATTA

179/251

TDECCATNGGTTCCATGGTATGTTGAAAGCCGATGAAGAATTCTTTGCTAAGACCCGGTACTCCATTTGTTC  
TCATCCCACACATTTGGATTTATCTGAAGAAACCGATGACGAAAACATTGCTACTTCTGCCAAATATTTTC  
GAAAGAATGGCTAAAATGGGTCAATGGTTAGAAATGGAATTTGGTATCACTGGTGGTGAAGAAAGATGGT  
GTCAACAACGAACACGTTCAAAAAGATGCTTTATACACTTCTCCAGAAACTGTTTTGCGTGTCTACGAA  
TCTTTACACAAGATTTCTCCAAACTTTTCTATTGCTGCTGCTTTTGGTAACCTCCACGGTGTTTACAAA  
CCAGTAAATGTGCAATTGAGACCAGAAATCTTGGGTGACCACCAAGTTTACGCTAAGAAACAAATTTGCT  
ACTGATGCTAAACACCCACTATACTTGGTTTTCACGGTGGTTCCTGGTTCTACTCAAGAAAGAAATTC AAC  
ACTGCTATCAAGAAATGGTGTGTCAAGGTCAACTTGGACACTGATTGTCAATATGCTTACTTGACTTGGT  
ATCAGAGATTACGTCAACCAACAAGATTGAATACTTTGAAAGCACCACTTGGTAACCCAGAAGGTGCTGAC  
AAACCAACAAGAAATACTTTGACCCAAAGAGTCTGGGTTAGAGAAAGGTGAAAAGACCATGTCCAAAGAGA  
ATTGCTGAAGCTTTGGATATTTTCCACACCAAAAGGACAAATTTGTA

YKL060C homolog 359aa (SEQ ID NO 620)

MAPFAVLKSGVIYGKDVKDLFDYAQEKGFAPAINVTSSTVVAALEAARDNKAPIILQTSQGGAAAYF  
AGKGVNDKDAQASIAGSIAAAHYIRAIAPTGYIPVVIHTDHCARKKILPWFDGMLKADEEFPFAKTGTPFLF  
SSHMLDLSEETDDENIATCAKYFERMAKMGOWLEMEIGITGGBEDGVNNEHV EKDALYTSFETVFAVYF  
SLHKISPNFSIAAAFNGVHGVYKPGNVQLRPEILGDHQVYAKKQIGTDAKHPLYLVPHGGSGSTQEEFN  
TAKNGVVKVNLDTDCQYAYLTGIRDYVVKKIEYLKAPVGNPFGADKPNKKYFDPRVWVRGEKTM SKR  
IAEALDIFHTKGQL

YKL150W\_homolog 906bp public: 1..906 (SEQ ID NO 621)

ATGTTGACTCATCATTTTATCGAATTTGGCTACTCCAAAATTCCTTAGTACCATTTGCTCCTCCCACTGCT  
TTGTCATTTGGTTTGGCATTCGAATATTTCTACTTCCAACAATTACATTGCTAACGAAACTGGTAAAACT  
TTCACATGATAGCAATGAATGGGTGGACTTGAATTTATCTTAAGTCAATTGATTTTACTCATTAACACCAA  
CACTTTGGTTTTCAAATTAAGAATGAGAATGATGTTTCTGTTTTCATCACTGCTTCATGTTTGTTCACC  
AATTTCTTACACCAAAGGGTAACAATGTTTATTCGTCCATATACCCCTGCTCTCTGATGTTAACCAATCT  
GGTCAAACTTGATTTCTGTGATTAAAAAATACGACGGAGGTAAAATGTCAAGTCACATTTTCCGATTTGAAA  
GAAGGIGAAACUTTATCATTTCAAAGGACCAATTTGTTAAATGCAATTCGGAACCAATCAATTCAGTCC  
ATTGCTTTGATTTGGTGGTGGTACTGGTATTACTCCATTTACCAATTTGTTGCAATCAATCACTTCTAAT  
CCAAAGGACAACACCAAAGTTAATTTGATTTACGGTAACTTGACTCCAGAAGATATCTTGTAAAAGAAA  
GAAATCGATGCTATTCCTTCTAAACACAAGGACCAAGTTAAAGTTCATTACTTTGTTGACAAGGCAGAT  
GAAAAGAAATGGGAAGGTCAAAATTTGTTTCAATTAATAAGAAATCTTACAAAAGAAATTAGAAAAACCA  
GGTCTGATTTCAAGCTTTTGTGTTGTTGGTCCACCAGGTTTATACAAGGCTATATCAGGTCTCTAAAGTT  
TCCCAACTGATCAAGGTGAATTGACTGGTGTCTTGAAAGATTTGGGTTTCGAAAAAGAACATGTCTTT  
AAATTTTAG

YKL150W\_homolog 301aa (SEQ ID NO 622)

MTTHHLSKLATPKFLVPTAGATALSIGLALQYSPSTNNYLANETGKTFTDSNEWVDLKLKSIDLTHNTK  
HLVFKLKDENDVSGLTASCLLTKEFVTPKGNVIRPYTPVSDVNQSGEIDFVIKKYDGGKMSSTFDLK  
EGETLSFKGPVYKWKWEPNQFKSIALIGGGTGITPLYLQLHQITSNPKDNTKVNLIYGNITPFDILLKK  
ETDATABSKHKDQVKVHYFVDPKADKKWEGQIGFITKEPLQKELEKPGSDFKVYVCGPFGLYKAISGPKV  
SPFDQGELELGALKDLGF EKEHVFKF

YLR029C\_homolog 615bp public: 1..615 (SEQ ID NO 623)

ATGGGTGCCTACAAATATTTACAAGAATTGCAAAGAAAGAACCAATCTGATGTTATGAGATTTCTTGAT  
CGTGTCAGATGTTGGGAATACAGACAAAAGAATGTCTATCTACAGAGCTTCCAGACCATCTAGACCACAC  
AAGGCTAGAAGATTAGGTTACAAGCTAAACAAGGTTTCTGTTATCTACAGAAATCAGAGTTAGAAGAGGT  
GGTAGAAAGAGACCACTTCCAAAGGGTGCCACTTACGGTAAACCAACCAACCAAGGGGTTAACCAATTG  
AAAATACCAAAAATCATTTGAGATCTACTGCTGAAGAAAGAGTTGGTGGTGGTCTTCTAACTTGAGAGTC  
CTGAAGTCTACTGGGTTAACCAAGATTCACCTACAAATACTTTGAAGTTATTTTAGTCCGACCCATCT  
CACAAAGCTATCAGAAGACATGCTAGATACAACCTGGAATCGTTAACCCAGTTTACAAACACAGAGAACCC  
AGAGGTTTGACTTCTGCTGGTAAGAAATCCAGAGGTATTAAACAACCGTCATTTGTTCAACAAAACCAAA  
GCTGGTAGAAGACACACCTGGAAGAGCACAAACACCTTATCTTTATGGAGATACAGATCTTAA

YLR029C\_homolog 204aa (SEQ ID NO 624)

MEAYKYLEELQPKKQSLVMRFLYRVHCNEYRQKNVLRASRPSPFDKARRLGKAKQGFVIYRIRVRRC  
GRKRPVPGATYCKPTNQVNLKYQKSTLSTAEFRVGRAGNLRVLNLYWVWQDSYKYFVILVDPS  
HKAIRRDARYNWTIVNPFVHKHREARGLTSAKKSRGINKCHLPNKTACGRRTWKKHNTLSLWRYRS

180/251

YNL030W\_homolog 318bp public: 1..318 (SEQ ID NO 625)  
 ATGTCAGGTACC3GTAGAGGAAAAGGTGGTAAAGGTTTAGGAAAAGGTGGTGCTAAACGTCACAGAAAA  
 ATTTTAAGAGATAACATTCAAGGTATTACAAAACCAGCTATCAGAAGATTGCGCCAGAAGAGGTGGTGT  
 AAACGTATTCTCGCTTTGATTTATGAAGAAGTCAGAGTTGTCCTGAAACAATTTTGGAAAAACGTTATC  
 AGAGATGCTGTTACTTACACTGAACATGCTAAAAGAAAAACCGTCACTTCATTGGATGTTGTTTACGCT  
 TTGAAGAGACAAGSTAGAACCTTGTATGGTTTCGGTGGTTAA

YNL030W\_homolog 105aa (SEQ ID NO 626)  
 M9GTGRGKGGKSLGKGGAKRHRKILRDNIQGITKPAIRRLAERGGVKRISALIYEEVRVVLKQFLENVZ  
 RDAVITYTEHAKRKIVTSLDVVYALKRQGRITLYGFGG

YOR285W\_homolog 546bp public: 1..546 (SEQ ID NO 627)  
 ATGTTTGCATTTAAAAAANTCTACTACTTCAATTCTCAAAACAGTGGTGGCCCCAACATCATCTCGTTAT  
 TTATCCACCGTCACATTAAGATCAATCCCAAGAACATTCCATAATGCCACTAAAGTTTCATTATTCAAT  
 GGATTAAGAACTACACCAAGATTTTATAGTGTATTGACTGAATCTCCAGAGGCCAAAAGTATATAAATAT  
 GCGATGTTAAGGATGTGGCCGTACACCCCTGAAAACCCCTGATTCTGTTTTAGTGGATGTTAGAGAA  
 CCAACTGAATTTGCAGATCGTCATATACCAGGACCTTTGAATATTCCATTTAAAAGTAGTCCCGGCGCA  
 TTGGATTTGTCAGAAGAAGATTCCCAAGAACATTTTGGATTTCCTAAACCAAGTACTGAATAAGAATTG  
 ATTTTCTATTGCTCTGGAGGTGTTAGATCTACTGCAGCTGAAGAATTGGCCAATACTTTTGGTTATAAG  
 AAAAGAGGAAAATTATCTTGAAGTTGGGAAGATTGGGTAAACNTGAAAATAAAAAGAACTAA

YOR285W\_homolog 181aa (SEQ ID NO 628)  
 MFAFKKSTTSILKTVVAPTSSRYLSTVTLRSIPRTFHNATKVSLENGLRTPRFYSVLTESPEAKVYKY  
 ADVKDVAVHPEINIPDSVLVDVKEPTFPGDCHI PGALNLPFKSSPGALDLSEEDFQEHFGF PKPSTDKEL  
 IFYCLGGVRSTAARELIANTFGYKKRGNVIGSWEDWVKHENKKK

YOR327C\_homolog 603bp public: 1..603 (SEQ ID NO 629)  
 ATGAAGATTTATTACATTGGTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTAACTTCAGCCAGA  
 GATTTATCACAGTTTTCCTTTTCCAAAGAAATCCCGTATCCCAATTCATGACTTTTTTCGCAGAAACC  
 GTATCCCAAGAACTCAACCTGGACAGAGACAAAGTGTGAAGAAGGTAATTATATTGGTTCATACUATTAT  
 ACCAGATCAGAAGGAATTTCTGGTATCATTATAACCCACAAACATTACCCCTCTAAGACCAGCATATACA  
 TTAATAAATAAAATCTTGAAGAATATTTATCATTGCATCCTAANTCTGATTGGGAAAAACATTGATAAA  
 GCAAATGAAACTTTACAATATGGACAATTAGAAGCATATTTGAAAAAATATCAAGATCCCACTCAAGCT  
 GATTCAATCATGAAAGTTCAACAAGAATTAGATGATACTAAGGTGTGTTTTACACAAAACATTGGAAGGG  
 GTTTTACAAAAGAGGAGAGAATTAGATTCAATGGTTGACAAATCAGAAGCATTTGCAAGTTCTTCAAGA  
 ATGTTTTATAAACAAGCAAAGAAAACCAATTCTTGTGTGTGATTATGTGA

YOR327C\_homolog 200aa (SEQ ID NO 630)  
 MKIYYICILRSSCDKALELTSARDLSQFSFFERNQVSVQFMTFFAETVSQRTQPGQRQSVEEGNYIGHTY  
 TRSEGISGLIITDKDYPVRPAYTLINKILEEYL SLHPKSDWENIDKANETI QYQGLEAYLKKYQDPTQA  
 DSIEMKVQQELDIPKVVV LHKPIEGV LQRGEKLDSLVDKSEALSSSSRMFYKQAKKTNSCCVIM

YFL037C\_homolog 474bp public: 1..474 (SEQ ID NO 631)  
 ATGCCAGTCGATCCAGAAAAATTAGCTAAATTGCAAAAGTCATCTGCCAAAAAAGTTGGTGGTTCAAGA  
 GTTAAAGCCAGAAGAACATCAAGACTGAACAAGATGACACCAAAATTGATTGAAGCTTTGGGTAAATTC  
 AAAGCTACCAAAATCGAAGGTGTTGAAGAAGCCAACTTCTTCAGAGAAGATGGTAAAGTTTTACATTTT  
 AACAGAGTTGGTGTCAAGGTGCTCCAGCTTCTAATACTTTTGCCTTCACTGGTTACCCACAAGAAAAG  
 AATATTACTCAATCGATCCCAAAATTTTACCACAATTGGGTGCTGAAAACCTTGGAAATCTTGAGACAA  
 TTGGCTGAACAAAATCCAAGCTGCTAAAACCTCCAAAACACTTCAACACTGCTTCTGCTAACGCTGCTGCT  
 GATGCCGGTGGTGAAGATATTCCAGACTTGGTTGACCAAAAATTTGACGATGTAGATAA

YFL037C\_homolog 157aa (SEQ ID NO 632)  
 MFVCPPEKLAKLQKSSAKKVGGSRVKAKENIKTEQDDTKLIEALGKLKATKIEGVVEANFFREDGKVLHF  
 NRVGVQCAPASNTFAFTGYPQEKNTITQLIPQILPQLGAENLEILRLALQLQAGKTPKLFNTGSANAAA  
 DAGGEDIPDLVDQKFEDVE

YFL070W\_homolog 330bp public: 1..330 (SEQ ID NO 633)  
 ATGCCACACAAATACCTACCACTGGTAAGAAGTGGTATTGTTTACAACGTTACCAAACTCTCCTTGGTGTT  
 ATCATTTACAAAAGTTGTGGAAACAGATACATTGAAAAGAGAGTTAACTTGAGACTTGAACATGTTAAA  
 CACTCTGCTTGTGCTCAAGAAATCTTGAACAGAGTTAAATCTAACGCTGCTAAAAAGAGAGAAGCTAAA  
 CCTAACGCTGAANCCCTTTACTTCAAGAGACAAGCTTCCAAAGCCAGAGGTTCAAGAATTATCTCCACT  
 GAAGGTAACATTTCTCAAACCTTGGCTCCAGTGGCTTACGAAACCTTTCATTTAA

181/251

YPLC79N\_homolog 109aa (SEQ ID NO 634)  
 MPFKYYHSGKTGIVYVNVTKSSVGVITNKVVGNNRYTEKRVNIRVEHVKHSACRQEFINRVKSNAAKKREAK  
 ANGETVYLKRQAAKPRGSRIISTEGNIPQTLAPVAYETFI

YBR089C-A\_homolog EMBL\_entry 279bp public: 1..279 (SEQ ID NO 635)  
 ATGGCTCCAGGTGAAAAGAAAGAGTCCTCTAGAAAAGAAAGGATCCAGATGCTCCAAAAAGATCCTTA  
 TCTGCTTATATGTTTTTTCGCTAATGAAAACAGAGATATTGTTAGAGCTGAAAACCCAGGTATCTCTTTT  
 GGTCAGGTGGGTAAATTATTAGGTGAAAAATGGAAGGCTTTAAACAGTGAAGATAAATTACCTTACGAA  
 AACAAAGGCTGAACCTCATAAAAAGAGATATGAAAAAGAAAGGCTGAATACGCTAAAAAGCAATTCGCC  
 TAA

YBR089CA\_homolog SWISS-PROT\_entry 92aa (SEQ ID NO 636)  
 MAPGERKKSSRKKNDFDAPKRSLSAYMFFANENRDIRVAENPGISFGQVGNLLGEKWKALNSEDKLPYE  
 NKABADKKRYEKEKAEBYAKKNSA

YBL092W\_homolog EMBL\_entry 396bp public: 1..396 (SEQ ID NO 637)  
 ATGGCTACTTCTGTTCACACACCCAAAAATTTGTTAAGAAATACACCAAGAAATTCAAGAGACACCATTCT  
 GACAGATATCACAGAGTCGCTGAAAACTGGAGAAAACAAAAAGGTATTGATTTCATGTGTTAGAAGAAGA  
 TTCAGAGGTACCATCCACACAACCAACATTGGTTACGGTTCCAACAAAAAGACCAAGTTCTTTGAACCCA  
 GCTGGTTACAAAGTTTACTTTGGTTAAAAACGTTAAAGACTTAGATGTCTTGTATTTCACACATAAATCT  
 TATGCTGCTGAAATTCCTCTTCTGTCTCATCTAGAAAAAGAGTTGAAATCGTTGCTAAAGCTAAGAAA  
 CTCGGTGTAAAGTCACTAATCCAAAGGGTAAATTGAACTTGGAAAGCTTAA

YBL092W\_homolog SWISS-PROT\_entry 131aa (SEQ ID NO 638)  
 MATSVPHPKIVKKYTKFKRHHSDRYHRVAENWRKQKRGIDSCVRRRFRCTIPQPNIGYCSNKKTKFLNP  
 AGYKVYLVKNVKDLQVLLHNTKSYAAELASSVSSRKRVEIVAKAKKLGVKVTNPKGKLNLEA

YEL059C\_homolog 2791bp PathoSeq: 1..2791 (SEQ ID NO 639)  
 TATCCATGGTAATGAATCAGTTAATACCACTACCAAACTGTTTATTAAATCTAGAGCAGATTTTAATACCTG  
 TGATTATTGAATTTGTTGATAACAGAGTCGTGGAAATTGGATTCTACCCCTTGATTGTAAAGAAATTGTCAAAATCC  
 CTTCAATTATGTCGTGATATTGAAGTTTCTTTTAAAGAAGATACCTCAACAATATGAAGCTTTTGGGATTTTCTCGAA  
 ATGGGAAATTAATTTTGTAAATGAAAACCAATGTTGTTAGTGGTGTACATCATTAAAAATTACTGAATCTCATTAT  
 TATTCACTACCGTACAAATCAAAATTATGTTTATTATTCAATTTAAATTCAAGTCAAGAAAATTAAGAATTTTCTGAA  
 ATTTAACCAATGAAAATATTGTTGATGAAAGAAATTAGACAAAGTGCAAGAGAGATCTATATTAATCAATGTAATGC  
 CAACGAAATATTCTGTAGTTTTCGAAGCCCTAGAGGTAATTTGGAACTATATGTCGAAGAAATATCGTATTAT  
 CAGCCATTAGAAAATTCATTAAACAAAAAATTATAANGATGCATTCAATTACTTCTCTCGTACACATAGAATTGACCT  
 TAGATATTTTACATGATTATGAACCGGAATTATTTTCAATAATGEGGAACATTTATTAAACCAATATCTTAAG  
 TGGAAATACCTGGATTATTTGTTTCTTGTTTACATGAAGAAGATGCAACCGTTACTAAATATAGAGAAACAATAA  
 ATGATGCTGCTGCTGCTGCTGGTGGTGGTATTACCAAGAAGAAGAAATCAACCGTGAAGGTGAACCTCTTCAAC  
 CAGCATTACAGAAGAAATTCCTATCACATAAGGAAAAAGTTTTCACCAATTTCAATGATTCCAAAGTTAATCGAA  
 TTTCGTAAGCCATATTAAATTTTATTATTAAABUCAGAATAATTGATAAATATTACAAACGATTTTACTGCTT  
 ATGCTTCTGAGAAACCAAGCAATTTGACTCAAGCACTCACATTAATTGGTAAATGGATAATCAAGAACAAGAG  
 AAATCTGCAGTCACTCATTATGTTTCTTCAAGATGCAAAATAATATATAAAGACATGTTTGGACATATATGATC  
 TCAAAATTAACCTTAGTCATTGCTCAACAATCAAAATGGATCCTAAAGAATATTTACCATTTTACAAAATTTGC  
 ATGTACAACCAAGAAATTGAAAAGAAAATTTTAATCGATGATFATTTGAAAAATATGAATTAGCTTTGAATGCT  
 TACATGAACAAGGTGATGAAGCTCATGAAGAATTTGATGATTATGTTGTATTACATGAATTATCAAAACGAGCTT  
 TCAAAATTTATACCTATGATAAACCAGAACCAATGTAATCATGGGATTGTTTGTCTGAACATTTACGTGAAACTA  
 AACAAATTTGCTGAAGCTGCTCTGATATTTGAATATTTGATTCATTTGGAAAATGCATTAGAAATGTTATATAATGG  
 CCAAGAAATGGAAACAAGCACTATCATTAGTTGAGAAAAGTGTGACCTTTTGGAGAAATTAATCTGATACCGCTG  
 AAAAATTAGTTGAAACATTAAGTGAAGATCATAAATATAGTGATGCTGCTGGAATGAAATATCAATTTTGGGGA  
 ATGTTGAAGCATCTATCAAAATATATTGTAAACAATATTTGGTATGATCATGCTATATTTATTAGCTGAAAAATCTA  
 AAAAACCAGATTTGATTGAATCAATAGTTGATGTTCAAATAAATGAAGCGTTTGGGCTGATTGCTGAATTAATTAG  
 CCGATTGTAAGCCCAATCAATTTCAAAATTTGAAAGACTTCCAGAAATGAAGAACTAAAAAGCAAGAAGATCCAT  
 TTTGCTTTTATGGAACCTCTGATGATTTAGATACTCTTGATAATGTATCGGTTCCTGCTTCTGAAACATCAACCA  
 CCCCATCATTTTCAAGATATACTGGTAAACTGCTGGTACGGCCCAAAACAGGAGCATCTAGAAGAACTGCCA  
 AATAACAAAAGAGAGAAGAAGAAACCTGCCAAGGGAAGAAAGGTACTATTTATGAAGAAGAGTATCTTATTA  
 AATCAGTTGGTCTTTTATTAGAAAGATTAGATCAAAACCAATCAGATGCGCTTAAACTTAATTGAAGGACTTTTAA  
 GAAGACATATGAAGAACAAGCTTATCAATAACAAGAATTTGGTGTGAATTGATTGATTTTATCAAGAAATA  
 TCGATGAATTTATATATGAGTGAAAAAGATCGTGAAAGAAATCGATGATAATGCTGAATCTATTTGATTCTATG  
 AATTCCAAAACCTAAGTATCAGAAATCCCTAAATTCATATATATAGATTATTAATCATGGAATGAAGCTAAGA  
 TAACTTTTATTTAATAGAACCAAGATCATCTTACTCCTTGATAGACTATCTTATTTATCTTATTTATTT

ATTGATATATCATATTCAGGAGGCAAAATTGTTTCATCAATTGTTCTTGTTTCATATTC AAGATAAAGATCCAGTAA  
CCCACAATGGCATTTT TATAGCATCAGTAAGTCTTTCTTTCCAGGCATAGCATAACACATATGTTATAAGGC  
ATATTTGTAGATTTCTGCTGGCCCAAGTTGTTCTCTAAAAGTACCATCTTTCAATATTAATCGTATTTTCTACTACA  
ACAAGCCGAGAAATACCTGTTTCATCTTTTATTTTCCCGTTTGGGTTTAAATTAACCAATCCCAAAAATTGTGCGG  
GTGACCAATCCATCCA

YDL059C\_homolog\_1 67aa PathoSeq: 1..67 (SEQ ID NO 640)  
ENKYSALVAVKIELILKDGTFEEOSGOAESTKMPYKHKCYASARZKAVTRAIKNAIVGLRQLYLEYE

[illegible]

183/251

AAGAATATATCCACCAAATGGTATGTGCTTATACCTACFTTTGTTTGTCTATCAGGTTGTTGATTCTTCCTATG  
 TTACAAAGCTTAAGCAAGTCGCTTTGGTGCCAAAGCTCTCTACAAACCAACGAATCCGATGGTTATTGGGGGTTCCTAT  
 TACCATTTCTTGTGTGGTTTTCAAAAAAGCTGAAGCTACAAATTAITGATTTCGCTGGTGAACCTTTTCAAAAGTATTG  
 CCCACCCAGAAGTCCCAAGCTTTTCAGTTCCCAATTTTCAGTGTCAAAGTTATTTCCACCGTTGATCCAGAAAACA  
 TTAAAGCTGTATTGGCCACCCAGTTCAATGACCTTTTCATTAGGTACTAGACACAAATCAATTTGCTCCATTGTTCG  
 GTGATGGTATTTTCACATTAGACGGTCTGCTGGTGGAAACATAGTAGATCTATGTTGAGACCACAATTTGCCAGAG  
 AACAAAGTTGCTCACGTCAAGGCATTAGAGCCTCACATGCAAGTATTATTCAAAACATATCAGAAAGAGTGGTGCTA  
 GAACCTTTTGATCTCTCAAGAAATTTGTTTTCCAGACTTACTCTTGATTCTGCTACTGAGTTTTTATTTCGGTGAATCCG  
 TCGAGTCTTTGAGAGACGAAAGTATTGGTATGGCTTTAGAAGCAGTCCGATTTTGATGGAAAAAGGAATTTGCTG  
 AAGCCTTCAACTTTTCTCAAACTATTTGGCCTCCCGTCTGTTATCCAAACAAATGTACTGCTTATTCAACAGCA  
 GTGAGTTCAAAAGTTGTAACTCCAAAGGCCACAAATTTGCTGTABTACTATGTCAAACAAGGCCATTGGAGTTGTCTC  
 ATGAAGAATTGGAAAAGCAACAAGGTTATGTCTTTTGTATGTAATGGCAAAACAAACTAGAGACACCAAAGTGT  
 TGAGAGACCAATTTGTTGAACATTTTGGTTGCTGGTATAGAGATACCACTGCTGGATTATTGTCTGTTGTGTTTTCG  
 AATTAAGTGAAGAAATCAAGAGTCTTTGGCCAAATTGAGAGAAAGGTTGAAGAAAGTTTGTGTTTGGTGAAGATG  
 CTCGTGTTGAAGAAATTAGTTTGAATCATTTGAAACTGTGTGAGTACTTGAAGGCTGTCTTAACTGAATGTTTAA  
 GATTGTACCCATGGGTCCCAACAACTTTAGAGTTCTTACAAAGAAATACCTACCTTCCCAAGAGGCTGGTGGTTCTG  
 ATGGTATGTCTCCAATTTTGGTCAGAAAAGGTCAAACTGTATTGTACAGTGTATTACGTTACCCACAGAGACACTA  
 AGGTTTACGGTAAAGSATGCTGACCAATTCAGACCAGAGAGATGGTTTGAACCCAGAAACCAAGAAATTTGGGTGGT  
 CGTTTGATTCCATTCACCGGTGGTCTCAAGAAATCTGTTTGGGTCAACAATTCGCTTAACCTGAAGCTCTTTATGTTA  
 CTGTCAATTACTTCAAGAAATTTGCTCATTTGACTATGGACCCAAATACTGATTATCCACCAAAAAGATGTGTCAC  
 ATTTGACCATGTCTCTTTTACGATGGTACTAATGTTGAATGTATTAAAGCAGGCTAGATTTATTTAGUGTATGTA  
 CCTATTTTAAACAGGATAATTTGTTTGCAAAAAAGTGCTGTAGATTTTCACTGACTGAGGGTCTTTTGTGTTGTA  
 TGTAGAACCAAACTATATGTCAGAACAAATAGGGATTGCCATTTCCCTTGTTTGTGATTGACAACTTTCTATGCCG  
 CCTTTTGTGTTGCTATACATATATATTTTGGGACTAGCATGTGTATAGACAGAGAGAAATCACTACTATCGAAT  
 CAGTTAAAGTAGATCTAGAAATAACTCAATGATAATTCGTTGGCACTATTTATAGAGTTTAACTTTTTCGGAAAT  
 TCTAAGTCTTACCAACAAATCTTTGACTGAICTTGTATGCTCCAAATTAATTTTATTAATTATAGCATCGCTCTC  
 GTATTCCCAAGCTTCTAGTGTATTATTTTGTATTATATCCACAAACTCAAAATCCATAGAGCTCATGTGAACAG  
 CTCATTGTCTGGCTAACTTCTTGGTGTGGGACATGTATTCGAGAAATTCAGATTACACACAGAGAGGGGTAAAT  
 TTAGCTTTGTTTTAGGATCGTCCCAATTGATGGAGAACAAATACCATTACAACTCCCAACACTCCGAGAAGTAT  
 ACCAATATCTGTTATTATATACGAGTACATGTGAAAAAGAGGGAGGCACCAAAATATGAACATTTCCATTGTT  
 CAGCATAAAAGGAACGTTCTGTACTTTGTGCAAAAGAAAGCAACCAACCTCCTTACTATTCTGAACACATTTCT  
 ATATTGAGGGGTATTGTAATGATACTTTGACAATCACTTTAAACAGCAAAACAAATTTGCCATCTCAACAAAGAGT  
 ACAAATATATATGTTTGTATAGGATCCCTGCTAGCTACAAATGTTTCAATTTTACAGAAATAAACCAAAATGTC  
 CCCCTCGCTTGTTCACCAAAATTTCTGCTATCACTCACTCCATATGTTGAATATTTTGAAGAAACAACTACTAATC  
 GTATATCTTAGTACCAGGTATTCTTATTGTGTTAAAGTGTGTTAAACAACCTTCAATACAAAGTATTTCGGAATACAA  
 ATTTAATGCNAAGCTCTCACAACTTCATCAAGATTAACATTTTGTGCTCATAACTCCATTGAATTTTGTATCTA  
 CTACAACTCTCAAGGTACAGTAATGGAATTCGCCAATAATTTTGGAACTTCAAAATTTCTCATCAAAACCCACA  
 TGTAGGAACAGGTGAGCTTAGAATATTTGGTATGCATTTAATGAAACCAAGGACCCCGAGAAATTCAGGCGGT  
 ATGGCTACCCAAATTTAAGCAATTTCTCTTTTGGGCACTGCTCATGGCTTTTGTACTCAATTTGTAGGTGATGGTAT  
 TTTTACATTTGGACGGTGTGGCTGGAAACAATGATGATCTATGTTGAGACCACAATTTGCTAGAGACCAATTCGC  
 CATCTCAAAATCTTGGAAACCAATATGCAAGTGTTTTCAAAACAAATGAGAAAGAACAGGGGGAACAAATTTGA  
 CATCCAGGAGTTATTTTATGATTGACAACTGATCTCTCTACACAACTTTTCTTTGGTAGTTCACTTGAGTCTTT  
 GACAGATGAACCACTCCGCATCTCACCTAGTGTGAAGATCTTGCTGGCCGAGATGAATTTCTCTGATGCATTTAA  
 TTATTCACAAACATCAATGCCCTACAGATTTTGTGCAACAAATTTTATTGGTTGTGCAATGGGACTAAGTTTAC  
 AAGTCAATTTGCTGCTGTGCAAGTTTCTGATTTTATGTTCAAAAGGCTTTTCACTTTAAGCCAAAGATGAAT  
 AGATGAACCAAAAGGGTATCTTTTCTTGTATGACTTACCCAAACAAACCCGTGATCCAAAAGTGTAAAGAGATCA  
 GTTATTCAACATTTAGTGGCTGGAAGAGACACAACCTGCTGGTTTGTGTCATTTGTGTTTGTGAATTTGGCCAG  
 AATCCCAAGATATATGCCAAGTTGAAAGAAAGAAATCTACAAATAGTTCCGGTCCCGGAGGATCCTCGTATTGA  
 TGAAATCACATTTGAGTCTTTAAACAAAGTGAATACCTGAAAGCTGTATCAACGAGAGTTTGAGATTGTACCC  
 ATCAGTGCACACAAATTTTGAAGTGTACTAGAAATACCACTTTACCAAGAGGTGGTGGTCCAGACGGTATGTC  
 ACCATAGATTGTTTAAAGGGCTCAATCACTTATGTACACAGTTTGGTAACACACAGAGATACCAAACTTTATGG  
 AGTGACCTTAACGAATTTAGACAGAAAGATGGTTTGAACAGAACTAGAAATTTGGGATGGGCTTATGTCCCA  
 TTCAACGGTCTCCAAAGAAATTTGTTAGGTCAACAGTTTGGCTTGGTGAAGTCTTCACTGAGTGAAGTCTTCACTGTTAGATCA  
 CTTCAAGAGTTTGTAGCATTTGACTATGGATCCAGAACTCGCTACCCCTCAAAATTAATGAATAGTTTGAATCTT  
 TCCCTCTTAGATGGGCAAAATGTTGAATGTATTAAAGCCAGTAGTATTATGATGTATAAACCATTCGAAATAA  
 AAAAAAATGTCCGCTTTTACTTGAAGTCTGCAATGTGTGCAAGCAAAAAAAGAAAAATTTGTAAACATTTT  
 CTTTCAACTCATUCCGTATCTCTTTAETTACATCCCACTCAACCAACGACAAACGAACAGAAATGAGTGCATATCT  
 AATTGGTCCGCTGGATGTGTTTGGCGATTTTATATACAGCTTCACTTTGAGTCCAAATAGATTTGGATACAACT  
 CACTTCCAGCAGCATCAAGAAATGATCTTGCAAATGTTTATGATTACACCACTCCCTCTGTGATCAACTCAGTAGCAAA  
 CTTGGAGACGCATCAAAACCAGTGGCGTTGCCAGTGGAGATGAGGTGAATTTCAATCAAGCATCAATTCAAAT



184/251

ACTGGAGTTTATCAAAATGAATCGGATTTAGATGAACCTAAATACAGCAGAGTTGTTATATAACGCAAGTGACTTG  
AGCTACAAGAAGGGAAAGCTGCATTGGCGATAGTGTCTGATTTGGCTTATTAATTAAAGAGCTCATTTATATACTAAAC  
ATTGTTGGATACTTATGTTTGCATAAAGCTTTAGATATCATCACTAACAAACCAAGTGTGTTTGTACAAATCTT  
TTGAAAAGTTTCAGCAAGATTTATACCTTTGAGTGGTAAATTAATGACATGATTGACAAACCAAAAGTTACCGGC  
GACATCAACAATCTTGCAATTTACCAATTGTATCAATTTATCCAGAAGTCACTTCTTTAATGCCACACGAGTTATTG  
GGACAAGTCTGATTTGGATTAGCGGATAAATTATTATGAGAGTTATGGCACACTAAACAACATAAATCCTTACTG  
GATTTATACTGAAAATATCAGCGATGAGATGTTTTTGTATCCATTTTACCACCTCACTTTTACAATTGTTT  
AAGAAATTTACTTTCAACTAGGTGAGGAATCTTTAGTCGATCAGTTTITACAAGACTATAACCTCTTCCATACTAAAA  
GATTTATGAAGCCAAACAATTTTCCAAAAGTGAAGATTTGACTTGTICAAAATCAAAATTTGCTGGCTTTTGAATA  
GTCACAAGCTTTATTTTCTAACTGAGTTTATTCATGGTGCAAGCAGCTGTCAAGTAGAACCAGCAAAATACGAT  
TTCAAAGATGATATATTAAGTATATCGAATTCTTGATAGGTTATCGAGTTATCGAACCATTATTATCGTACGT  
TCTCAAACCCGCAATGCAAAACTCAGCAAGGTGACGACCTGGTCAACATGTACCATTTTCAAGAGCATTTGCTTCAA  
AAGAATTTCCACAGGACTTACACCAGCAAAATTTCAATTATCTGGCAATCAAGAATTGTTGAATGCAGTTAGACCC  
GGATATCAAAAATGTATCCAAATTTGATTGACATTTCTTTTGAAGCTTAGATCCATCGCTTAATGAGACGTTGGTT  
TCACCTTTTTCAGAGCTTTTTCAGTGTGTTTATATCTAATGCGGCAGTTGTTACGACCTCTTTAAGGGACTCA  
GAGGAAGATTTTGTTTTATCTGCTGTTCAATGAAAGTGACGAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
GATTTCTGACUCCAAAAACCAAGAAAACTCAACTGCTTAGACCTTACAAAGATTCCCCAGCCCGCTGAATTA  
GAAAGGTTCTACTTTGGCTTTCCGCTACACCTACAACAATAGACCTGAATTTGCTGCGTTATTTTGGGGGAACGAC  
CAGGTAACCTCATGACCTTATAGGATTTATTTCTTGGGACTTGTCTAATAATACGCTCTCCGTTGATCACTGCAACA  
TTCTGCTTACTATTAGGGTCTTTGGCACTCTGCTGGTGCAAGGCAACTTCAAGGATATGGGAGATCTTGTATACAC  
AACATCAACAACGCAAGTACGAGAAAAAATGATTTTCTCAAGATATCTTTGACTCTCTTTATGATTCTTGAAA  
TATTACATTTGACTCTTTAAATGAAAGCTTTGAACAAGATTTAAATGCCCCAATTGATGTTGAATCAGAAGAAACAA  
GATTTTCTCTTCAGCACCACAACAAGCAACAGGACCTTGATGATTTCTGGCAGAAATAGAATTTGTTATAGAGTTG  
GCCGAGGATTCACCTTGTCTTCATTTCAAGGGTTTATTCAATTACTTTCTGCAATTTGTGAAGAAATTTGAACACTAAG  
AATGAAAGAGCAAGAAATCAAAATCCGTGGTATACACTAGATTTCTCAACCAATCATTAAGGGGTTTTTAAATTC  
GATAATTTGATCAATGTTAGCAGGTTCTTCAAGTTGATGCTAGCATTUAAAGUACAACAACCCCAAAATTTATTT  
GATTTGGCAAATGTTTTCTGTCAGTATGACTCGAGAAATATATATGACGAACCTCATTTCACTTTTATAGGCGAT  
TTTTGTTACCAACCATAGTCTGATCCGTATAATTACATAICAGATTTCCGCTTTACTCGATCGATCCATCTACCAGGG  
TTGCATAGTTTGGCAGAGATAAGAAAGATGATGCTTTTACACATATTAAGAGAAAGTATATCAGTAAGAAAAAT  
GTCCCCATCAATCAAGCATTTTCAACCAACCTAACTCATTTAGTACAGTTGGGAATTTCACTGTCTTGGTGAAA  
AAATTTGTTAAACCCATACCGCAGATAGTAATGAAGCATTCACCAAGTACTCGTTGTTGTATCTCTTGTGATTTAGGA  
TCAGGGTATAGATTCAACCAACCACTTTGGAATTTGGCCATCATTTGAATTTTAAATGCAAAATGTGTTTGCACAC  
TCTGCTACTATTGCTAATTAACGAGATAGGGTCAACTTGCACCTTAATTTGCTAGAAATTTAGCACTTATTA  
CAGCAACTTCGACTGCCAAGCTTTCTTATTGATCTGGCACCAGAAATTTATCTGTGACTTGAAAAATTTTAAATGCGATA  
TTTGACTCGCTTATTCTTGGTGTTCATTTGGACTTTGAAGCTTTGTCAAAATGTCATCATTCAGTTGCTGTGAT  
AACTATCTATTGAAACAAGACATTTCTGCTTTGTTTAAAGCTTGTAAATTTGGATTTGATTTCTGTGAATGAA  
CCAGCTGAATCGGCTGCATTAOTCTCACATCCCTCTGGCTCATTAATTTCTTTGTTGACACTTCAAAATCTTTT  
ATAACAAGTTGTTACCAATATTGGGAACCAAGATACGACAGCAACCAATTACATTTGTTGGGACAGGCTATGGGAT  
CGTACTTCTATGAGCTTTTCGTTAGCAACCCCTAGAACCAATTTTGAATGATATATATCATCCAAAGAACTTGGGA  
ACACATGGTGTGCTGATTTCTACGAAGTGATATTTGCTCACTTATCTGCAAGTTGTTGCTCAATTTGCTTATGCT  
AGTTTGTGAAGAAATACTATTTTCAACAAGCAATTTTCAATATTTGAAGAGATTAAGCCCAATGAAATTTTGTATTACC  
AGAGTTTCAAGCTTCTGCTGATCCCTTACTCAACAACGATAGATTGATTACCAATTTGAAACAATGACAGAGTCA  
ATAAAAATCAAGTTTGGCTTTCAATTGACAACTTTGAAGAACTCGAGGACTCTTTGAATATGAATATGAGATATG  
GATTTTGTGTTTGGGCAATCTCAATCAATTTGATGGCAAGTGGCTACTACTGCCCACTTTTGTGTTGGGATACAAA  
GTGAAAGGGGATACATTAGACTTTGGTACAGACAAACGATCAAAACACATTACTAAAATCTTTCTTAAATACATTG  
AGCATTTAGCTTTGATTTAAATTTCTGAAATTTGATTACAATTAATGGTAATAACCATATTTATTTGATGCTTTGGTCCAGCT  
AAGCTTTCTGCTGCTGATTTTACAGATTTCTTCAAGCTTGTGCCAAGATCCAAATTCCTGCTCAATCAACATTTGAAT  
CAATTACCTGAATATGAAGAATTTGTTGAAAAATTTGTTTAACTGTCAACCTAAACTTGATTTGAATACCGTTTGG  
TCTGGTAACCACTTTGATGGGGATTTGCAGATTTGATGCTAGCAATGTATTTGTTGACAACCAAGCAAGCACCAC  
GCTTTCTTTTCTTTATTAACCAAGAGAACTTAAATTTTGCAGTATTTGTCATTTGGAATTTCCATAGTGTCBAATCA  
AGAACTAAGCGGGAGTATTTCTAAAGTGTGACCAACGACAAAGGAATTTGTTAATCGTACACCTAAGGTTGTTG  
ACATTTTAAACATTTCTAAATTAATTCATTCAGAACTTTGAAGTGCAGAAATACGAATTTGGCTTGACCAAAATTT  
AACATGCTGCTTTGATTTGAGCAAGTAAACGCTCAAAAGAAATGGTACATTTGATTTTCTGTTTAAACAAAGCTT  
TTCCGCTCTTTTGTGCCAAACGCTCAAACTTAATAACACCCGAGTCAAAAGCAATTTGTTGCCGAAGAAATTAAGTT  
CAAGGAAGTAAGATTTCTGACTTTGTCACAACTACCTCTGCTGCCACCCACTTCAAGCATCTGCACTTGAATGCT  
TTACATTTCAATGCTCAATTCAGAGATTTTGGTTACTCAAGTGGAAATCAATTCGCTCAATTTCTGATCTTGGAA  
GTGTTGCAAGTTATTAATTTCCAAAATCAATGACTATTTTGTATGCTGGACATACTGTTTCTGAAGAAATGTTTCA  
TTATGTTGTTTATTTGTTGAATTTTATGATCAGCTGACTTTTGGGACAGAAAGGTTGAAGATTTTGCATTTGGA  
ATTGAGAGATTAATGCTTCTTATTTCAAGCTTGTATTTGACAGTATTTTAACTCAACCCCAAGCTTACGCT  
TCAGACTTGTATGTTAGTTGGCAACAAGTTTTTGTGTTAAATGTTTGTGAGAGAGTCTGTTTGAACCAAGTGATG

CATATCATCAAGTCGGTAGATAAAAAAGTTTTCACGGTGTATTGTAATGACGCTATCTACTCAAGGGGTCCATCT  
 AGAATCACTTCTACTTTATTCCCTCAGTCATTAGTTTACCTTAGGGACTTTGGTCAAGGTGATTTTATTTTGAAT  
 CCCTTGATCAAAAAAATACGCATTGCTGTTGCTAGTCAGGTCACTTAAGCGGACTGATGCCATGATCAAAATGTC  
 CAGGAAAAAAATTCAGGAGTGACTTTAGATCAATTCATATTGACTTCNTGGCATTCAAGCAACGCTATATTTT  
 TTTGTTAGAGTGGCCAAATCGA/AAAACGGGGCATTGCAGTTGATTCAAAATGAATTGTTTTCAATTTTGCATCAG  
 TCGAAGTTTTCAGATTGATCCAGATATTGGTTAAGTTTACGAATTGAAGAGTTCAAGATCCACAAGACTGTC  
 AMTGTAATAGTTTGTAGATACTCCACTTTCCGATAAAGTACTGCTTGGTGGATCCATACAAGTTTGGCAAGTGGTAAAC  
 ACTATATCATATTTTGAAGTCCCTTGTACCAATATTTAGCTACTTTACAACAGTGTATTGTCAATGGGACCAAAAT  
 TATCAACCTGCCAATTATTTCAAACTAGACAACCTTATGAAGAGTGTAAATCGATTGGTGGTAGGTGTTTATGAAAAA  
 GATTTCCTTGGTAGAGACCAACAAATTCCTCAACGCTTCTACAAAGAGAGAGTCAAGAGTTGGTATCGTTGAAA  
 GAATTTGGTGAAGTTGTTTATTTTGAATTGATTCAATTAGCTCAATTATCTGCTAGTTTCTGGTAGTGACACGACCA  
 ATATATTTTGTCTTGGAAAAAAATATTTTCGCTTCTCCGAAGATTACAGCAAAACCATATCCATTAACCAAC  
 AAGTATGGCCGACAAATACAGAATTTGAAAAGACAGATCCATCAAGTTTTCAGTGGGAATTAAGGGTCTTCTGT  
 GACTGTAAAGTTACACAATGGTGTGTAATATAAGGAATTTGCAGACAATTGATGGGTATTGAATGTGGTACT  
 AGATGAAGGTAAAGAACTGTCAATGGCAAGTGTACTAAAAAATATGGAGATGTGTTTATAGAGGGAATAATGG  
 TATGTATAAGGAAACTATTTGGATATAAAAGCGTTTACTAACATTTCTGTTTCTAGTGTATATATAAGTGA  
 GCTTGAAGTAGGTTGTATAATTAAGTATTTAGTGTATGTCAAATGCTAAATCTCTGACGAATGAGCGCAGAT  
 TGGACGAATCATATGTCTGCTGTAGTCCGTGCGAAAAACTTTTCTGTTTCAACCCACACAACAAACAAACCA  
 AAAAAAGTAAGAAAAAATCTATCAATCAAAAAAGTATTTTCACTTTCCCTACAAACCAACAGTAAGTATTTCCAA  
 AGATGTCACTGCTGATTAGAAGACAATTGTCCACTTTGATTCTCTCCAAAGATGGCATTCAGCAAAAGTATGTAGG  
 ACTGCTAGAAGGTGTTGAATTAGGATTTGATTACTAACCTTATCACTTGTGAACCTTGGAGCTTGAACCTTGAACCT  
 CAAAAGAAATGGCTGAAGTTGTCAAGTTCTACAAAGTATACCAAGGACCAAGCTCCAGCTGCAAAAGAAATTCAA  
 CAATCCATTTCGCCAGATACAGAGCTGCTTACTTTGATGGCGATAATGCTTCGCTAAACCATTAGTCCACTTGGC  
 CATTTGCCGTGTATCTTTTGGTACTCTTGGAAATACCAACACTTGAACATGCTCAACATGAAGGTCATTAGCTT  
 AATGTTCAATAGATTAAAAAGAAATGTATAAAAAATTTGAAGTATATTTAGTCTTGTGTGGGCGAAGGGTACACCA  
 CATTGTAGTGGGAGATAGTTCTGTGTAGACCAAGAAATGGAACCGCATACGACAGAACAGAAAAACAATGATCGAC  
 CACACCCCTCCCAATCAACACACAGAGGCCAAGTAGGCGCTTCTTATAAAGAAATGTAGTCTTCTTAAGTGTAGT  
 TGTAGACAGTATTCTATAAACCGAGTGGGAGCAATCTG/AACTTCCAGTGTACTCTCTCTGACAGCAAGAGAGAC  
 CCCTTAAACAAAAAAGTATCTTACCAAGCTGGCTTGGTCAAGACTCATTTGGGGAAGAAAAAATATCCA  
 ACATTTTTTTTTTCCAAATTAGACGACAACAACACAGGTAATTGATAACATTTATCATCAATCATCGAAGGCTTACG  
 TTATAGTTGCTTTGATTGGGTCTGATTTTTTTTTTTTTTTTCTTAATCCACCTAAAAACAAAGAGCTTAAACGCACTCA  
 CTAAACGAATAAAGTANTCTTGGACATTTCCATTTATAATCAATTATGAACAAATCAAGACCCAGATTCCACAATAC  
 CATTAATAAAAGCTGTATCCACCAAAATCTACCATCAATTTCCACCTCCACCGCAACAACTTTGAGTCCAAACCTT  
 CCAACACCAAGAAATGTTACGTAGTATAAGTGGCAGCTAAAGTCTAAACACGAACCTTGGCTCACTCTCAACAGGGT  
 CAGGAATCGAACAAATCAAAACAAAAAATAGCAATTTCCCTCACTATGTACCTGATACATACAGACAACCCCA  
 CCAGAAATCACTCAAAATCAAAATATTCAGGCTCCAAACAGCTGTTCATGGGAATCAGCAAAAGGACTGTTGTTGCCA  
 CCACCATCTATTTCCGAATCCAAACACTATGAACCTTCCGCCAACACCACTCCAGCTCCACCAACCACTTGCAAA  
 CAAAAACCACTGCCAGCACTTAAACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 AGAAATCTATTGGTGATTGGAATTTCTGTAAGACTATCGGTGCTGGGTCAATGGGTAAAGTGAAGTTGGCACA  
 CATAATGCCACACATGAATTTTGTGCGTTAAATTTATCTAGGGCAGCTAAACCTTATCAAGAGACACATCTCC  
 AACGACCTTCTCCGCAACCAACCAAGAGCAGCTCAGAGACATAAAAGTTTGAAGAAAGTCTGCGAGAGAC  
 ACAAGAACTATAGGTGAAGGGCCATTCGGGAGATTATTGTATCATCTTTTCAATTTGTCTTTTGTATGAGATGGTA  
 CCTATGACAAACCATTATTATATGTTATTTGAGTATATTGAAGCAACCAAAATCTTAGATTATATTGTTGCTCAT  
 GGATCTTAAAGAAACGACAGCTAGGAATTTCCAGGGGCAATTCATCAGCTTTAGATTATTGTATCGAAGC  
 AATGTTGTTATCGTGATTGAAAATTTGAAACATTATCAT/AAACGAAAAAGGTGACATAAAGACTATTGATTTT  
 CCCTTCTCTAATTTCTATGCCACCAAAACCTTGTAAARACCTATTGTGGTCTGTTATATTTTGTGCTGCACAGAA  
 CTATTGAGCGCAAGCCGTATATTGGGCCAGAGTTGATGTGTGCTTTTTGGGGTGTGCTTTACGTTTGTGTG  
 TGTGGAAAAGTACCTTTTGACGATCAGTGGTTTTCGGTTTACATCAAAAGATTAAAAAGGGATGTTGAGTAT  
 CTTGCTTTTTCTTTCCAGAGAATGTGTGCTATTGCTTTCAAGAAATTTGGTTGTTGACCCCACTAAGACACCATCT  
 TTGTACGAAGTTTGTCTGCATCCATGGATGAACAAAGGATATGATTATAAGGTGAACAATTATCTTCTCTAGAGA  
 GAACCTTTTGTGCTTACCTTAGATCTTGAATTAATCAAAACCATTTGCAATTTTGAAGCTAGGCACGGTGAAGGT  
 GTCGCTGATGAGTTGACGAGTATTTTACGAGTGTGAAATCAAAATGAGTTTGTGAAAACCTGGTACAAAATTTACT  
 GAAACACGAAGAGATATGCGTCTTCTCAGAAATGCACAAATATTACCTGATCCAACTGGCGGGTTCACCTCTTGT  
 GTATCTATTTACTATTTGGTTGACGAATTCAGAAAGACCAAAAGGCAAGGAAGAGGCAATTAAAGGCTCAAGCA  
 CGTGCTCAAGTTCCGACAATCGCTGTTTCTTACACCAAAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 CAACCAACCAACCAACCAAGAGTATCTCAGGCCATTTCCAGAAACCAACCTGTACCCCTGAGGAGATAATCAAC  
 CCTGCAAGTGGCAACCAAGGCAAGCTAACATGACAGCAACCAAAATTTGTGGAACATTTTCAGAGACCCCTCA  
 AGAACATTGGACCCATCCAAAGCAATCAGTGGATGAAAAACCAAGTGCACCAAGTTCCATCTATTTGCTGTTCCAGAA  
 CAGACACACCAACATCTGCTCCATCAGCTTGTGTTAAACACACACATGATGATGAAGATCAACTTTCCAT  
 CCTGAACAACAAAGTCCAAAGAACCTCTACCCCAACAACTTTGGATCTGTCAAAGGTGGTTGGCGGCTCATCTGGA

186/251

TCTGCTATATCAGCCCTAATGCTGGTAGTGGTGCTGGCTTCAAATTCCTTTGTTAAGAAGATTGCTCTCGAAAAA  
 TACAAGGGGGCCAGTTCTCTTAAACCTTCAACATCTCCACTGTCAAAATGTTGAAGGGCTCTCGCCACACCAACT  
 AAGGCCGACCCCAATGCTACGCTGCTGTTAGTATGAAGGTTACTGCTAAAGAGAAACAAACGAATACAAAGACCA  
 CCAAAGTCAGAGTTAATCAAAAAGAAACGCCACATGGTCTGTTCTTCTCCACTTCAAACAAAATGCAAGGATCC  
 ATTCTCTGTTGAGTATTGECACCATTAACCAACCATTTGATACCAATACCAACACGATTGTTTTCAGACGGTGCTAAA  
 CAACAAAATTTGACTGTGCTTCTACAGCACGTCATATGCAACCTACAGCCAGAGCAAAATCTGTTGGTGGTGGT  
 CATATGCGGTAAAGATTGCTATGACGCGGTATCACACGGACTGCAAGATCCGTTCGCCACCCCTTCCAACTCTATG  
 GCAAGCCAGAATAGCCAAGAAGTTGTTGGGAAAGATACAAGCGAAGGCTTTTTCATGACGTTCAATTGGATGAT  
 CTTCATATACAGAAGTTCCACAACCTCACTGAATCGGAGATCATTTGAACACTATAATATTTCCAAACCTAATPGC  
 ATGCCATCAATTGACGATTCTAAGACATTGTTTTCAAAAGGTTTTCAGTGTTCAAAACACATCAGCCAAAGCCG  
 TTGCTGTATTAGGTATAATATAATTAACGTGTTGAGTAAGTTGGGAGTTAAATTCAGGAAGTGAAAGGTGGA  
 TTTGATGATCAACACACGCTTCGGTACAGCTTAGTCACAGTAACGAACCTTGATGAGGAGAATAAATCTGATGGC  
 GATGCTTCAAGTCAAAATCGAGTGAATTCATTTGAAGTGAACCGAAGGAATCAAAACACCTAGTGCACAA  
 CCTTCACTTCACTGCTGCTCTCATACCCCAACGCCCATCGGCTCCTAAATCACACAAATCAAGTAATCTATTT  
 GCAAGCATTCCTCGAAATGTCGCCAAGACGTAAGTTTTCCATTTGGTAATGCGTTTCAATACTTACCGTAAAAAGAT  
 GGATCTCAAGTTATGATGCCACCAATACACCAGCTACAGCTAAAGTGATTTCATGGGTTGATGACGACGACGAT  
 AAGCAGAGAAATGGTGAAGACGACGATGACGAAGATGACTATGGATATGATGACTCTGCTGATTGCGCTCAATGGA  
 TATGCTGGTGGTATGATGATGTTGATTTCTTCGCGTATTGAGCAACGTGCCAAACATCAACGAACCTGTCAGTAGT  
 TCGAGTCAAGAAAGCTAGCAAGTCGCCAATTTGAAGTTTGAATTCATATTGTGAAAGTCCCATAGTGGGATTGTAT  
 GCTCTCAATTCAGAAATATTTGGTAAATACATGCAATTTATAAGACACTAGCTAGTCAGATTTTAAATGAAATG  
 AATTTATAGTTTCATTAAGTTCTATTTATTTAATCTATACGCTTCGAACCTGCTAATCTCTTCAACAAGCGCGATC  
 CTTACTTTGAAGTAATCGTAAATTTTCGATTCCCTAATTTCTGGGCCAATTGATGATCAGACTGTTGTTTCCAT  
 TGTGGAATGCTTGACTTGTCTTTCCAATAACTAATGGTAATTCGAATTTTCTTGTGGGGTTCGGCTGTTGACTCA  
 AGTCCAAGAAACCTGGTTGTGTTTGGCTAAGATACCATAGGTTCTGCCACTTGGGTATATTTCACTCACTAGTA  
 ATGCTGAGTTTAAATTCGAACCAATCATACCATATAGTATAGCCCGCTTCTTAAACTCAATTTGATAGGTGGCGA  
 GGCAGGAAAGAAAGAGAGTGTGACTAATTTGACACAAATTAAGAAATTAATTTAATCGAGAACGATAACTTCTCG  
 TTGTTCTGGTCTGGTGTGGGATTAGTTTCTGTTTCTGGGTTGACTCATTATTCATTTGCTCTCAACTTCTATTCT  
 TTGATCTCTTGACAATTTACCCGATCTATGTTTTCAGTATTTTCAATTTTCACTCTCTGTTTCAAACTCTCTTTT  
 GCGAGCATATTTGATTCT  
 ACTTCTTTTACGTAAGTGGCAATAGCTTAAACCATTTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 TATTTCTGTTGTTGAATTTGTTCAATCATGGCACTAGACTTACCTCCCAATTTTCTATATAACAACTTATGGGC  
 CAGACTCTTTTGATTTTGGTCAAAATTTCTGTTGAACCTGTAAGTGTCTCTGTATATCAATTTCAAACTTAACTC  
 TTTAATCATCAAAACTTTCTCTCAAAATAAATCTGTTGGTGAATTCAGGTGATAATTTCTCTTGGGAATGGT  
 CAAAGGATAAATAAGTTATTGTTCTGTTGATATAATCGATTATCATCAATAATGAAGAAATTTTCACTCAGTGACAA  
 TTTGATATCTGCTCAACTCTAGTTGCTAGTCTCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 GTAGTTAATTAATTAATGATACAGATGTTCAAACTTCTCTGTTGATGTTTAGAAGGTCAAAATTTTACCGAATCTTCTT  
 ATTTCTCTGTTTGGACACCAAGTGGAGAGTCACTCCCAAGTGAGAACGGAAACCAAACTCAAAATCTTCTAATCT  
 AACATGTTTCAAGTTCTTGAACAGAGCTGATTAATTTCAATTTTAAATTTATTTGATGAATGAATGATGAATGGA  
 TGGCTCAAAAGCCCAATAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTT  
 TCGGTAATTTGAGAGGAGTTGATAACCAACACCTATTTCTCTCTGTTTCTTACCGCAACTAATCTGTTGTTG  
 AATCTCAATTTCTCTCTGTTTGGTTAGTAAGATTATAGGTGTTTGTGTTGGACAAGGATGCTATTTGGTCTTGAT  
 ACCAATATTTACCGAATGAGATAGGATGACTAGCACTATTTGGCACTGGTGTGATGAGTGGCTTCGGGATACCAT  
 GGTGTTTGTCTCAAGAGAGCTTGAAGCAAAATCTGTTGAAGAAATTTATTAGTATATACAGATTGCTGCTGAGAAAT  
 GGTCTTAGTACAGATTGGTATTATTTGCAACCAAGGAGACCGGTACCAGAAGTTTTCATTTGAAGCATAGTTTCTA  
 AATTTCTCTCTGTTATATTTATGCAAGCTATAGTCTCTTAACTCTTTTGTATATGTTGATATCAATACTCG  
 CAAAGAGATTCTTGGCATAAACAAGCGCTGGATAAATCAACAGTCTTTTGAACCAATAAATAATCTCTCTCTCTC  
 AGTGAAATGGACAGAGCGCAAAATTAAGCTAAGCAAGACATGAAGCTTGTATTATTTCACTCATGCTTACA  
 ATGCTTGAATTAACAGAAATGACTTGTAGCTGACTGTCAAACTACATTTAGAACCAGACTTTCTCTAGCTGATAGA  
 AAPAGATCAACCAACAAAGTCTTAAACAGCGAATCTTGAATTTCTGTCATGGATCTTAGTATGAGACTCCCGCT  
 AACCAATAGATGTAATAAATCTGATATCTTGTTCGGGGCTGTTGCTAACAAATCTTATCTTATCACTTACTTGT  
 TCTTGTATTTACCAACAACATCTAAAAAAGCCCTTGTATTAGATTCATCAAGAGAGAAATCTTATGCACTAATCA  
 CGAATTTGACGAACCCGCAATATGCTTTATTAAGAAATGTTTCAGATAAATAATAATCTTGTGCTCAAACTG  
 AATCGGAAAAACCATGTTTTACGTCATTTACGTCATTTATGTTACTTTGCTANTATTTGCTTTAGACCAAGACCA  
 GAAGTGAGAAAAATGAAGGGGGGAAATCTTGAUAGGGGCGAGTAAAAAGGCGGAGCGGGCGGTGGCAAA  
 AAAAAATTACAACCAAGCAACACATTTTAGTGGATGCGTAAATAGTATCAAAATGTTTCAATTTGCTGCTGCTG  
 TGTGAGGCCCAAAATCAACCAATTCATTTCAACAGCAATCACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT  
 AGGCCATTAAATGAGGGGGGAGAGGACATAGGAGATCAATTTGTCATTAATTAAGAGTGAATCTAAATTTGA  
 AAGGCCCTCTAGAACACAGACCTGTTGAATTTCAATTTAAATTTGATCAAAATTTTATGTTGATTTGATATTT  
 TACAGTATGAGAGAGCACTGATAACCATAGATAGTATGTTGATTAATATCTCTGATTTACAGTTTAACTAT  
 CUGTAGTTGCTCAATTCAGAGTCTCTTTCAGATATCUGAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT

YLR377W\_homolog\_1 80aa PathoSeq: 1..80 (SEQ ID NO 642)  
NLGSNPNNAKRMAEVVKFYNKLPLQGPAPAAKKSNNPFARYNAAYFDGDNASGKPLVHLAIAVVFQYSLEYQHLLKH  
ACHEGG

[illegible]

188/251

GGGGTCGGTATCAGAATGGTAAATTTCCGATGATAACGCTCTCTACCTCGTCARATTTGTAATCGGTTTCAAGAGG  
AGTAATTACCTCCCTTAATTGAATGCGGTCAACGGCTTTGGGTGTATTGCTCAATCAAACCTCTGTAGTCTCAACTC  
GTTTGCCCTCTTCAATATCAGCACAGCAATTTTCGTCAAATTCGGATATTCGAACACCACCGACTTTCCAATAAT  
ATAGGACTTTGATTTCTGTCTAACGACAAATAAGCGTCGCTGTATTTCAACTCAAAGCACTCTGTGTGATACA  
ACCACTGTTTCCCCAGCAAGTCGCCCACTTGACAGTAGGCAATCGTTTTTTTGTTCATCGCAAACTTGGACTAGCATT  
ATAAGGATTAATAATGCAACCCCACTGCTTCGCAATTCGCGTTTCCCTGGAACAGACCCTTCATGTATATGGTAGAA  
AAATGGTCTTTCATCTTTGGGCAACCCCTGTCTATCAATATGAGACGTGACATGTTTACCTTTCTTAGCACTAAA  
CACCACTGTTTCTTTGACCTGTGTATCACCTCCAAAGGGAAAGTCTGCAACAGCAACGACGTTTCTAGGGTTTTT  
CTTGATTTTAGGTGACTTGTCTGAAGCAGCTATTGAAACTAGATAGATTAAATATGATAATGGGAATTAAGATCAT  
CTTGCTCAGACGTTTATGTATAATCTTACAAAATATGAAGATCAAGATTATATGACGATTTTAAAGAGANT  
TTTAACCTTAGACTGTATTAATTAGGTAAAGAATAACTTTGGTTCTGTGTGTCTGTGTTTGTGATGAAAGCTGCAAA  
AAAAAGAAATACAGCATTTTACAGCATAACCAATAACTATAGTCTGCTATTGTGTAAATTTGGTTAATTTCTGT  
ACAAAAATTTGAACATAAAATTTATCTCAGACAGCTTCCATTCATTCGACATGACTAATCCCTGACAGGAACCTTA  
TGGAACGATGACACACGAAATTTGTGGGCGAGACACACACCGCAAAAAAAGAAACATGACCTTTCTGCGUCAA  
CAATTTCCCCACACTTACTCACACGAGCCACACAATGAGTAATCCCAATCTTAGAAGAAGCCACACCTGCT  
AGGACAGCTCTAGTCCACCCTACCAAGCCATCTAAATCCATCGSATTAATTTATCTCTGACGAGATAGACTTTT  
TTTGTGGAAGCAACAGATGCTCCTCCTTGGGGTTGTAAATTTTCTTTAGGTCACACCTACACATACATATCTCAC  
CCCATACAAAAATCCCAATTAGGTAGTATGTTTCAACCCCCCTTATTTTTCAGGTATAAATATGTCCATA  
AATCCCGAATAATGAATAAATTTGTTTCTTCTTTCTCTCTCATATTAATTAATTAATAAATAATTTACTTTA  
ACTTTTATTACATCATGACTAGAACATAACAAATGGACTGTACATGAAAGAGACCTCAAGAACCACCAATGGTTTAC  
ACACAATGGCCACTCCGATACCGATCCAAACCAAGTAAAGAAGCAATGGTGTCTGTTAGAACAACTTGGGGTCAACC  
AGGTGATGAATTAGATGACAATGAGGTTCGTCAATACCAAAAGTCTTCAGGTAGAAGAACTCCAACCCAGCAAT  
GAATCAGGAGAGATTAACCAACTTGAATGACAATTAGATAACCAATTGATGAATAGAGAATCGCGTTTGTAT  
TTATATATTACGTAATTAACGAATTTACGCTGACGATATATCTTCTCATTTGTTGTGACTGTTTCGGATTTGTGAAT  
TTCTTTTCAATCTCTGCTTTCCAAACCCCTTCTTTTPTGCTTTCTTTCATAAGCCCTGCTTGTTCGCCAACACCTG  
TTGCAAAATAAATCAGTATTCATGTCTCTCATACCTTATGTTTACCTATTGTCTCTGTAACAGACAGNATCCATTTTA  
TCATAAAGCCCTTTATCTATCTCAGTTGGAACCTGTTACACTTTAAACAACCTTAGACTTTGCCCAATTTGCTAANC  
AACTCTGGTGTGGGACATATGGTGGCCCTAATATTATTTCCATCAACATATCTGCATTGCAAAACACATAACGAT  
CTTTCCAAAAGATTCATTATTGGGTAGTTTAGCCCTTGTATTGATTGACCTCAGCATCATATGAAGACCAACCA  
ACAACTTTGGGCTCTTAACCTTTGTGGCTCTTTGTTTACAAATTTTGAATATTTGATATGTCCTGGGTGGAACAAA  
TCAAAGCCACCGCTCAATGTAGACAATATCCCAATCTTCAGCTTTAGGACTAATATCTCTTCCAAATTCGCCACGA  
TTCAATAAACAACAGATCTCTGGATTCAACCCAGCTCTCGTGGTGGCGTATCGTTTAAATCTATCCAAATTTGTCT  
TTGGTCAACAAGCTTTCCGGTAGTTCTCAGAAATTCGTTGATAGTGATGCTTTTGGACATTAACAACATTTGCCCA  
ACCAATTCAGTAATTCGAATTTTCCGASTACGTTTAAACAACAACCAATTCGCCCAATTCCTTGACTACCTGATAA  
CAGTCTCTCACCCTTGGCATCAGTTGTTATATCTGCTCCATGAACACATATGGACACCCATATTCATCCATTAAT  
TTGGGATCAGTAACATATGGTGGCTTGGCAATTCGCTTTTGTGGTCCATTACATGCTTCAACAGGCACTAATTTCT  
TCATCCAAATTTAATAACTGTGGGGACCTTATTTAGCAAAATTTCTTCTGTCAGGTGTACACCAACATACAACTCC  
TTACCCCAATTTGACGTGCTTTTAACATTTGCCCTTCCCTTGGGCTTATCATATGTTTAGTACTTCAATTTTCAGCACT  
GTTCACAAATCAAAAAACAATCCATGGGTGAGCAAAATCAAGACCCCATCAATCCAGATTTGACAAATTTTCAAT  
CTTCTTGGCTTTTCTGATATTATTGTAGAGCTTGATTTGAAGAAATGTGATATGGAACAAGGAAAAAAG  
TTGCAAGAGGATCAATATTATTTGTTTGTCTTGATGTTCCGACACCTCGTGTACATTACATAATCTTACATAAA  
CCCAGATCTTGTGTGGCCACCCATTAATGAATTTGTGTAGTTGGCTTTTCTTAAATAGTCCAGTGGACTTGAC  
TGTTTGTGGGCGAGACCCCTGTACTGAACCTGCCAGCGTTTGGCTGACCTTCATAAGTTTCTGTCTGTCTGTCTG  
GCTTACGTAACCTCACACCCCTGGCCCGACACCTTATGTTTAAAGCAATTTCTCTAAATTAATATAAATCATTCCTC  
ATTTCTCTCTGCAACAGCATGTAGCCAAACAAAAAATCGCCCAATCAGCGAGGAAACGTAATCAATAAATCAAT  
CATTAATTTCTGTGTAGTTTGTCAATGAGCGTATTGGGCAAAATGTAAATTTTCTGTGTGTATGTTTATCACCT  
AGTATGAACCCCATACATGATAAGTGCACCCAAACCTCGAAATATCAAACTACCAAGGAGCCCAATCCCAAC  
ACAGTCTAACCCACAGCACAACTCCCTAGAAAACACTTGTCTCATGATCCATGCTTGTGATTGAATCTGTTTCCA  
TACTTGTGTGACCACTGTTTGTGTGCTAATCTTTGGGAAGACGACCTTGTTCCTGCTCTCATCTCAAAAGGGTT  
AACCTTAGCAATTCATTTCTTCCCATATTCGTTGAAATTAATCCATACAAATCAATTCAGGGATATTTCT  
CAATGATCTTGAATTTGTGACATGTTGATTAGTTTGTGATGCAAAAGGAAAGTGTATAAAAAAGAAAGAACCAAC  
TGAAATAACTTCCCGCTCAAACCTGACTTGGCTCAATTTGCTATATTCACTGGTACCATGATACCATTTAG  
TTTCTTGTGACATTAATAACAGCTCCCTTTCTTTTGTAGCTTATCTCCCTCTAAGAAACAGCTTTCCAAATA  
TGTGTTCACACTCTGTCTTATTTGGTGAATTTATAGTCACTCTTALACAGACACATTTAAATGGGATATCTCTT  
TCTCTTAACTTTCTTTTGGCCACCAATTTCCAGATCTTCTTAAATGGGATCTTTTGTCTGATCTCTGTA  
CATGAAGAACTTACACGATATCACTACCCACAGTACCCAGTTTGTGAAAACTTTACACACGCTCCGGTTGGA  
AATCCGTGATAAATGCTGCTTTGCAATTTTCTGCAAACTTTTACTTCCCTCTTTTCCAATTTCTGAGAAACAC  
CTCCACAGCAGCATCATCACTAGAAAGATTTGGACAAAGGGGTTTGTGGTGTATGATCGGGGCATCACCCCA  
TTTCTCTGATGCTGACTTCTTGGGATGAGGGGTACTTCTTTCTGTTACCTGAGTATCAGGTGCACTCTTCACT  
GGCTCTCAATTAATTAACCTATCTTTGCTTAGATACCTTGAATCTTTATGACCTCTCTCTTAAACATGGAGCT

189/251

GCATTAGTAATTGTATAAAAGATCGACTTGC TTATTTTTTTTTTTTGGGTGAAAAATCGGTCTAAATCC TTCAAC  
 ACCATTCC TTTTTTTGGCTACAAAGATCTC CGGATTTTCAACTCTTCCTTTCCTCCAAAAATGATTACAAGAC  
 TTATTGGTATAGCAAAAGTCAGGGATCTATCGCACATACCTGACCGCTTCCTTCTAIGAAITTGTTTCCCAAAACT  
 TTCCACATGGTGGCCCCCACAAGATTCTTTATGTGGAATGACAAATCTTTACGTGAGAGATATCGTTTGGTTAC  
 AGAGTGAAGCCATCCAGACATTTTCGTGAGTACTATTAATCTTCAATATAAACAGGGCCTATACAACGTTGA  
 AGAATCCATTACTCGAATTGCACATTTCCACTTGAAGCTGCCCAATCATGTAAATATCACCGACGATGCGG  
 TGGCCAAAAAATAATCAAGAATTACCAGCAAAAGTCAATGGAAGCGTCAATGAACATTAAGGAGATGCTTTATGC  
 AGGTAATGGAACCCCATGAGCAACTAGAATTAGCAGAGCTGGAAAAACGAATGGAGACCTTGGAGCCGAAAAQA  
 AAGAGCGTATAAAAACCACCGAAGAAAGGATCAACCAGTCACTAAAAAACACCCCATGAGATTGGGAAGAGTTAA  
 TGATGGATGCTATTCGGTTAAAGTATTGGGTTAATATACAAAACGGAATCAAGATTGGGAAACACCTAAACCAG  
 TCCATCTCACTCATTAATAAGCTATTATTTACCTCTTTATATTATTATATACACGAAAGATGTACACACAC  
 ACATATACGTCAATTATTTCTTTCTTTATACGTTCTTTACTCGCTGGCCACTGTTTCGATCGTCACTCTCTCTCT  
 TCCACTTCGTCTTTCTTCTGCTGCTCTCTTCCACTCTCTGCTCTCATCTAAGTAGCTAATTGGACATTATAT  
 TGCATGAGTCAATCTCTGTTTCTCATCTCTCTGCTCTTGGATGCAATTTAGCUATTCTTCTTGGACCGGTG  
 GCACCTCACTCGTTGATTTTGAACCCAAACAATTTTAGCCCAAAATCATCTGACTAAACCTTGTATTCTTTAT  
 CTACACTGGTTTCAATCTCGGAAACATCTTCACCAATATCTCCAGCAACGTCGTTCCAAAGAATGCCACATCA  
 ATATCCAAATACCTCGAAGCTGGAAGGTATATAGATATCATACAGCAAGGACAAACCAATCTCACCGTTTCTTCT  
 CCCGSCATCAGTCCGACCCACAGGAATTAATGCATACCGTCACAAAATATCTTGGACAAGAGCCAAAGTCG  
 TTCTCTCAAACTTGGATGCCATGGCAGTTAGACCTTGTTTGGAGACTAGGTATCTGGCATGGATTAAACCATAT  
 AATAATCTCGAGAAATGTGCCAATAACGCTTTGTTTGGCAATTTCTGATGCAATTCGTTTACTTGTACCATTCGGT  
 GAATCATTTCTATTGCTGGTATTGGTGGTTGTATTGTCTAGTGTATGATCTTCTGCGCTTCAACTTGGTAAATCC  
 AATATTGTGTATAATGCTTCTCTATAATAAGCTACTTCCACACACAATCCAGTTAGATTGAATCATCTTCAATA  
 AAGTCTCTGTGACATCTGTACAAAATAATCTGTACCAACAATTCACAAAAGCTGTTGTATCCAAGGTATATGCTCT  
 TCTTCTGGAATCCAGGCAATGTAGTGTATATACGGCAAGCTATGTTAATCTTAATTTTTTTTTTTTCCGTTCT  
 TTGTTTATCAATGGAGGTAAAAAAGAAACAGTGGTGGCAAAATTTGGGATAGACAAATTTGAATACACCT  
 AAATCTCTCCATTTCTATATAATATTAACACAGCCACTAGCAAAATATGGGAATGATAACACCACCTATTTGTT  
 ATTGTAAGGCTTTTCTCTTTTGATTGCTTTTGTGATGCTTAGGCAAAAGCTGACCCNAGAAATTTCTTTTCT  
 TCGCTGAGTGTATGACTGAGTGTGTGTGAAAAAGAGAGCTTTCGAAAAATAAAAAACACATACCACAGAGAC  
 GAGTTCTACCAATAATGCTTTTACCTGATTACATCCATATCTATATTATTATCAATATTTCTTGTGCTTGTAG  
 CAAAACAAATTTGGTGGCAACCAATTTGGGAAATTCACAAATCAAGAATTTGTATGCTTGTATATTTAAAGGTTTCTCT  
 CAAAC

YGR008C\_YLR327C\_homolog\_1 79aa PathoSeq: 1..79 (SEQ ID NO 644)

MIRTNKMFVHEKRPQEPKWFTHNGHSDTDPTRVKKNAGAKNNWGPQGEELDDNEVRNYQKSSGRNENHEMKQER  
 LNNL

YGR034W\_homolog\_2004bp PathoSeq: 1..2004 (SEQ ID NO 645)

CCTTTTTTTTTTTATTGTCTTTTATTATATATTCAGTCAATATAAATATCTCTGTCAATTTATTTCAGCTTTTAC  
 CACCTTTTCTTGAATCAAAAGCTTTTCTATCTTTGTCCAAATGTAATTTAGTAAACGACAACTTTAGATGGATGAA  
 TGTGTATTGGACAGAGAGCACCATTGTGATTTTCTTTTGTAAATTTATCAACTTGAATGCAAAATTTCAATCTAT  
 AAACAGAA TTAACCTTTACCTTCAGAACCTTTTTTAGAACCTTTAAACAATTAAGAACTTATCATTTTGTCTAATTC  
 GCAAAGATTTGACATTGTATGTTGTCTTAATCTTTTGGATAATGGAGCAGATAAAAGAACTCTCTTTTCAACTG  
 ATGAGCACTCAATAAGCTTTTCTACCTTTAGAACGAGATGAAGAAACGCTATATAAATGGAATTTTGTATAG  
 TATTTTACTGAATGTTTCTTACTCTTTGTCTTAATAGGAAGAGTAAAGAAAGGAATATATGGAAGGGTTAT  
 GATTTCATTGATTGATTGATTTTTCAAGTTTTCATTCAACAAGTTTGAAGAAATGGAATCTCTATACATAATTTCA  
 TCAATATCCCCAATTTGTATTTTAAATATGAAATTCAAATTAAGGATGTTCTTTATATTGAGTAAATCTGCA  
 AATCATTTATACCTTCTTGGTGTACTACTTCAGTCAATGGTTTGTCTTGGAAAAAAACCTCTTTATTGAAACTG  
 TATTAACTTAATTTCTAATCTTTCTTTGTTTGTCTATCTCTCTTTTCAATGTATATATTTCTTTTATTCTTT  
 CTTTTTTTTTTCTTTTCTTTTATCTTCTTTTCTCCATATCTAATTCAAATATCTATTTCTATACCTTGACTGAT  
 CTTGGCCATTTTGTATGATATATGCTATCTAGTATCGATCCAAAAGGAATTTTTTTTTTGAAGAAATTTGAATA  
 TCTTCAAAATGAGTAAGTGTATAGAGAGATGAATTTTTTGGCACTGTGGTCTAGTGTAGCTCCCTACTCAAAAAA  
 AAAAAATATATATATATAATGTATTTGGTAAGCAAACTGTGGTAACAAAAGTATTTTGTGATCTGATATATAC  
 AGTACATTAGGCTATAGCCCTAACACACATTTAAAAATTTGGCATTACCAATCAACATCAAAATTTCTTAAAAA  
 AATATAAAACGAATAGAAAAAAGAACTTTTGTGAGCTATACTTATTACAGTCTTCTCTATATTGGCAAAAAA  
 AAAAAAAGAGAGCCAGGAAATACCTTTATTTTCAATATATCTGTGAAGAAATTTGGTGGGTTCAAAAAATGAGG  
 CTATAATTAGCTCCCGCGGGACTCGAACCCCGACCCCTGAGCTTGGCTTGTCTATGCTATTAAATTTACACAAGACA  
 CCGGAGGGCCAAATGCTAACCAACTGCAACCGAGGAGCATATACTACGTTGTACCGTGACACGTTGCTGTCTAGA  
 GACCAATATCAAACTCTGCGCTATGTGAGTGAATCTCACTCAAAAAAATTTGACCTATTTTCCATACCAGTAA  
 GTTTTTGGGCTTATTATTTAGAAATAAACTCAATTTACTTTAAGAAATTTGATGATTATTTAGCTTTCTAATTTG  
 TTTGCTATAGCTTTTTCGTAAGCTAGTTATAGGTATTTACAGCTTTATGTCTGATATTTGTTGATGATAACTCGG

190/251

ATAGCTATCTCTAAACACTTGAACACATAAGCAGCAATTACAAAGACGTAGATTGTATGACAGTAAACCAAATCG  
 ATTGACATCTATAAATAGTAAAAAAACCTTTTCATCAATTGATGGTATCTTAGATTTTGAACCTGATTGATAGT  
 TTCTCCCCCATTTGTAAAAAATTAAATTAACC TTGGAGAAACAAGAAGAAAGAGAGGAGAAAAAATCTCATTA  
 AAGACGAAGACAAAGAGAGAAATGTGCCACCACCACCACCAAAAGAGAAATCCA

YGR034W\_homolog 120aa PathoSeq: 1..120 (SEQ ID NO 646)

VSSSRSKARRAYFTASSVERKVLSSAPLSKELRQQYNVKSLPIRQNDENVLVYRGSKKGSEGVNSVYRLKFAIQV  
 DKLQKEKSNGLSVPINLHPISKVITKLHLEKDKRKALIQKRGKRAE

YMR273C\_homolog 935bp PathoSeq: 1..935 (SEQ ID NO 647)

TCTTCTTCTTCGTCTGTCTGTCACGTTCACATCTGATCGCCATCCTCACTGCTCATATTTTGTTCCTCTAAATGTAAAT  
 GTATGATCAACTAAGTTGAGGTAGGCATACATAAAATTCGACAAACAAAACCTTGCTCTCTTAGTGAACGCTTAGGG  
 TTAGCAAGTTTCAAGTGTGACAACTCTATAAATGGCAGCTCAACATGAACCTGGAATCTTAGTCAAGCATCACT  
 AAAGTTGATTGAGATGGTGGTGGCAAGGGGAACCCAAAAGCTGAATCAGTAAACTCAATAGGCTGGTTGGCCCTT  
 CATGTACGTTTATTGATTTCTTCAACTTTTCTTGGATATCTAACTTCTCTTTATCTTTCATTCTTAGACAAAAGA  
 TCTTCCCTTGGCTTCCCTTGCACCTTCTCTCACTTCCAAAGAACCTCCTCTACTACCTCTTCTTTGTATCAGTA  
 AGTTCACTAGAAAGGTTCCTCTTTTGCATATCTGTTCCGTTTTTCTCTGCCTAATTGATTTCTTTTGGACAAATTCG  
 TCAACTTTTAGCATCCCCAAATCTTTGTTATCATTGTATTATTGAATAGGAGTTTCATCTCATCAACAATAACT  
 ATTTGTGCTCTGAATGTTACGAGATCTTACATCTTCAACCAAGTCATCAGTACCAGAACTCAAAACATCTGCTCTTC  
 TCCCCAAGAGTGAACAAAGTCGCTTTTGAGATGTTCAATGTTGAATTGATGTATCGGCGAGCAGGTTACAGGGAAC  
 TGTTCCTCCCTGTTCGTCTTGAATCTTCAACTCTTCTGCTCTTACGAGTGGCACTCACTTGTTCGCAAAATCTCTTCT  
 TCTCTGATCTGTCTGGATCTGTTTGCACATAAATTCAAAGGTGGAAGCTTTTCTTTATTCACTGAATTCCTCTGT  
 TCTGACAAATTTGGCCTTGATTTCTCTTGAATAACT

YMR273C\_homolog 198aa PathoSeq: 1..98 (SEQ ID NO 648)

IKRTSRANQPIEFPTDSAFGFPLPFPSSQSTLVMLDYRFPVIVRAIYRLSHLKLAKFKRSLRQVLLSNFMAYALN  
 LVDHTLHLLEQQNMSSSEDGDQMER

YPR028W\_homolog 3616bp PathoSeq: 1..3616 (SEQ ID NO 649)

ACGATATAAATTGGGGGGAACAATATATTGTTGAACCTTGAATTTTGTGTTAGATGAGTGAGTTTGTATATAAAG  
 GGAGAGATAATTGTAGAGATAATAAATTTCTGTCACCTGGATAAGTAGAAGTTTATTCTATTATATATCAAGCCTT  
 TTTTATCCGCGAAGATAAGCAATGAAGGCTATGGAGCCGATTTGGAACATCTGATAAATCCAATGAGTTTTCAC  
 AACTACTCTGACCTTGTTACTGCCATTTCTTTTATTACTCTGTCACATCAAAACAGTAAAGCAAGACATATATGTT  
 AGCTTGATGGACTAATTGCAAAATCAGCTCATTAATTGAGTCAAAACCCACGACTACTACACAAACGGACAAACAAA  
 CTAATCAAAAGCCAAATAAAGCAAAACATGAATGGAAGACACAGAAATAAAGATTGTGTAGTGAAGAAAGAAAG  
 AGAAAAATGAGTTCTATTCCGAGCAATGAAAGCAAAAGAGCAAGGAAAAAATAATCTAATCTAAGGAGTTG  
 GAAGAAATTGTAAATTTAACACACACAAACACACAAACCAACTCCTAATAAATGAATTTCTTCCCTTAAACGT  
 CACATTTTGAATTTTCAAACAAACATTCAAAATTTTCTCTTTTCTAATTTTCTTGGCTCTCTTTTCTCTCT  
 TTTCTTCTTCTTATTCACCCCATTTCTAGTATCTATAGATCAATTGTTATAATCTCAATCATGCTCAGTTT  
 CCAAGCTCAAGCTCAAAATTTATTCCTCAATTTGATTAAGTATGTTTAAATCCACAGACTTTTCTCATTTGCCAAT  
 TCAACGAATTICATTCTTAAACCAGTTTGTGTATCTTTTAAATTTCTCAAGATAACAGACCTTTTTCAGTCTT  
 TACGATATAAAATTTTAAACCATCTACTAACGATTCCATTTCATAGTCTACTAAAAATTTCCGTGTTTTAGATC  
 AATTTGAACAAAGATCCGGTTTACCAAGATCATATGCTGTTCTTGGTGTCTGGTGGATTATATTTCTTTTTAAATCT  
 TGTTCGAATTTCCGTGCTATTGCTCAACTTTTATCCAAATATTGCTGCTTTTGTCTATCCAGGTTATTAATCACTTG  
 TTGCTTGAAAACCACTACTAAGATGATGACACCAAAATATTGACTTATTGGGTGTATTTGCATTTATTAATG  
 TCATTGAATTTCTGTTCAACACACATCTTATACTATGTCCTCCATCTACTATCTTATCAAACTGGATTCTTATCT  
 ATCTTTCTCTCATTTGGTGGTTCTACTTTGGTTTACAATAGTGTATCAAAACCACTTTCTGATAAATATGTCAAAG  
 TTGAAAACCCAAATGCTAGCAAAATTCAGAAACCCGCTGAAGGTGTTCTACTGGTGTCCACTATTAAGTTAAAC  
 CATTTTCTTGAATGTTCTAATACAGAACTACTCTGACCAATATTTCTGAACTTGTATTATATATATATATAC  
 TTTATTTATGCAATTTTGTGAACATAATATATCTTGTATATACAGAAAGAACTCATTTATCTCATTCATTCTG  
 AACATATACACATTCAACATCTTCCAATCCAGTTAATGCCAATAAATTTGATCTTCTTATGTTTGAATGAATTTACT  
 CTAAACAAATGAATTTTGTAAATTTTGAATTTCACTTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA  
 ATACACTTTTATGTTGAACAGTTTACCAATGGCTACCGACAGGCATACATTAATGATAAACTTGACGTAATATC  
 AAACCTTTGGTGAATATAGAGCTCCAGTTAATTAATCCAAACCATTAATTAATCCAGCATATAAGACAAATGCCAT  
 ATTTGATTTCTACAGCAAGCTTCTTAAGCATTTGACCAAGTATAAGCTAAATCTCCATGAGCGTATTTGTGTCTAC  
 GCTTTGATGACTCATTAACAAATTAATCTCTGCTTCCGCAATTCATTTCTAATACTGACATTTTCTTATAAACTCAAT  
 CCAATTTCAATGGGATAGTATGTTAAAGTGGTTTTCGGAGCTCGATTCAATTATCTGCTGGGGATTAAATAATGCGT  
 TGTGTTAATAATGAATAATCTGTGTTGGAATTGACGTTGCAAAAATTTGCGATAATTTTGGTTGCAAGTTTTC  
 CAAATTTCAAAATAAAAAATTTGTGATGCAAGTAAAGTTGAATCATCTTGATAAGAAACACCTTCAATTTGGGGT  
 GATCTCCATAGAGGCATTACTGACAAATGAGCAACATAAGAGTAGTGATTGCTGGTTTAAATAAAAACATTTGCC

191/251

AAAAAAAAAACNTATTTCATGCTCTGAGTATCCTAGTTTTTACCACAGCAAAAACAGACCTCATACACAACAAGAACT  
 TCTTTCTTAAACAATATGACTTAGACTAGAATAATAAACAAGAGAGAAGCAACCAATCAAGTAGGTAACAAGTCAAT  
 GAAGACTAAGAGGACCGACCAATGAATAATCACAAAATAATGGATTACTCGATAATCAATTTCTTAGAAGCTTCATT  
 CATATATCAATTTTACCCAGTGTATGCAGAGTCTCTTACATAACTATAACCPAAAAATAATATCACAAAGCAGGATT  
 CATAACCCCGGGATGAAAAATATACCCGTTAGATCTGCCAAACAAAATTAATAATAAATCCATTGTGATGTATTTTAATT  
 TCCATCTTTTATCTTTTAGGCATTCTGCGCTTGATGGAAACCAAAAAAAAACCAATCAAACTATTAAATGTCCA  
 ATAACTTAGGTTTGTGATTGACGAGTAGATGAATCAAGGTCGTGTCCGTCGGGTACAAAAAGAAAAAGAACTTGAA  
 GAATTTTACTTTTAAAGTTTCTACAAATTTACAGAACTCTAACAGAGTCATTCTTTAAACAAGTTGTACAGCCACTC  
 TCGAGAGAGAAAAAGATAGATACAAGATTTCAATAGAAACATAATGATGTCTATTAAATGTAACCCATTATTTCCAT  
 TATGCTGGGATTAAATTAAGTGAAAAACAATCTTACTGGAAGAGAAAAAGAAATGAGAAGATATAAATA  
 CCGCTGAGGAGTAGAAAAATAAGAAATCCGAAAGTTTCTGCTCTCACTATGGTCTGTGCGCCACTTACCAAGGA  
 ACGAAAACTGTGACAAATTTATTTTCCAGTTGCTTGCAATTTTCAGTTACACACTAGTAGTCAATGATATGTAGC  
 ATTATGTAAAGGACATTAAATCTTCTGCTCTGTGTGCTAAATTAAGTTTAGCTCTTTTATAAATTTTATTATTATGCG  
 ACATGCTAATTTCAATTGGGATTTTAGTATCTCACTATTACCACTTCCAGCTATAAATAGCACTTTAATCGAATTA  
 AACGAGGCTGGAAGACAATTAGGGAGGAGAAAAATATCCAGATTCCACAGACAGANTACATTAGAGTGTATGAAT  
 TCCAACAATTAGACGAATGGAAGTGAAAAAGGGCAAGAAAAAGAGAGCAAAATACCAAAATGAGCAATATT  
 GAGAAGTTTGTGGCGATGCGAATGGTAGCAGTAAATCTGCAGTTTCTGTATATTCATTGGATCATTGTTGTGTCT  
 AGGGGGGGTGGGATAC

YFR028W\_homolog 149aa PathoSeq: 1..149 (SEQ ID NO 650)

VLDQFEQRSGLP RSYAVL GAGGLYFPL LUNFGGIGQLLSNINCZVIFPGYSLVALKTTTKDDDTKLLTYWVVF  
 FINVIEFWNSNFILYYVFFYYLLKTKGLIYLSFQGGSTLVYNSVIKPLSDKYVKVENPIASKIQBTAEQVSTGVH

YFR033C\_homolog 24142bp PathoSeq: 1..24142 (SEQ ID NO 651)

GACCAAGGGGAACAATTTATTTGGGGAGGATGAAGGTTAGCCCTTAAAAACCCCCACAGTGGGGGTTTCCAAAAT  
 TTGGGCAAGCTCCATCTTTGCAAAAAAAGCTTTATCCACCTGCTTCCAACTAGAGAAACATTTTCCAAATTGGTACAA  
 TTGATAGACAGGAAACTTATACTGATCTCTTGTGAATATTCAAAAGAAAAAAGAAACCCAAAGAGAAACCTT  
 ACTTAATCCAGCTTAGTATCATATATTTTATCTTATTTAATTTAACGTTACTACTACCACCCTTCCATTTCCCT  
 CGAATACCAATTCAGAACACACAATAACCAATAATAGAATGTCTATTTTTCAGAGATTTATTAAGAAATCAGTTGTTT  
 CAAGTCTTATGCTGAAGAAATATGTAATTAAGAACTTATTCATTTTCTTGAACATGTAACTGTGCTTTTA  
 GATGCTTTATCTTTGCAAGCAATTTTCACTTATACTAACGTTACATTTATTTTCTTTGTTTAGCCAGTTGAAGA  
 CGTAGAAGTTGAACAACCAAGAGATGCTCCAGAGAGAGAGTTTCCGAAGAACTGTTGAAGAAAGAGAGATGA  
 TGAATGAAGATGATGAAGAGATGATGAAGAGAGAGAGAACTGCTGACCCATTTGATATCTTTGGGTGAAGAAATG  
 TACCAAGACCCGCTGCTTGTGAAGCAATTTTATCACCATTTCACACCAGTGTATTGAGAGAGTCAACCAACCAAGA  
 ACAACCAAGATTATGAACACAAACACTACAAAGAGATTGTATTGAAGAGTTTTCATTTTCAACACTGTGTAA  
 CGATTGTGTTGCCCCAAGATTATTCACACAGATTGAAGTAAATTAGATGAGAGATAGTATAACACTGTGTGGGGAT  
 AAAACGTTTTTGTCTTTGAAATAATAAGGACATAATTTCAATACGTCATATTTCAATTTCAACTGCTTCACTTAT  
 TAGTATTAAGTTTCAATTTCTGCTCTTAAATGACCTTTTCACTGCAATTTTGGCCCATTTTCTTACACTGCTGCT  
 TAATATCTGCTTGAATGAAAAAAGCTGAAAAATTTAGAAAAAATAACTATACATATAACCTTCTTCCCATTTTCTCA  
 ACATCTTACTACTCTGCTCAATTTTAGGAGGTATATACTTCCGACAAAGAGTTTATTAATGAGTGTATTTTCCAA  
 TGTATTTCATATATATAATTAAAAAAGCTATTGTTATAACTCTTACTCTGACATAGAATGTTTGAATTAGTCTG  
 TACTTTCATCACTGCAATTTCTCAGCAATTTGCGGATTAAATTTACGTATAATGCAACTTCTGACGAGCTTCACTTT  
 GACCAACTCAAGAAACATTCTCGAAATATTAAATAAAAAAAGTACCTGATTAGAAATATCTTACTTTAGAAAGT  
 GATTGAGAGAGAAATATGTAAGTGAAAGACCAACAAGAGCTATAGTAAACCCCTTCTAGAGAGAAATTTCT  
 AAGATATATGAAGCTTCCCAAGATTTATCTACAAACCATTTCTGATGGCTCAATTCAACTTTTGGATGGATGTG  
 TACATGTTGTTAGCTTTGATTTAGCCGTTAATAGTAAAGTTCTAAGAAATATAATAAATAAGAGAAATCAACCCCTGGA  
 AATGCATAAAATATGAATCAAGAAAGCCCGCAATTTTCTTAACTGCAAAAGAGAGAGGTTGAGTGAGAAAT  
 TAGGCCAATTTGGAAGCTCGACAACTTTAAATATTGCATATGCGCTTTGCATATTTCCGGTATATAAAGCTATA  
 TGTGTCATAAATTTGTGCATATTTATGCATGATTTAGCAAGACTTACACATAGCAAGAGAGATTTTGGCCAGTA  
 AAAAGGCTCTTATTTCTGACAAATTTTATAGACAAATATAAGTTTCTTATTTAGTACTAAGTATACTTTAAGTAT  
 TTCTCACACAAAGAACTTATCTTCAAGTGTCAAGTGTGAAATCACTTTAAAGTCTTCAATTACTCACATAAAT  
 AACCACTTTTATTAATAAATAAGCTCATACTTAATAGTTGAGACCCCTATATTTACCCCTAGTCTTGTGTTTATC  
 ACAAAATAGTCTTTTATTAAGTCTCTTACTTTTTCCAAACTTTTCCAGTAAATGGGTATAAATATTGTCAA  
 AAACAATTTTAAATACTAATTTTACTAATTTTAACTTAAATCAACTTTATGAAACACTCAAAATTTGGTATTA  
 TATAGCTTCCATGTATCTGGTATACATACACTACCAATTTTGAACAATAGAGTCAATTATCTACTGTAAAGTCT  
 TGTTTATTTGCTGTTTATAGGCTATTATCTACTTAAATAGTGTGGATAGATGATTTGAACAAAGTACACAC  
 CACCAAAAAACAAATATGCAAGATGACTTAAGCAAAATTTGTTAGGGAATTTCTACTTTTCTACTAACCAATTTCA  
 GCTATAGGAGCAGGGGAAAAATTTGTACAAATCTAACAAAGAGAGCTCTGACATTTTTCAGAGAGCCCAATAAAA  
 TTCCGAAATATCTATGGTACATCTGACAAAAAGTTGTTAATAGTTAGGATCTCGCGTTTGTACTTTTCTATAT  
 AAACAAACACCACTTTATAGAAACCAACAACAACTTAAATTTTCTTATTAAGTAAAGTCTTTTAAATATC









195/251

GC AAAACAAAAA CCGG GATTCAAGGACGATGGT TGATATGAGCCACAT TGAAAAC TATGAATTUGCTGATTTGAC  
 TGATAAACAAAATCCAAACTTTAGATATAGCAAGTAGCTGGTATAGCTCTGCGTAGTTTATTCAGTAATGCATGTC  
 TATTGAAAATGCTATGATGGTTT TAGAAGGAATCACTACATAAGAACATTCAAGATGCTAGGATTTTCAGTAACA  
 GAACCACTAAATGACTATTTTCTCTGCTGGTGTCTGTTGCACAGTAAAGAACAGGATTACACAGCCATTACCCATT  
 GACCTCAGGCACCTGTTGGCCATGATATAGTAGTGATAAATCAAAAAAGGGACCAAAATTATTGCCAAAAATA  
 ACATTAGCATGAACCTATTGTATCTATTATTGGGAAAAGATATGTGAATCAACAAGTATTGAACCTTTTCGACCTT  
 CATGACGGTTTGTTGTTGGCTGTGAGTATTTTGTGTAGACTAGTTTACTGTATAAGCCTTTCAATGGTTTANTACA  
 CTCTGCCCTAAGGCATTTATTAA" CAGGTCTGATATGCAACGCAGTATAATGCAAGGAATGTCAATCCTTTCTTTT  
 ATGTTTTCGCATGCTTCTTGGAGACTGCCACATAAAAAAGAAAAGGAAATATCATCATTGATACATATATACCTT  
 TCTTTTACATTATCCCTTCTTTTCTCTAGCCTTTACATTACTTAACCTAACAGTAATATCCATTCTGTCAAC  
 AAACGGCTGATGATTATTAAATTGCCAAAAGTCCCATGCCAAAAATCCAGTACTCTTCACTCTAACCTCGTCTCCCG  
 AAGAAATCATTGATTGTGGCCTAAATATTATTTCTTTTACGATTCTTTCGCAACGGCCGAAACGGCCCACTTT  
 CAATGTTTAGTAATAACAGAAATTACATAAATAAGAGAACCTGTGATCCTTTCTCCATTCTTCTTTCTTTGATTT  
 CATCTGTGATTTTCAATTCCAAATACAT"TAGAAAT"ATCAAAACUATCAAAAAAGTAATTAATTACTACCAAC  
 ATATGATAAACCACCACTTTAAAACGATCAAGATCTTTATTGAATAAGGTGTTACCTATCGATATTGAAGGTGAT  
 AAACATTCTTCTCTTTCAGTAGTAACGAGGAGTTCTCCAATTCTAAATCATGATTCAGAGTCTTTACACCTGAT  
 AAAGCCCAAGCTTCCAAAATTCAATAAAAAAACATCTAAATCAACCAAGTAGGCACCGATCTAATAATAAAAAAT  
 ACTAAGAAAAC"TAACCCGCTATAAAAAAGTGTGCGAATTCCAGTCAATCAGAAAGABAGAACAGAAAATCGCACCTT  
 TACCAATCAAAAAGAGGATCAGATATACTCGATCAAGAGATTAATTAGATTGGATTTTAAATCGTGGCTATAGGG  
 TCTTTGATTTCTTCATACATCTTTGAATTGATGAAAAATGAATACGTGACAGCATTATGTTTATACCTTTT  
 AAATGTATCACTGCTGCTAAGACACAGACAGTATGCTGGATGGTGTGAT"AT"ATTCATGGAAGAAACACCAAG  
 "TAAAGTGATGTTTCATAGATATAGGACTACCAAAAAGTCTGTGTGAATGTTACGAGAAGCAAAATATTATTAGT  
 GTGTAGCAAAAT"AT"AT"ACCAAGACAGAGAGGAAAAAAAACCCATTTCTTGAATAATCTTCTTTTCAT  
 TCCATCTTTCTTTTCTTCTTAATCAAT"CTTTAAAT"TGAAAAGTTCATTGGAAATCGTCAAGTATGTTTAT  
 CAACATTTCTAATTAACCTATCTTAATAATTAGGGAATAGTGTAT"ATTTGCTTTAAAGATATCCGATACITTT  
 TTTCTCTTTTGTAGTTTGTGTTTTGTTTCTTTTATGATTAGTTTCTATTTTAAATTAATTTCTACATTCTGT  
 ATTGACGACTACACATATCAACGACCTAGCACATCCACCCACCAACATPACACAACTCAAACTTATCAGACACA  
 TCTAGCAAAATGAGACAAATTCAAATCATATTAATTTCCCTTGTGTGTTTCCATAATAAGATGTGTTGTTGAGAT  
 GTTGACATCAATCAACAAAGAGTGGAGAACTTTTCTGGTAGTTCTGGATCAGCAAGTATCAAGATTACCTGG  
 GATGATTACACACGATTACAGACTCACCGAAATCTTTGGATTAATGCTTAAAGGGTACACAATTTCTTTATGTACTGCA  
 CCTACTTCAGATGGGGATATCCAGTGTGTTGGATCCATTAGTCAAGAACGAGCTATTTTCAGGTAAATCTAATAACA  
 G"TTTCCATTGCCGAGAACTCAGTACCTAACGGTTATTACTATTTCCAAATTTACGTTACTTTTCACTPAATGGAGGT  
 ACCCATTTTCAATTTACCCACGTTTCAAAATGAGTGTGATGTCGGTCCAACTGCCACTTTGGATCTCACCCGAA  
 ACACGATCAGTCCAGCGGATCAAGCTCAACGATTTCAGTACTGCAACTACTGCTGACTCCAAATCTTTTCAGTT  
 CCATATACCTTACAAACAGCGAAGACTAGATACGCAACCAATGCAAAATGCAACCCAGGTACCAAGTCACTGCTACA  
 AACTGGAGTATGAAGTTCCCAACTAGTGTCTTACTTACTACTCAACAAAGGCTGGCACACCAAAATGTGGCTCT  
 ACTATTAACCCAGGTTGGAGTTTACTGCTGAATCTGCCGTTAACTATGCTAGTCTTCCGCCCTATCCAAACATAC  
 TGGTATCTCTGCCAGTGAACGAGTGAATAGGCTACAATTAGTGTCTGTACAAAAGAGAAGAAGATGGTTGGATTGA  
 ATGAGGGAAACCTCTTTATAACTTAGATAATGCTAACATTTGATTTGATTTTCAATTTTCTTTTCTTTTCTTTT  
 GTTTGTTTATTAGCTTCTTAACATGTAACTAGTGTGTTGGTTGTAATAGTTGATTTTCTTTTCTTTTCTTTT  
 GCAAGTAGATTGGAAGTAGGCTGTGTGGCGTGTCTGCGTAGGTCAGGATGATGATGAAGACGACGACGCGTT  
 TGTGTTGTCGAATGAGATCTCTTTTCTTGTCTATCTTTCCGTTTACTACACAAAATCCATTTCTGAAAGCCCC  
 TTTCTGTGTTATGAGTATTTTCTTTTCTCTCCCATAAATGAACCAACATGAAATGAAATTTTATATCATTTGG  
 GCAGTGGATTAACTTTATATGAATTTCAATTTATTTTCTGTTATTACTTTTCAAAAAGAACATTTAAGCAAG  
 TACAATATAAATAAGTGTACAGCTTGTCCATTATCAGATTAACATTTTACTTTTAAATATCAAGCCAG  
 TACTGTTTTTACACATCACTGCCACACAACGAACTTTCTCACTCAAAATACCTGCTATCTGTTTAACAAGCCACT  
 ACAGACTTTTAAATTTTAAAGAACAAATAACATACAGATCCAGCTCAGCTCAAGACACAAGCAAAAGACCCGCT  
 CATACTTTATCCCAACCATGTGTATGAATCGACCAAAATATCAAGAAATCTCAGTCAAGAACCAACAACTTGAA  
 CTGCTTTTACAGATGCTTTCCACTAAATTTGATCAGAAAAGCAACAATACAGTCAATGACAAACAACTATG  
 GCAAATAGAGAAATTAATTTTATAAGTTGATTTTCTTATTCACTTCAATAGTTTGTAAATACTAGGGTTGCTA  
 TATTATTCCACAGAACTAATCTCTAGATTTCTGCCAACTTAAACGAATTAATATATAGATGGAGAAATGCAAT  
 GATTATATAAGCGGTTCTTCGAATCGATTGCMATAGCTTACTTGTGTTTGTGAATATATACAAATTTAAAGT  
 TGACTTTAGTAGATATTGTGACAAATGGAAATGCGAGCGGAAATTTCTGTGGAACCAATCTCGATCCGAGGT  
 TCGCGGATAGTGTCAACAAACCGCAACACAGCTCTTCCAAATTCCTACTTTCCGTTACACATATATATAGTATACAG  
 TATACCTTTCTATTCATTTTGATAATCTACCCAAAAGAAAACAGAAATTAACCCCAATTGCTCTCGGTAGGAAT  
 ATTACAGATATGAACCTTTACATTTTGTGTTTGGTTGCAAGTGTGTCATUACAAACCATTTTCAGATCACCATCAC  
 TTCTTGATCAATTATATGGAGATTTACATGCAAGAACCAACACAGCACCAAAATTTGCAGGTACAGCAGAGGCTC  
 CAATCAGATGGTCAACAAAAGGTTT"TAGCAATGAGATCCMAATTGACG" GCTGATAAAGATGATACTTCCG  
 ATATTGCTAETGATCAGAATATGTTTGGTGGAAATTTGACTATATCCCAATTTCAATCATTTGTTTCAATTT  
 CTGATGACTTTTCAATAAACATCCACTACAGATCACAAAACACCCAAAATATTCATATCCGCTATTTGTTGGGGCAU

YFR033C\_homolog 114aa PathoSeq: 1..114 (SEQ ID NO 652)  
EDVLEVRQPPADAPBEEVSEETVBEEDDDDDDDDDDEDESEETADPLDCLREECTKCAACKPFDHHPHECIERTKE  
QETADYEHKHVKRDCTEETFEHLQNCVNDCAVAPLEN3LE

[illegible]

YCL166W\_homolog 13/90bp PathoSeq: 1..15790(SRQ TE NO 655)  
ATGATAAAGGATTCTGTCAAACTCTCTTGAAATGAATCTTAAAGGACATGACATATAAAATATTGTAGATCCTCTCTTTA  
CAACAAGATATAACACAATTGTCCTCCCGCAGTACGACAGCCCTTTCTCTCAGCACCACATTTTCTCTCTCTCTC  
AACTTCCAACTTACTATAAATATCTTGGGATTCCTCCATCACCACCTCTCTCTCAACAAATACAAACAAAAAAG  
CAACCCCTCCGACGAACTCCCAACTTGAAAGAAAGCGTTACTCATATCTAGTGCAGATTATASCTCGTTTGGGTTGA  
TCTATCACTCTGAGTTCTCTGAAATTTGGGATCCGGTTTATGAAATTAACATTAAGAAATTTATGTCTTGGATCATC  
ACCCCTCTCTTTGTTTAAATATATTAACAACAACAAACGCGGTCTATTAACTATACCACACACTCAAAATATATAT  
GAAAAATGAATTAATATATGATTATAGCGAACTAATCTCTTAGAAATTGATTACTGATTAATTATCTTATCAACAA  
AAAGATGTTTTATRAATATAAATATATAAATAATAAAACGAACTGATTAATCTGTTATTATTATTACCCAAACTG  
AACATGTTCTCAATTATCAATCTCTGGAAATTAAGAGAGAAATATTTGCTTAAATTCCAATTCGATTAAATCAACT  
GATAAAATATGATCCCT  
ATTTTGCAATTCGGAATGATATATAACCCCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
ACTATGATCAAAAGATATAACCAACTTGAAGAAACAACTAAGATTTATCTATCTATCTATCTATCTATCTATCTCT  
TTCTTTTCTATTTGTTTGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT  
TATCT  
TAACTCAATAGCTTTTAAACTATCATCTGTGAATTCACACATCAACAGTTGTGCTACCAACAGTTGTTGTGTAATT  
TATTTTACTACCAACCATCATGACATCATACCACTAGTACTATATTACTAGCAGTGTACTGTGCTGTATCACT  
ATTTTCAATTTCTCTCTAATGCACCTCTTGTGAGTTTATATATAATGATTAGCTCTCACTCAATAATCAATTAAT  
ATTGTTGAATCAGCAACTCCACCACTACTACCACTGGCAGTGTATTTGTTATTTGTTATTTGATTCAATTAATTT  
AATIGCTTCTCTCTAATTTTTTTTATTAACCAATAGTGTGATTTGTTATTAAGAAATTCGACCAATATATAATCTCT  
TTGTTTCTTAAACATTTTGTCTCTTACGTTTCACTAAATTTTCTCAATTTTCAACTTACCAAGTTTATGTTCTC  
AATTTTGAAAATTCATGATTAACTATATCTTGAACCAATTTATGCAATTTCTCGTTCTCTCAATTTGAAATAAA  
ATGACTCTTACCAACCAATTAACCAAAAGTTGTAGCAATAGCATCTTTCACACTTGATCTCTTTCAACATTAAC  
ACCATTAACCACTTTGGTGTATTATTACCATTGTAGACTCTTGAACCTTGGTTTTCAATACTTTTCACTCACTGC  
CTTTTTCAGCAGTTCACTAGTACCTTTTACCAACATTTACATCAACTAATTTAGTCATAAAGCTTAAATTTGCTAA  
AACAGGATTATCAATTTGAACATAAAGGATAATTAGATGCATATTTAATAACTTAATACTAGTTTCACTTTCATC  
ATTTATAGGATTAATTTATCT  
TCAACTTTGATGAGCAATCTTATCAACTATTTTAAATGTTTAACTGCACTAATTAAGCACTTTTATTTGT  
TTTGTGTCCAGCATCT  
TTCTAATCAATGTTTCTTACCTTTATTTCCATTTTGTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
TTGTTTTCTGTGTTAACT  
AACCTTTTCAACACCTATACCTGAGGTATCAAGGGGAAAGACCTCTGTGTGTATCAAAATTAACATGATTAATC  
TCCAGTATAAGGTAAATCCATTCGATTGTCCTATTCAGGCATTTTTCACGGCCATAACCTCGTTTAAATTAAGGTCT  
AACTGTGATAATTTATCT  
ATTCACGACGACATGAAGTTAACTTAAATTTAGGATTTAACTGAGTCTTAATCGGTAGGAATTTATCAATGAATTTTCGATA  
ATTAACATATGAATTTAGGTGATTAGATCGCATTAATCAATCAAAAAATTTCTGTAATGATTCCTTTTCAATTTT

ATGGATTTTTCATATTAAACCAACTAGCATATGATGGTATAAATAATTAAATGTGTTTGTATATATTGAGGTTF  
 TTCCTTTGGTGGTTCTTCGGTTCATCTTCACCTTCTCTCTCTTGGTCATCTCTTCATCTTCTTCATCTTCTCTC  
 CTCTTCTTTTGAATTTCTGGTCTTACTTCTTTCTGTTGTTGGTCCATATCAACATCTTTATACGTTGTATTTGTTF  
 TACTTCTGAACCTAGCAATACTAGTATTTTGGTTTGAAGACAAAGGTTTCAGTCCCTGAAGCACCARCAACCGAAGT  
 TCTAGTTGGTGTGATTCATTTCCCTTTTCTCTGTACTTCTTCTTTAATTCAGATTCTTTTTCATCATTGT  
 AGATTCACACATTTGATTTACATTCAGATAAATCAGAAATTTTTTCTGTTCTCTCTCTCTCTCTCTCTGGTTF  
 TCTTCTTCTGTTGATTAGATTCGATTCTACATCTTTTGAATAATCTAGATCATCAATTTCCATATTAAATCGTC  
 ACCATTTATTAAAGCAGATGTCTCAAAATCATCATTAGATTTATCAGGGTCATTATTAGAAATTATAATTTTCATC  
 AAATGATGGGTCTCTCTGAAATATGTTTCAATTCCTCATCTTCACCCAATCTCTGTTTAGATTCTTCTCTTTC  
 ATATTCTTCAGTATTCCTCTTTTGTGTATTTCTGTGAAACCAATTGATCTTCTTCACCAATATCTACATCCAC  
 TTTATCTTGATTTCTCATCAGCATCAACGTTGGTTGGTCTCTGTTTTCAGATTTCAGAGGCAGCATCGATTGCCAC  
 TGGTGCATCTGGTATATCAAAATTCATATCATTATCACTATTACTGTCTTGTACTGTCTATCATTTGGAATGGT  
 ATTGTCTTGATGTTCGTTGACTCAACTTTATTCAGACTCAGCATCATCATCTTGTGTGTGTGTGTGTGTGT  
 ATTTTATATCTTCAGTTGGGTTTGT  
 TAAATTAACCACTTCTTCAATTATCATTTGCAGCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
 TCTATCTTCTTTCT  
 CTCTTGTGATGTTCTATTCATCATCTCTGCTGT  
 AGGGCTTTCTCTTGGAGGTGAAGCACTCATATTTCTCGAAGCAGTAAATCTATTAATGTATGTATATATATATAT  
 GAAAGTAAGGATAAATGATTAAAAAAATTTGGTTGCAAACTTAAAAAATAAATATAATGAAATAAAAAATAAA  
 AAACCTTCTGT  
 GGGGAAAGTTCTTTTCT  
 TTTGT  
 ACCACATGACATTACTTAAGCTTTCACCTTATTACTGCTATGCCATATCTTAAACTCTTGTCTAAGCTTCAGTC  
 CAGACAAGTATGTCTAGTCTTTTGAAGTAATGAAGCCTCTTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGT  
 TTCATTATTCTTATTATCCACATATATATCTTATAATAATTAGGTAAAAACAAACAAATAAATGTAAGGAA  
 TTTAATAGGGAACCTGAACAGAGTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG  
 TTGGCAAAAGGTCAAATCTCTCTTATATATATATATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG  
 GGCAMATGGTAAAAATTAGGGCAATGAATTTGAATATATTCAGAGAAAGAAAAAGGGGGAAAAAAGAAAAA  
 ATGAAATGAATTTAATAAATTTATTTTGT  
 TAATGGCTTTTCTGTATATATATATCTCTATGTATATATCTTTTATTACATCTCTCTGGTAAATATATATATA  
 TA  
 ATATAGAGGAATATTTCAACTACTAACCATCAGCCAAACAACTCAAAAGAAATATCAAAATCAGACAAABAC  
 CATTAATTCATATTAACCAAAACCAACAAAGCAAAAGCAAAATCACAATAATATTAATCATGCAAAATTAATGA  
 TCAGTCAATAGGAATAAGAGAAATGGGAAAGAAAGGAAAAAGGAAAAAGGAAAAAGTAGATGGGAAATTTAACTC  
 CAACCTGTTTCTTGTGTGTATATATATAGTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
 GCGGTCTGCTGT  
 TATCTAATGCCATATATATCTTTACTTTTCTCTCTATTTAAACTAACTGCATCAGATCTATTTCAATCCGTTGT  
 TGTGTACTTTATGCTTGTCTTGT  
 CCCACTAGTTGTCAACCAAGAAATTAGATGAAGCATATATAGCCCAAGATTAGAAAGCTTGTCTTAGGTATTAC  
 TTTTCTCGTATGATATTCTCTCTACTACAATGAAGAAATGGCTTAACCAATAAATAATGATAATTAATCTCTG  
 CTGATTTGGAATTAATAAGAAATGAAAAATTCACCAAAACAGAAACAGGAAAAAATAAAGAAAGAGAGAGGA  
 AAATTACATTATACCATCAACAGGCGATTAAAGTTAACTTGACACAATAATAGAATAACTAACTTGAATGGGT  
 GGTAAACACTCTTACCAATTCAATTTGTTACCTTGAATCAAAATCTCTTCGATGATAAATAAATAATCAAAATAT  
 CGTTTACAAATTAACCAATTAACCTTACAAATTTGGACTAATTGATACACTTTCTCATTTGTTTGAATGGAGATATTATA  
 CTACTGCTCTCCAGAAAAATTAACCAAGTATGATGT  
 AAATTGAAAAAGCCTTGTATATATGTCTTCTTGAACCAATCAAGAAACAACTGTATTGGGAAATAACTAACACC  
 ACCCAATTAAATAAACAGTAACCAAGATACATACCTTAAATTAACCACTAATCTTAGTTTCTCTTAGTTACCCTT  
 TTCTTCTTTGTTTATTCGGTTGACTATGTAACAATCTTCAATCAATTTCTTCTTTCTTTTACTTCTTCTGTTCA  
 ATAATTATATCTTACTCTTGACTCAAAATATTATCAAAATACITCCCTACATTTGTCTCTCTCTTATGATCACC  
 AATTCACTTCTTCTCTCTGATCTTACTACATAACTTACGTTGATTAACCTCTTCTGGAAGTTTGTGAAAAATGTAT  
 TTTTCTTTCTCTCTCAAGAAAAATAATGAACCTCAAAATCTAAATAATCTGCAATATAAGATATCAAGCATAT  
 ATGCTAAGATCACTACTGAAATTTGAAGGCGAAAAATATGGTAATCACAATAATTTCAACACAATCAATCGGAGTT  
 TAAAGATTGCACACACACTAGGAGGAAGAAATTAATAAGAAAGTTTGTAGTTTATATTTATTTGGCACCTGTCA  
 CACACAAATAGTAATTTCTATATGCTTTTCAATTTATTCAAATTTAGCTTATCAACCAAGAGCTACATATAGATAAGT  
 AAGTAAGCTTTCTTTTGTGTATTAACCTTGTCTGATTTTATTTGATTTGCTCTTCACTCTCATATAATCTTTTGG  
 AACCAATAAAAAAAGGACACTGTTTGAAGCAACCTTGAATTAATAGTTTCTTCTACTTACTTTGGTGTCTAGATTTA  
 GAGCATTACATGTGTCAATCTGTAAACAAGTTGATAACAGTGACTTGTGAATAAATTTTCTCTGAGCTTAACTCT  
 TATCACAAGTAAGTATAACTCTCTACTAATCTTTTTTTCAGCAAAATTTTCTTTTCTTTCTTTCTTTCTTTCT  
 TACTTTAGGGCTATAGCCCTAATCCAGTATTTCTATCTGACATAGATTCTTAGTATCCGCTCTCAATAAGCT  
 ATACATAACACTTTTTTTTTCTACTGACATCCCGCCTTGGCTCTTCAATTTGTCTCGCAATGAACCTGAGGATAT

199/251

GGACCTATTGACACGATTTTTC AAGGCTTGGACTGGAAATATGGTGGACTCATACCAATTTTGTTTAGACTTG  
CCCCCTCCCCCCCCCTCCAGTTTGGCASTTGGCAATTCACAGTTCCGATTACTATACAAATCATAC  
TTAAGTACACAAACAAATTTCTTCTCTCCCTTTTGGTTTGAATTTGGGTGAGAACGAAAAAATTTCTAC  
TAACAAATATTTTTC AAGGAAAAAATTTTTCACAGTTAACTTTCTTCTCCATTGAAATCCACATTAAATAC  
AATTCACCAATGGTTCTTACGCTGCCACTCCTGCTAAACCCAGCCAAATCAGCTTCTGCCCGTGGTTCTACTTG  
AGAGTTTCATTCAAAAACACCAGAGAACTGCTCAAGCCATTAAATGGATGGAAATAGAAAAAGCTCAAAAATAC  
TTGGACCAAGTTTTGGATCATCAAGAGCCATTCCATTAGAAAGATACAATTCATCTATTGGTAGAACCTGGTCAA  
GGTAAAGAAATTTGGTCTTACTAAAGCTAGATGGCCTGCTAAATCTGTCAATTTTGTCAAAGATTTATTAAAGAAAT  
GCTCAAGCTAATGCTGAAGCTAAAGGTTTGGATTCTAGTAAATTAATTTCTCATACTCAAGTCATTCATGCT  
CCAAACAAAAGAGAACTTATAGACCTCATGGTACAAATTAATGCTTATCAATCTACTCCTTCCACATTGAA  
TTAACTTTGACTGAAGAGATGAATTTGTTGAAAAACAGTTGAAACAAAAACAAATCGATTTGAACTCAAGACAA  
AGAGGTAGATTAGCTTCTCABAAACGTTTAACTGCTGCTTAAATAAATAAAAAATGGAAACAAATAAGGGAA  
TGAATTAAGATTGATAGATAGATAAAAGAAATCAAGTCTTGTTCATTTCATTTCATTTCATAAAATTCATTTTT  
TTATTTATTGGAGAGAGAAAAAGCAAAATGCTCAGTATTGGTATGTTCATGTTTCTCTAAATCTTTTAGCGG  
TATGTTCAATATGTATATTATAATAATAAAAACTTAAAAAAGAAAGAGAGAAATCACTTTCTGGGA  
TATCAATTAATAGATATATGCTAAATAACAACAACTTACTAACTCTTTACAAATATGTATATTGGATGAAT  
TTAAACAAATGTAAAGAGTAAAGGACATTTTACTTTACATAACGTATTTCTATCATAGTAAATACCTCTTAGACT  
GTCCGATAACACAAGAGTTTAAACCGATATGGGATTAGAGTTTITAGTTTTACTATGTATATCTGGAAAAATTC  
ATTTCTTTAATGCTCTTTTCATGTAAAGCTGGAAAGCCGATATCACTTGTPTTAGTGAGGTCCTCCCTTCCCATCTC  
CTGGTTTGTGGGATAAAGTTTCATATCATATCACTATTAAAGCCCCAATTGATGCCAAATTTGTGAGACTGAC  
TTCTTTTCATTCATCTTAACTGCTATACTCCGAAATTTGGCATATTAATTAATTAATTAATTAATTAATTAATTAAT  
AGCCTTAATATAAACCTGGGTATATATATCCAGATAGAGATTAATTTTTTGTATATCATTTGTATAGAGGTTTCT  
TAATTTTTCACCAATTTGTTTTTGGCCATCTTTTTTAAACATAGTAAATTTAAATTAACCAATTTGATAGAGTA  
AAAAAATACCTTAAACTCTCTTCAGATAAACATATATCCATTAATAAATCTTTTCAGAGTTTCAAAATAAA  
CUATCAACCAATATATGAAGAACTAAGTATAAAGATTATGCTTCTTACATACCAATTAAGAAACCAACCTA  
GTATATTCCTCTCATATAGTCTGACCAATAATAGAAATAGAAATTCATCTTACAAACCCACCCACCAAGTGAA  
GAGAGACGAGAGAAAGAGACACAAACGAAAAAATTCACGAAACTAAATATCCATCTTTTCACCAATTAACAT  
GTCTTTATCATTAATAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
ACTTTAGCCTTCCCAAGCAAAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
GCTGCTTATCAATGCTGTTTTCAATACTTTTAGAAGAACCAAGAAATCAATTTCTTTATGTTGGCATTCCATTGCT  
GTTGTTTGGAGTATTGCACTAGAGCTAGAGATTATAATGAATCTTGTACACATAAGAGAGGTAGAGAAAGATTG  
GAAAGAGTTAATGTTTAACTTTTATGATCATGATCATCAACATTTGGCTACATATACTACTACCATTTATGTTG  
TTGTACATAAGTTTTTCTTTATTGTTTAAATATATATATAAABAAAAAABAGAAATTAAGTCAATTTGAGACAA  
ATTATGAATAGACATCAAGCATTATTTTATTTTATTTTATTTTATTTATTAATAATTAATTAATTAATTAATTAAT  
GACAACTCTCTTATTTAGATCTTTTATAAACTTTTACCTAAGAAACAGTTTAAACATCTTTCTTTTAAACCTCTAGA  
TTCTATCACTTTGATCAATTTGTTTCTTAAATTTAGCAACCAATGATCTTTCATATCATGATTAATTTTTCAT  
ACCAATTTGTTTAAATTAATCTTTTACATTTTGTCTTGAATTCATCATCTTTTTCACCAATTAATTAATTAATTAAT  
TTGACGTTGTTTCAGGGTAGCAATCAATAAGCTTGATTAATAACCAAGAACATTTATTTATCTTTAATATCAGT  
ACCGATTTTCTCCCAATTTGTTTCTGGAGTACCAAAACATCCCAATTAATCATCTTGAATTTGGAATATTCTCCCA  
GGAACTCAAAATGCTCTTAACTGTTTTTAAATCTTTTTCATTAATAACCACTCATATCATATGCTTATGCTCCAC  
GGGTAAATAAATGAATAATAAGCAGTTTGAATAAACAATAAATGAATGTTTTTTCUAAAGAAAAATTTATCTAA  
ATCAACATTTCTTCATCAGCAGTAATTAATCTAATAATTTGACCTAATTCAGTTTGGAAAGTCACTTCATGAA  
TAAATTAATAAATCAACATAGTAAGGATCTTGACGGAATGTTTTTTCMAACCAATTAATAATGGCCCTCTCTAA  
CATAAATGAATCATTAATAGCAATGTTGTTAACTCTTCAACTAAATACCAACATGGTTGACCTCTTCTAGTTT  
AGATTGATCCATCATATCATCAGCACTTAAATAATAGCTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT  
TTTTTTATATTTCAGTATCATTTAACTTATCTACTAGTAGTATTATTTCAAAATGGCAAAATGATTCAAATACAGATAA  
TCTTCGATTTAATTTACCTCTGGAGTATTATAATTTAACTTCTCAACAAACCAATTCATAGGCTCTTTGAGGCAT  
ATTATAGAAACTAAATTTGTTTCAATTTCTTCACTAAATCTTCAAAACATCAAGAAATCTTTCTCTACAGC  
AAGTTTATCAGACATTTGAGAGTGAATGAGTTGGTTTTTGGTAACTGCTAATTTGTTGTTGTAAGAGAGGAAT  
GGGTGTTGTTTATTAGGAGTAATTTTTTTTTCATGATTTATAAACTTTCCCGAGGGGGGGGGGGGAGAGGC  
AGATCGGCTGAGATCTGTGTTCTGTATCAATTTATGTTTGGTTGGTTGGCTGGAAAGTTCTTTTAAAGCCATAA  
ACATAAATAACATAAACCCAAAAATTTGGACAGGGGCGATACCGGTAAAGATTATCAAAATTAAGATTT  
TACACCATTTGGAAGAACTACTACCTCTTTTAAATATAAACATTTATGGTTGTCACTTTCTATGTTAAATTAAT  
CAATTACTTTCAAAACCAAGAGAGGAGGAG  
TTTTCAACCATGTCGCTATTATACATCAACTCTATTCTTTAATGCTCTCTACTACGTTTACTTTTACCAGCTCTTG  
AAGTTCATTTACCTTTCTATCTTTCTTTGTTGAAATCCATTAATTCAGCTGATGAAGCAGCATCATTTCTCTTT  
TACCTCTTTTTTTTACCACCAATCCATATTAGCATCTTTAGCCAAATCTTTTGAATTTGGTTTCTTTCTTTTAT  
TATCACCACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACT  
AATCATCATCTACT  
TTTTGTTAGCTCTTTCTTGTAAAGTAGCATGTTGAATCTGTTTACCAATTTTTTCAATTTCTCGTTCTTTTATG



[illegible]

201/251

YJL166W\_homolog\_1 91aa PathoSeq: 1..93 (SEQ ID NO 656)

CAPHEHTYMGWQSLGSPKQKYITQYTIISFYAAKPLKCAAYNAVFNTFRRTKMQFLYVAIFVFWVSIWTRARDY  
NEYLYTKEGREELERVNV

YPL271W\_homolog 7123bp PathoSeq: 1..7123 (SEQ ID NO 657)

ACACCTCGATGCACCTAATTGAAAAAGAAAGAGATCAAAACAGGAAAGAITTGAAGAAATTTCAAAAACAAGAAAA  
CAAAAAAAGCGTTAAACAGAACTCTCGAACCATTTGGAAGAATTATCAAAATTGGGGAAACAGCATTTGGAAATTCCTT  
TGTGTTAGCCATTGGATTATATTATGTGCGSTTTTATACCCCAACTACAGCCGTTAAATTTAGTGGGGTCAGTATT  
AGATTCACTTAAACAATAACATAAAAGATAAAGATGGCGATTAAATTTGTCGGGGATATAAAGTTTCTACTGTATT  
TCCAGTAATGATACCGCTTATGGCTGTTAGTSCCGSTTTGCTTCTGGGCCAGAAATTTGGGTATTGAATTTATTGGG  
AGAGAGATTAGTAGCCACATTCCCTGCTACACTCATGAAAAACTTATTGCGTCATGACCAGAAATTCCTTTGATAA  
TGATAAACACAAAAGTTGGTGATTTCAATCAGTAGATTATCGAGTGATGCATACATTGTCACTCCATCAATCACATC  
TAACCTACCTGATGGATTGAAAAACTTATTTATTGGATTGTTAAGTTTCATATATGATGTATCTGATTTAACCCCAT  
GCTATTGGGAATGATGTTGTTAATCTCACCTCCCAATAACAAATTTGGTTCACTATTTTATGCTGACAAAAATCAGCAA  
ACTATCGACCAATTTACAAAATGCCACTGCTGGGTAACTAAAGTATCTGAAGAAACTTTGAATTCATAAATTT  
AATTAATGCATTTACTGGTGAGCAAAAGGAATTAAGAAAAATATTCTACCGCTTTGAGAAGGGTAGTTTCATGTTGC  
AAAAACAAGAACATTTGCTCAATCAAACTATTTCAGTATCTATTTATTTCATTGTACCACACTGGTTATTTGGCATG  
TGTGGCCTTGGCAGTTTATTTGATGACAAAGGTACAATGTCCAGCTGGACATGTGGTGGCAATTCACCATGTATCT  
GGAAATTCCTCAATTCAGCATTTACAGTTTAACTACTACATATTTGGAAATTAATGAAAGGTGCCGGTGTCTGT  
TAACTTTTTCGATTGATCGATTATAAAAACAAGGTCCCTGCTATCCAAAGGAGAAAAAGTGAATCATGTGAGACCC  
TACTTCCGTCAAAGGAGATATACAGTTTAAATGATGTCCACTTATGTTATCCAAACAGCTCCGGAATCATCGATATT  
TGACCATTTGAATTTCAAGATTTGTTGGAGGAAGTACTATTTGATAGTTTGGCCCAAGTGGTGCAGGAAGTCAAC  
AGTTGCTTCTGTTATCTCTACCGCTTACGATATACAACCTGGGTGAATTTTAATTTGGCGGCAAAAATATAAAGA  
TATTCAAGTCCGGGATTTGAGACGTTATATATATCGGTATTGTTCAACAAGAACCCAGTGTATTTGTTCAGGGACTAT  
ATTGSAANAATATTTGTTTATGGGTTGACTTCTCTGAAATCAACAGGTTGACCAATGCAGGATATTATCCATCTTTT  
CAAAAGCCCAATTTGTCATGATTTTATTTGTTACTTTCCCTGATGGATATGATACCATAATTTGGGAACAGAGGTGC  
TTCATTTATCAGCTGGTCAAAAGCAACGTTATAGCTATTGCTAGAGCATTTGATTAAGAACCCAAAGTTTGTATTTT  
GGATGAAGCAACTTCTGCTCTCGATTCAAAATCTGAAAGTTTGAATTAATGABACATCGAAAAATTTGACAAATTA  
ACCGTCAATGACAATAATTTCTATTGCCCATCGATTATCAACCAATTTCCAAATCGGAGTTTGTGTCTCTCTAGG  
TAAATATGGCCAAGTCTGTAACAGGGGAACTTGTTCGAATTTATTTAGTAACTCTGATTAGAGTTGTGCAAAAT  
GTTAGATGAATCTGCAACTTCACAAAGCAGCAGCGGATCGACAAGAGGAAGAAGAGGAATTACAAACAAGAGATCG  
TCATAAAACTCAACAAGATCAACGAGAGCATATTATTCGAGAGGCAGAGAGATCGAAAAATGAACAAATTAATA  
TAGTAAGGCUAAGAATCTAATGAATCAATTGCCACTGGATATGAACACACAAATTAATTACTTACAGAAATCAATATGA  
AGAAAAACACCGCTGATTAAATTTGAGTTTATATCTTTCTCTCTTCCCTTCCCTTATATCATTTGATTAATTAATTTG  
AAAAATGACCTTCTTATTTTCTTTTAAATTTAGATTAGAAATGCAAAAAAAATTTATAAATATATATTTATTCCT  
ATTCPTAAAGACAATTCAAATTTGATCATTTGTCTGATGATTTCTATATTCATGAAATTTCTATCTTAAATTAAT  
ATTGGATTTGAAACATCTTAATCAAAACATATAAATTTCACTTATATAGGAGGAGGCTGTGGGAAATTTGTTAAT  
TATCAGTTCTTTCAATGCAACTTGGTTCCACTTGTTTTACCATCTTTGAAAGTTTAACTTTGGCTTCAACAAATC  
CTCTTTTTCAGCAGCAGCTTTGAATCTCTGTTTAAAGACTTTCTTAAAGTTTGCAGCAGCAATTCCTAAAGCTT  
TGTATTAATGATACACAGCTTGTGTTGATGACAGACAGCATAGTTGTTATTTATTTATGATACATAATTAATCAC  
TGTGGGTTGTGAAAAATGTAATAATTTCAAAATTTGAAATTTGAAATTTTCTCTCTCTTTGATTCTTTGTGAAAG  
AAAAATTCGATTACCTTTTGAACATGAGACACACCAAGTTTCTTTATTTGGTTGAGAAAGATTCATGCAACAT  
GGTAGCTTTGATTTCTTTCTCTCTCTTTCACAGCTCTTTCTATTATGAATCTAAATTTACTATTAATTTATTT  
GGATATTACTATTTCTACAAGTCTATATACTTAAC7AAGATTTATGTTTTCTTTCTCTCTTTTGGTTTGGATTAT  
GAGAGGCATTACTCTCTTTATGTTGACCCAATTGATAAAATCGAAAAACAAGAAGGTTGCAATTTGCTTTTCAG  
ATTGTAACACCATTTGTTTAAATGAGTTGCAATTAATTTCAACAATTTGCTTGCATATTTGATTTCATCTAAATTC  
ACAAGTTTTCTGCAATGATTAATACAACCTTTGATTATACTTTGTACAAC7GATTTGATTAGATGGTTTGTAGTGG  
TTGGCTTTGTTTGTAAATTCCTCAATTAAATTCATTAATTTGATGGTAATATCTCGATGGATCATCATTAACAATTT  
TCTTTAATTTCTCACTGTCAATTTTAGTTTGTGAGATTTTATTTCTCANTAAATTTATGACCTTTAACTCCCAAT  
TCTTATCTAATGTCAAAATCTCATCAATTAATCAAGGTTCAATGAATGCCAAATTAATATGCAGATTTACTCGGA  
CTTTATTTAAAGTCTCTAATAAATCTAATACTCGATTCTTTGAAGAAATCATATTTTCTTTAGCTCTTAANAAT  
CCAATTTAGCTTTGTTTACCAGTGGCCAAATTAGTTATTTGTCCTTGTCTTTTGAAGATTTTUGATAATTTGAT  
CATCTATTGCTCATCTTTGTTTCACTGCTCAATTTGAATCAGATTCAATCATCATCGGAAGAGTCAATCACT  
CATCAAAATTTAACTTCACCTGATTTCTTGGTGGGGATTCTTAAAGCTTTGAGCTAGTTTAAATTTAGCTTTGTTT  
CAATTTCAAGTATAGTATCTTCAATGTTGTTGTTGCTGACTCACTGCAATTTGCTGCTGCTGTTGTTCACTATCA  
TATCACTTACCTATCATCTCTGTTGTTATCTTCTGGCTTCTTGGCCCCCTTCATCTCTCTCTCTCTCTCTCTCTCT  
CACCGTCACTCTCTTGAATTTCCCATCTCTCTCAAAAAGTTTTCTTGGACCTTGTATTCTCTCTTGGCTTCTA  
ATACATCAAAATTAATAGTTTAAACATGCTTCATTTGACAGTAAATTTCCCGATCTCATCAACTTGACATAAAAGT  
TTTCCCAACTAGAACTCACAATTTTAAATAAAGTAGATTTCTTGAATAAAACTCAATACAAATTTCACTCA  
ACACTAAATTAATCATCTACTTCTTCTCATCTTCTTCTGTTGCTATAATTTGTTGGCGGTAGTGAATTTGATTTCAA

202/251

A T A C T A A T T T C A A T T C A T T A A T C A C C T G G A T A G T C T C T C A T C T T C C A T A T A C A A T T G G A T C A A A C A C A T T G A A A  
 A C A T T A A T T C A A A A T A I A C A A T T T A T C I G A G A T T T G G T G T T T A A T T C A A T G A T G G T G G A T A A T T A T T C T T C A G  
 T T T C T T G T T T A A C T A T A G A T A T T T C A T C A T C A A A T T C A A C A G A C A T T A T T T T C T G G A T T C G A G A T A A T T T G T  
 T A A T C A T T C T A T A C A A A A T G T T G A C C A A G T T T T A T A A T T T C T A T G G G A A A G T T T C A A A G T A T A A T T T C T G A T A  
 A T A T T G A A T T C A A T T T T T C T T T A C A A A T A G A T T G T A A A A A T T T T G A T A T T T A A T A T C A T T G G T G T C G A A A A A T G  
 A A T A T T G A A G T A A T T T T G T T A A A A T A G A T T C C A A A A C A C T A T C A G A T A A T T T G T G T G A T T A T T G T T A T T A T G T T  
 T A A T T A A G G A A C A A T T T T A C C A A A A C C A T T T T A A A A T A T T A T C A T A G A A T T T T A T T A T T G T T G C T A G T G T  
 C A T C C A A A G T T G T T T G A G T T T G T A A T T T G A T A G A A A A T T C T C T A T A T A A T A T T T C A T A T T G A T T A A C A T T T G  
 T T T T T A T T T G T A A A A T T T C A T C A A T G G T A T G A G A T T T A C T A A T T A G A T C A A A A T T C C A C A C T C C A C C T T T A G A T T  
 C A T C T A A A A C A C A G T A A A C A A T A G G A C C C A A T T C A G G C T T G G T T T C T C G A A T G G T T T T A A C A A A A G T T T T T A  
 A A G T T T G T T G A C A A T C T T G T A T A C A T T C T C G T G A C G A T G C A T G T T G A T T G A T T A A A C A T C T C A T A A A A T T T G  
 G T G T A A A T A A T A T T G A A C C A G T C A C C T T C T C T A A G A T G T G A C A A A T T T A G T A A A A A T T T C A A A U C U C C A A T  
 A T T T A C G T T C A T T A G A T G A T T T T T C T G A A A A T A A A G T T T C A C C A C A C A C A C T T T C C A G A A T T C T T T T A A T G A A A  
 C A T A T T C T G G T T C T A T T T T A C C A C G T T A T T A T A T A T G T T G G T G A T G T G G T T T T C T T T C T T C T T T G A A G T G A  
 C C A A C T G A T T T T G C A T T T C A T C T T C A C A T T T T G A A T C A T C A G C A A C T T G A T T G A A T T T G G C A A C C A T T A A A T C C C  
 A C A C A A T G G T A A C C G A G A A T T C C A A C T A C T C T T T G T T G A T T T T T C T T C T T T T G G T C A T C C C C T G T T T C T T C A T  
 C A C T G A T T A C T T C G A C A C T T T T T A A A A C T T T A G C C A A C A C T G G T A A A T T T C C C T T A T A G A A T G G A T C A C U A T T T T  
 T C C A A T T T G C T T T C A T A T T A G T T A C A T T T T G T G A T A A T T C C C C A C T T T G A G G A A C T G A T A A A T A A A T T G C T A A A C  
 C T T C A G T T G A C A A A T T C A A T C C C A G A T A T T A A C C A T A T T T A A T A T C T T C A T A T A A A T T T T C T A C T A T A T T C A A  
 C A T T A C T A T A T C T A A T A A T T T A T A A A T T G T A C A A G T G A A A A T C C A G T T T C T C T A A T C C A A T T T T T A A A A T  
 T A C T C A A T T C C A A T T A A A A T T C A A C A A A T T G T A A C A T A T C T T C C C G T C A C T T T T C A A A A T A A T T T T G A A A T  
 T A A T T A A T A C T T G T A A A C A A A T A G C C T A C C A A A T A A A A C T G C T C G T T G T T C T T A C C T T T C A T T G A A C T G G T T A  
 A T T T T G T A G T T T C A A C A A G T A A A T C T A A A T A T T T C C C A A C A G T T A A A G T T C C C C G A T T A T T A A T T C A T T G A C A A  
 C T T C A G T T A A T G C C A T A C T A A A A C C A A A T T T T G C T G A T T G T C T A C T A G T T A A A T C C C T T T A A A C T A T C T A T T C A  
 A C G C A T A T G A C C A T T C T T C T T C A T T A T C T C C A G C A A C A A T T C T G A A A T T A A C A G A G T G G C T G C A T T C A A A C G T T  
 C T T T T G G T A A T T C A G A A C C C A A T T T A A A A T A A T G A T C T C T C A G G A C T G C C A T A T G C T C T A A A C C G T T A G T T T T C  
 T A G T G A G T T T C A G T A T T A A G G T A G T T G G T G G T T G G T T C A T T T T T T T T G G T C C A A T T T G A A C G G T T T T T T T  
 T T T C T C T A C T T C T C G A T G C C T C C A A C A A C C A C G G A C C C A C C A T C G C A G A A A A A A G A T T T A T G G T T A T T A C T T  
 C T A T A G T T T T T T G A C G C G T T T A A C T C T T A A C A C A C G A A T A T T A C A T T A T G T T G T C T A C A A A A T T C A C T C T A C G G T  
 C A C A T A A A T C A T C C T A G C A T A T A T C T A T C A A G A T C C A A G A A C T C C T T C A A T C T T T T C A C G G C A G A T T C T T C T G  
 G G T T A A T A A T C A A T T G G A T T T A A C A A T C C G T C G A C C T A A A A A T C A T G C A A G C T C A T A C T G A T A C C A T A C T T A  
 C G A T A T C A A C A A T T C A T A A T C A T T T A C T A A C C C A T T C T C G A G A T A A T A C C A T T A A G A T A T G G G A C G A G T C G T A T A  
 G C T G T G T T T T G A A A T A C C T T C C A A C C A T T C A A T T T T A G T A A T A T T T G T A T T A T A T A T G A T T T A T T A A T T A C T C  
 C T G C A G A T A C A A T T C T A A T A A T T T G G A T G T T T A T A A A T C G A T A A A G A T T G G C A A A T T A C A A G A T A A T T A A T C G G  
 A T T T T G A T G T T T A T A A A T T A G T T A A A A A G G T G A A A T A A T A G A A G A A T T G G A T C T T C T C C A A C C A G T C G T A A T G  
 A T T T T G G T A T A A T A A T G C A A A T G A A A T C A T C C A C A C T A A C A C C A C T A C C A C U A C C A G T G A G A A C A A T T C T G A T T  
 A T A T C A T T A T C T G C C C T T T G A A A G T G G T G A T A T T G E A G G C T A C A G T T G A T A T T A C C A C G G G C A A G A A T A T T A T  
 C A A C T A C A G G A A A C A C T A A T G A T A A A A C C C T T A T T A T C A A T C A C G G A A T T T A T T C T T C A A T A T C A T A A T T C A A  
 C T C A T G T C C C T A A T C C A G T C A T T T C T C T A C T G A A T C T A G A T T C A G T G T T A G T A T C T G G A T C A A C A A C T A A T A A A G  
 T G A A T A T C A T A G T G A T C C C A T T G A A A T A T C A A A A T C G A T C A T T C A G G A A T T C A A G C A A T T G T T T A C T T T A A

YFL271W\_homolog\_1 50aa PathoSeq: 1..50 (SEQ ID NO 658)

MSAYKQAGVS(LN KALAIAAQ(LRNSLKPFKAAAEKRGFVEAKV)TFKDG

YJR115W\_homolog\_81440bp PathoSeq: 1..81440 (SEQ ID NO 659)

T T T G A T A T C A T T A A T G A G G T T T T A G G A A T G G T A A T T T C T G A A A G T T T T G T G A A G T C G A C A T T A T T G A T A A T E A T  
 A A A A A G G T T C T G A T A T G A T T G A A T A T A A T A C A T A A A T G A A T T G A T T A A C A T T A A T T G A G C A A A T A A A G A G T A A G  
 A A A A A A A T A A T T G G T T G A T T T G G G A A T A A G G A A A G G A G T G G G G G A C A C G A G G G A G T A A G A A A A C T T A A A T  
 A T A A A A T G G T C C C T A T A G A A A A A A T A A A A G G A G G C C A T T C A A A T T T A A A C A C A G G T T A A A T T G T T G C C G C  
 C A A C A T A T T G T C G C G G A G A C A C A G T C G G G G T G S T A G T A G T A G T A T T A C T G G C G G T G G T G G T G G T G C G T G A C  
 C C T A T T G T C T C C C A C T G G G A A T A T T G G C A T G A T T A C T A A T A A A C T G C G G C T A C T A T G A T T G G G T G G G T G T G T A  
 A A T G A C C T C A A G G A C T A C T T A G T T A G C A C C A A A C A A A A A A A A A A A A A T A A T G A C T G T G A A T C A A C T C A G C T T T A A A C  
 T C A T T T C T T T T T C G C A A T T T C A G T G A T A T T A A T T G T T G A A A T A T A T T C A T A A T C T A A A G A C A A C C A G G T T  
 G A A T T G T C C A C C A C A A T A A G T A C A A G T A G C C A C A A A T T G A G G T A T T C T T A A C C G T T A A T T C A T T C A C A C A C T  
 A C C A C A A A G T A C A G C C T T G G T T G T A T T G T C A T T T T A T C G A A T C G G T C T G G T T C A T G G T T A G T T G A T T C T T G A T C  
 G C A T T T A A A G C A T G G A T A A T A A T T G T T A C A A C A T T T G A A T C T T A A G C A A T G A T A T C T A G T T A G T A T G A T A A T G  
 A C T A C A T T T G T G T G G T T G T C C A C C A A T T G T C C T A T T A C C C A T A T G T T G G G A G A T A T T T T T G A A T T T G A G A T T C  
 A G A T T T T G T C A T T A T G A A G A A A A G G G A C A A A C A A A C A A A C A A A T T G T G C G A T T T T A G T T C T G T T T T G G A G A T  
 G A A A A G T T G T T T C A A A C A A A G T T T C T G G G T T G T T G G T C A A T C T T T A A G G G T A A G T A A A T T C C C A A T G T T T C C A A  
 A C A A T G A T T T T T G T A A A A A A A A A G A T T A C T T A G T A A T T G T T A G T A G A C T A T T T T T T C C G T T T G C C T T T T T C



204/251

CGGGTGTGTGCCCATAAAGGAAATGATACTAAACATCATAAATACATATTATTTATTTTAACTTTTGTGT  
CATTTAACTTTTFTTTTFTTCCCACTTTTFTTTTCCCTTTTCTTTTCTTTTGGGCTTTCGTTTCCCTTTTCCCT  
GTTAAAATTACACTAAAGAGCCAAAAGACTTTTFTTTTAAATATAAATATCCACAGAATTCCTTCGAAGATAT  
CTCAACCACCTTCAACAAATCATTTTATTTTATTTAATTTTATTTAATTTATTAACAATCCTTCTTTTATTACA  
CTTGTTTTCCCTTCATCTTTTGGTTTAAATATATATATATATGAATAACAGCCCAACTCATATTTCACTTGATTA  
ATTATACAACCTCAGTTCAACTCAATGTTACAAATCTCCATTACATATACCTTCAGAAAGAGAAGACACTCTAATG  
TATCTTCATACCCAACCTGTCACCTACTTCCACCACTGCCACCACTTTUACTTCCACTTCCACTTCCACTTGCA  
CTTCCACTACACATTCCTCACTGAATACCACTTACCAACACCAACATCAGCAACAGCTCCAATACCAAGTCCCA  
AACGACAACGCAATCTAAAGCTCTCATGTCTGGTATTAAATTAATAAATTATACAAATGCCAATCAAAAATTGATC  
TTTACAAAGATTCTGGATTAAATGCGAATTACAACAATTGATAGAAACAACTGTACAAAGATTGAATCAAGAAC  
CTAAATCAATACATATGAATATTCTTCAGAAATCATTTAATGAATTTATATTAAATACCTCCCAATCATCTACAC  
CTTTAAGATTATCTACACAACCAACATTAAATAGTCACTCTCGGAGGAAGTTTCCATACCTATAGATGATGAAG  
AACATTAACAATCTTAAGAAAATTAACAATTTGAGACTCTTAAGAGAAAATCATAAATTAAGCAAGATAA  
CTACTCCACCAAGAGCTCCAAAGACAAGAATCATTTATTACCTGGTTTGAATTTCCAAATTTGATTTGAAATGA  
CTGAATCTGCTGGTTTAGGTTTGAATAAAAAAGAATAATGAATTTGATGTCATGTCTGCTCTGTCTTGTCT  
CTGTTCGATTGTCTACCTTTTGTTTAATFGACTTAAACAAAATAACCTTCCCATCTCTCCCTTCCCCCTCTCCCC  
CTCCCCCTCTCCCCCAACATACCATACCCTTATTTTGTATGATGATGATGATGATGAATAATGAAGCTCACAGAG  
CATATGAAGATTGACTTTTCCATATCCAGAAAAAACTATTAAACAAAGAGACAAGTAATTAATGTTTGTATC  
AAATTTTCTTCAACAAAATTCATTTCAATTTAATTTCTATACTTAATTTGAGAGATTTGATTAACCCATAATA  
ATAATATGATGAACAATCTACATTTTCTATCTGTCTTAAATGCTATTTTCAATTTAGTTTGAATTTGATTTGATTT  
TGTTTGTCTATCTATTTCTTTATAGATCTTTTAACTAATAABCAATCTTTTGTTTCTACTATATGAATTGCT  
CTTCAAAAGTCACTGCTATAGAGTTATCTGACAATTGGTAGTTTGAACAGTTTTTGAACAGATAAGGTCTTATA  
GCACAGTTACCTTACCCACCAATTTGATGATTCTAGTAATGTAGGACAAAGTAATAATCTGTAAATATAGCTTAAA  
AAAATTATAGATATGTAGAAAGTGGAAAACTTCTTTTGTGTGTGATTTTGTAACTTATATTAATAATATCTCT  
GCTTATATTTTGTATACCACCAATCATGCTCTATTTTGTATCATCATATAAAATCTTTATGAATATTGACAA  
AAGCCCAATAACAGAGAATTCACCTTCTCTAGTTGGATTCTTCAAGATGTTATAGATATTAATTTGTTATTTG  
TAAAAGTGTGTGTGGACCAATTATTGATCAATTAACCTCCGTTTCTTTTCTTTTATTTGATATATTAAGTATTCATTG  
ECGTCTGATAGTCTACGATATAACTACAATGCATTAGATCACCACCTAACAATTGATTTCTTCGCTCTCTTTT  
CCTCTTCTCTCTCTTGAACACGCAAAACCTCTGCTTAAAGGGAATAATTAACAACCTAATAATAAACCTATGGCTT  
GT  
ACCCGAAAGTAATTTGAATCATCTAATAATATAAATATTACTTTTCTGGATCCCCCCCCCAGGAAACCAAT  
TGTTTTTTTGAGTGAATTTCTGAGCTGCGACATCCCCACAAAATTGATTTGAGCTCCACCAATCACACCTCAC  
TTTCAATCAGGCTAGTACATGCTGTAGTCCCTTGATGGTCCCATACGCGTATCATTTATTTCTACTTTTGTGGT  
CCCTATCTAATTTTGTGTGGGAGAGGGGTGTGTGTGTGAGGCACTTTATTAATTTCTTGGACCTGATTTTAGT  
TTTCCCTTTTGAATTACATCAATAATTTTCTTAAATAAAATATATCAATAATAAATGATGGCTTAATTTGT  
GATGGTAACCAACGAACATCTAAGAAATTGTTAATTAATTGTTATTGTGGTGTGTGTGAAGAGAGGAAGAATGT  
AAGTTTGAATTAAATTTAGACGGTGCTTTTCTCTTGTTAATTTAGTGATAAATTAGTTTCTCATAAATCTCTT  
TGTTCTGATAAGTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
AATCTTAGTGCATATTAACATAAATTTGACAACTGATAATCTAATTTGATTTTACATAATTTGATTTTGGAT  
TTTGAATTAATTAATTTTCTTTATGAGGTGAGATGCTGACCTTGACAACTGGCTTTTATTAATTAATAATTC  
CTTACACACACACATCAATTCATTCAATTTAATCTTTTGGAAATATCAACCAATTTAAATTAACCATCAACGA  
CTACTGTCTTGGCTTAAGTTCAAAAAATACCAGGAATCTAACCACCAACAAAGACCAAAATCGGATTTGATAAA  
TCTTCCCAAAATTCACACACCTTATTATATTATTCACCAACCAATTTGTTCTGTGGATCAATCTTTTGTAGTTTAA  
TCTGGATTGCTATGTGGATCGAAAGGGGGAGGGTTTGGGAATTTGGCCATAATCTATAAGAAATTAATTCACAAAA  
ATTTTAATTTAATTAATTAACAGTAGTCAATTAATTTCTGTGGTTAAATTAATTTCTACATACAAACATGTGGGA  
AAGGGAAGAGGAGGGGGGGTGGCAGGTGATATTGTCCCGTGATAACATAAGATTTCTGAATCTATCTTGTGCTAAT  
TGACCAAAAATCTTATTTCTTCACTATTGATCTCTGGATCAATATCTCTAATTTTTTCTGAACCTAAGAGTAC  
GTATATTTACATCACTCATTTCCCAATACAGTATAAATTTGATTAATTTCTATTTCTCTTACTCACCTTTGATTTA  
TATTTTCACTGAATATAAATGTGGGGTTATAAGGGGGGAGGATCAAAACATCTTATTATCCGCTCTCTCCCTTT  
TATTTCTTTTAAAGCCCTCTAGTGAATTAATTTTAAATTTGATTTTAACTTTAAGAAAGAGTATAGATCTAACAC  
AATTAAGATAAACTAGTAATTTGGTAATTTGATTTGAAGTTTGGGAAGGAACATATATTTGTCTTTCAATTAACGA  
GACAGAAAAACATAACCACTACTCTTAAATGTAATTAATTAAGGCTTGCTAATGGTTTAAAGAGCAATTTG  
CCGCTCAAAACATAATACATTTCTACCTTTTCAATAAATCAACACCTAAGGATTTCAACATTTCTTTACAGCAGC  
AACCACTTTCTTCTCAAAATACCTTCTGACCACTATTTTGTAAAGAAATTTGGGGCAACCAACATTTCACTCAGGTTT  
ATACTATCAATTTTCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT  
TTCAGGATCTTGAATTAATCTCTTGTGGAAACCAATCTCTGGGAATCTAATAAATTAATAATCAAGTATAAGA  
TTCAATTATAAATTTTCTCTTATGTCAGCAACATTTATTAAGCAAGCTTCAAGAAATCAATCAATTTCTTTTCT  
CACCATAAAATCACTATATTCTCTCTTAATGTATCTCTTAATCTATTTCAATTTCTGATTTCTGAGTACAGTATA  
ATGTTTGGCTCCATCAAGATTCAAAATCAATTTCTGTCACCTTTTAAATCGTTTCTGATTTGAGAAAAATA  
TTGACACATCAGATGATTTCUATCAGCAATTTGATAAATTTAGTAGUACAATCATAGCTTAATTTAGAAATTCGTTAA

205/251

TGGATGTGTGTGTGTCGGTAAATCAATGATTTTGGCACCTTCATTTTSCAATTTTCAACAACAATATCCATGCT  
TCTTTAATTTGGTGGGATACCCCTAACTACACCATCATCTCTAACAACAGCAATAGTCAATTGATTGATTTTTCG  
TGGGCTCATATACACGCCAACCAATTCGTAAACACACCCGATCAAAATTCACGGTTTTCATCATTTATATAACT  
TTTCATCCATAGTTCCAAATCATCAATACTTCTAGCAACTGCTCCTATTACACTTGGTACTGACTCCTGACCAATC  
TGGCCACACAGCTATTCCTCTAGCAGAGATTCTTCTTGTGCTTGGACGTAATCCATGACAAACAGAAATTCCTTC  
TGGAGATCTAATTGATTCGCCAATATCACTACCAACTCCCAAAACACTGCCACCAATGAAACGACTGCTCCTTC  
GCCAGAGGAGATCCTCCTACTTGATAATAATAAATTATATGGGTTTITAGTAAATCCAGTTATATTTATCCCGGA  
ATCCAAATGTAAAGCGCTTGTGGTTCATTGGTACGCATGTAGAATACTGCTCCCAACTGAGATAAATTTGALT  
AGTCATAGCACTCTTTTTCCTATATTATCAATCATGCCAACGTATCCACCATGAGCAATTTTACCTCTTATACA  
AATATGTTCTTTAAGTGTAATGGGAATACCATGTAAAGGCCCAACTACTTTATCATTTTCTTGTAAATATTCAATC  
TCTTCTCCGCGCTTGTCTTAGTCTCTTCAATGAAATATCTACAGCAAAATTTGGTGAATTTGGTGGCAATGAT  
TGGTCTCTTGGCAAAATGCTTTAAATACTTCAACAGCAGTATACCTCTTGGATGCCATTTTTCACAAGTAACCT  
ACCCGAGTATCGGTATCTCAAAATTCCTCTCCGATAGCAACTTTGTGAAATATAAATCGACGGCATTGGA  
TTGATTTTGGTTAAAAATATCCAAATGATTGTGGTAAATTCAAATCAACAATTTTGTGGTGTAGAATTGGCCAGTT  
AAGCCGGTATTGTTCAACCTTGGGTAACCACTACTGGTGTACTTTTCAGAATCCTCATAAATATCAAGAGGATC  
CTTTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
TTTACATTATTGTGGGGAGCAGAGTACAGCAATAAATATAGTTGAATATTTATGGAGTTGAACATTCCTTGT  
GGTACGCAAAATTAATTCATATTGGGATTTCAAACCGGTTTCTTATCGTTGAAGAGCTAAAAAAATTAATTC  
GGAATCTTTGAACCGCTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT  
TTCAATTTATTTCCAAACAGCTGAGCTTGATATATGATATTATTTGCTCAAAACATAAACCATAACTTAAGAAATAA  
TAGAAAAATCTGGTCAATCAAAAGATATATGCTTTCCTTTGATATAAGCAGGAACGAGATCAAAATAATTCAGCA  
GTGAACGATCACACAATGAAGCAAGGGGAAAAAACAATAAATTTTTCCTCTTAAGCACTTGGG  
AGTGAATTCATTATATCAACAGCCCGGACGTCCTCCAGAGAAATGGATTTTGAAACAAGAGAGACAATGATG  
GGGTTAGATCTCTGCTGCACTCTTTTACCCTCAATCCAAATTAACAATCAAGAAATGTTATCCCTATGGGTCCAT  
TATATACTCTTTTAAACAACAACATCAATCTCCTGTTCTAGACCAAAATTTGATATTAGTTTGTGGAACATGCTC  
GAGCAGTATTAAATCTTTATTCACCTATAAATAACTCACTTTGGACATGTCAAAATATGTAATTCATCTTAATCAAC  
TCCAGCAATGGTTGACTCTGAAGCTCAGCCAATTTACCTTCCCAATCTCAATCCAGAATTAACAACAGTAGAGT  
ATAAACTGGTAGATCAAGTCTTTTACCTCCAAATTTTATGTTGTGATACCAATTTTGAAATGATGATA  
TTGAAAGTGGTTTCCAAACAATTAAGAAAGTTTAAAGTGTCTTTGAGTCTTTTACCAGAAGATGCAATTAGTTG  
GGTTCACTCTGTTTGTGAACATGTGAGAAATCATGATTGGGTAGCAATGACAATTTAAGTTACACATTTAAGC  
GGAACAAAGCTACACATTTCAACAACCTTCAATCTTCCCTTGGATTAAATGAGTTCCGGATTGAGCACTGCTGGGT  
TAAACCAAGCTAAGATAAATAATGGGTATGATCAATTTGATTTGTAATATAGGTAAAGATTCTTTACAGCCATA  
ATATTGCGGAATATCAATTGACAAGAATTATAGAACTTGGTACCGGATAGATTTCCTCATATTAATATAGTG  
AACCTCCAGAAGAGCCACTGCTGACAGCAATAAATTTGCTTTGTTATTTGCTAAAAACCATTTTAAATTAATCTGC  
ATCATTTGACTGGTGGTCAATTTAATGGGTGTTATCACTGGTGTATGATCTTTTGGACAGGCAAAATTTGATA  
AATTTGCTAAGAACACCACTCACTTCCCATCATCATTTTAAAGCCCAACAACCTACCAACACCAACCTCATCGA  
CATCTCATCTTCCCAAGGTGATTTAATTTATTCACCAAGCAAAAAATTTTATGAAGGAATAACTTAAACCTC  
TTGTTACCTTGGGGCTTAGTTTGTGATTTTTCATTGGAAGTTATGATCAACTCCGACTTTATGAAATGGATGAAG  
TATGCTATAAAAGAGGTGGTACTGTTGTTTAAAGTATCTTTTAGTACTCCATTTTCAAAAGTTTATATAA  
GATTTTCAAAAAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG  
CTTTAGCACTTAGACTGGAGTTGATTTGAAATTTGAAGGGCTTATTTGGGAATGCAACATGTTACCTTTTAATA  
AAACTGTTTCTGCTAATGCAAAACATGATAAGTACCAATATTCTTGAGAGGGGAAACCAACAGTTGGAATTTGT  
GCAATGCAATCCACAATCAACTTATGCAATTATTTTGAGAACTAGATAGTCTTCTCTCTCTTCAACAATAC  
AATTTCTTTTCCATTATCAACATCCATCAGGTGAGATGAGATTACGTGTACGACAATTCCTGTAAATATTATTTG  
CTGATCTCGATACATCAACTTTGGAATTAGGGTTTGATCAAGAAACCTGCACTAGTTTGGTTGGCCCTGACTCAA  
TAAATTAAGTTACAACCAAGCAATACAAAGTGGCAACAACAGCTAGTATTTGTCAAAACATTTGACACATGGA  
TTGATTTTGTACTCTCTTTTCCAGTTTATACCTGCTGGTCAGATTGAATCTTTTGAATTTGSCACAGACATTTTCT  
TATTTCCCGCAATTTCTTACCCTTAAAGACGATCAACATTTTAAATGCTTTTCAACACCTCAACCTGATGAAACCA  
GTTATGTTAGACATGCTTTATGCCAGGAAGACACCCGAACTCATTTATTAATGATCAACCAACATTTATGCTCT  
ATGATGTAATACATGGGGGCTGTTAGTTGATGAACCACTGCTGAACCAATAAATGAACCTGAACCAAGTATTAT  
TGGACTCTATTGATTTAGGACGATCCAAATATTTGTTTGGATACATTTTTCUAAATTTTAAATTTATCATGAGAG  
CTCAGGTTGCTGAATGGAGAAAGCTGGATATCATGAACAAGAGGGAATATCAATTTTCAAAAGAACTTTGGGAAC  
CTCCGAAAGGCAAGCAATGATGCTTATTAATGGATAGATTCCCTTTGCTAGACTCATTTGATTTGATTAAGCTG  
CATCTCAGGCAAGATTTTAAATGGCCAGTTGAACCTTAGTACAACCTATGCTACAATGTCAATCATCTTATG  
GTATTTGGAGACCGAAGTSAAGTTTTTACCAGATGATACCAACTTACAACTCTTTATCGATCATATACCAACAGTAG  
CTACAGCTAAAAAATAGACAAATGCAATTTATATAATTAACAAATAGCAATTCATTTACCTTTGGCTCTAGCAG  
CCCAATTCCTCTTTTTTAAAGAACTGACTTCTAGCTGGTGTGTTTCTCTCTGAGTCTGATCTATCCATGATAG  
AATCATCTCTGGAACGAGTTGTTCTACTCTCTTCTCTCTTTTAAATGTGAATTTTGTGTTATCATTTGCAAGTCA  
AATGTTCTTTAACTTTCCCTATAAATTCACCATTTTCAATCAAAATATTTAGTTCACTACCTTTGTAATTTGATTC



207/251

CGTCAACACCAAGTACAAATTGGTTTCAGTCTTGTCTTCTAGAACTACTTGAAGGAATTCTGAATGATAAGTAGAAC  
TTGCAAAATTTCAATGGATCTTCAATATTTGGTCACGGATGGTGGTAGCAATCTAATGAAATTTGCAAGTTTGGATC  
TCTTATTTGTATCACTTCTGTGTGCTTCTACTGACCTCTTCTTGTTCGGGGTATCTTCAGTAACCTTCATCAACCT  
TTCTCTTGAGGGATGCATCAAGTAATACTGTATCTGGACMTTCCAACTGCTATTGTCAGATGCCAIGTTATCAAACT  
TTTCTATATAACTTCCACAAAAAAGAACTAGSAACAAGATCTGATAAATCTATTGAAAAAAGAGTTTGTG  
GGAGAAAAGAAATGAGGAATCAAGTAAACAAACAAGCTGGAGATGTCGGCGGAAAAACATTCAACACGGCTCCGCC  
CAAGTAATGGCTGAACAGAGAGGTACATTAAATGTTTCATTGAAGAACATTTCAAAAGCTGATTTCATGTATT  
TTTCTGTTTTTATTAAATGGTATTATGCTTATAAGTGGATGAGGAGGCTATGGTTTCTTAATTAGGCGCTTTTT  
AACTATTACTTCATTGCTCTCATTTTTTGACAAAATTTCTTGGAAAACCTGCAACCAAAATTTCTCATGCCAACAAC  
TTTAGTCAGAAATTTCTATCAACTGCTTATAAATCTGCTATTAACACCCACAGGATTTGTACATTTCTAGAAGCTAT  
AGTATCAAAAAGCGGAACCTTACTAGCACTACATACAACCTGGTGGTGTATGATCACACABATAGATTGACAAAAGCTC  
GTCATTGAATGGAATGCCATACATTGACTTTCTGCTTAAACAATAGATGGCGCACAAAATTTAATATAGATATAA  
CAACCTGAGAACCTCAATAATAATAATAGTGAACCTGCAAGAGAGAAAACCTTCATTGTAACAGTATACCTTTCTCTA  
AAACATTAATAACACATTTGAACATTTCAATATTTCATAGGCTGATTAGATTGCGTGAACAAAATCATTTGGTCT  
CTGACAGATTTTTTCTTAGGGTGGTGTAAATTTATCTTTACTCTATGCGAGATTACGAACACTTCCCCCGCTC  
CTCCACCTTCAGTTCAATCAAGCTATATATCACTTTTCTGTTTAGTTAGTTTCAAGAGATATAAGATGTTTAAA  
CTGAAGATCATAGGGAAGGCCATTTTTTTTTATCGTGTCTGTTTATGTTTATTAAGTAAGTTTTATTTTAG  
TTAAGAAAAACAAAAACAACCAACACAGCATCTCAAAAACAACTTCTTGGTACTACCCTAAATTTTTTTTT  
ATTGCCATTTCTGTTTTGGTGTGTTGGCATCAATCAATAATCTGTTCTAGTTTCACTTTTCCCCTCA  
CATTCATTTAATTTTGGATATTTTCATTCATTAAATTGATAACACTCAACAAATCAACAGCTTATCCAAA  
ATATAACATTCACACATACACTTTTTTTTTTCCACACTCTTTTGAATAGATTTAGTACTCCCCCTCAACACACT  
CTTGGCAATAGGAGATAGAAATAACATCTTATACAGCAACAGAACTACAAACCCCCCCTTCATTCAAAA  
ACCAACCAACCAACCCACAGAAACATGGGTTCCAAAAACAAACGATATAGCTATTTACAGCATCAACGAATCAT  
CATTTCAATGCAAGAAATGAGATTAATAAATACCATTTAGATGTATCAACATTTGATGTTATAGAGTGAATAAT  
TTCCGTAATCAACACTGTTCGACTTTGTTTGGTATTTTACATGTTGGTCTTAATCTTTTATCATTTGCTATTA  
TTAGCAACAGATATCTATTCTTTGCTTAAATATCTGTATTCATAGATGGGCTAGTGTAGATTTACAGGCTTAC  
GCATATTTCCATTGGCAATGGATTTTCACTCATCTATAAATTTTCAGTTTGTGCTACTATTTTATTCATTTGATA  
TGGGCCATACATATTTCCACCCACAGAAATATTGCTTGGTTTTATCTAAATCCCATAGCCAAACACTCTATCTG  
ATAAATATATAGATAATTTTTGTTTTATTAACAGTATCAACGAAGCTCATTTTTTTGATTTGGTGTGTTTTTTA  
ACTTATTATGAGATAGATAATGCAATACAAATATTAGTGGCTGACACCCCAAGACAAGTTATCAATATATAGCA  
TTAAGATACATAGCCACTGGTGGAGAGTTAAATAACAATATTTGAATAACATTGAACAAATTTGCCAATACAAAT  
TTCTACTTTGCTATATTATTTTGAATTCATGTGTTTATCTGGTGTCTATCTATCTATATCTCTCTTGGGTTTGT  
TTTGGGATGCTTTGTTACATTTCCATTAAAGATCTCTTTGAGCAACCATGCTTATAGAGATTTTAAAGATTACGCT  
TGTCACTTTGATTAACGAAAGTATTGCTGATGCAGTTAGGTTGCAACCATAAACCAAGAAAGTGTGTTGGAGCAA  
GGTATATTATCGGAAGAGAGAAATTTGCTCAATTTGCTGTGTTTGGAGATCTGCTCACCTGCTTATAATGACTACTCA  
AAAATTTTTTACCGTACAGATACCACTGCCACATTCGAATCAAAATATTCCATTGAATTATAAGAAAGATAGATCA  
AATTCACCAATAATTTCCAGAGACGATTTTGGAGGCCACAGTAACCAAAAAGTATATTTCCCCCATTAATGATCAA  
AATAATGGAATTTGGAAACGCTTAAGTCAATTGAGAGACAGCTATACTCAACCAAGTTATGGTGTAAATAGAGAA  
TCTAAACCAAGTTGATTGATAGTAGGTACGAACACTGCTTTACAACTCCACACAAAGATCAACAGCTTCTGCTT  
TTGAGTGAAGATCAAAACGAATTAATTTAAACAAACCAACGATCAACAGCTTGCACATGACACATCAAGAAC  
CACTTGAACACCCACCAAAACGCTTATCACTGACATTTCAAGAACAAATTTGGTCAACAGAAATCTACCATCTTCC  
TTTTAGCCCAATGAGAAAGCTCTCTCTCCACCATTAGGGCGTGAGATGACACAGAACAGTCAAGACATAAATCT  
TTAACTGGATATGACCAACCAAGTACAGCCCTTACCAAGTCAACACACAGATCATCCACATAGACACAAAGTAT  
AATGATTATGCCGAATCATTAACGAACCCCTTTGGGAATCCAAGCTCAATATATTCAGGATCACTGGATCATTT  
TCAAGACCCGATGAAAACAGATTATACAGATGAGGTATAAATCCGTTATACAGCAGATTAAACCAATTGAAAAA  
TCAACAAACGGAACCTTATTAATTCATTTGAACCTCTCATATCAGACATCCACTGAAACCAAGTTCAAGCTTCTGTT  
ACTGATGACTATCCNATTAATCTACAGGATAGATTACATTTCTCACAAGACGAAAGTAAAGTGAACCAATCAGAA  
GAGGACCAACAACAGGCTAGTCTTACAGGAATGATATTATAGATGCTTTTTAGAAAGATTGAATGCCCACTCA  
GAAAAAGAACCTCTTATCCAGTAAAGAGGATTTTGGAAATCTTTGAACTTAGTGAAGCTGACACAGAAATG  
GACTTAAGTATAGACTTATTTTATAGAAATGAAGGTTTATATGATAGAAATGTCACATTTCTTTATTTATAGT  
AGATAAACAATAATTTTAAACACACATACATGTTTCTTACTCAAAAATTAAGGCTTAAACAATATTGATAGCA  
TATCTACCAAGAACCCACGAACCTTATTCATTCACCTTTCTCTCATGTCTATCAACAGTATTTTGGTTTTCTG  
TATTCCAATTTCACTTTTGTAAATTTCTTCATCACTGATTGGTGGAAATAGGATATCAACCAAGATCATCATCTCC  
ATTTCTTAAATGTATACAAGTACACAGCTAACCTTATCTACTGACGGCAAAATAAGCAATAGTATTTCTCCAG  
AAAATGGAGCTCTTACTCTGTACAGGCTGGCTGATTTGATCACTTTTCTGATCTCTGTAAACGATCATGCCCT  
TTCTTGATAACAAAGGATGTTAGTATCAAAATGCTATCATTTGTTTCAAGAAAATTTGGAATTTTTTTTTTACTTAC  
GTGCTCTACTAATTTACCCATAGCTAATGATTAATTTGTTGTTGTTGATTAACTGATGTTTGTGTTGAAA  
GTTTACCATGACTTTGTATTTTTTTTTCTTCTGTTTTAACAAATCAAGCTGTTTTATGAGTGGACTTTGAA  
AATGTATATGCAGTATTTTTCTCCAAACAACAATAACAACATCGAGTATATCTGTATAGCATAAGAAATTCATGCTC



208/251

CTCATTAACTGTGAATTAAACTTTCGTAATAATAGCATTGCGCTGTAAACATAAAGAGAGTAGAATTAATATACATA  
CAGGTTTTATTAACCGGTTTTTCAGATTATATACAGAACCCTAAACTACTTAAATGTCCTTTTGATGAACCCCTTGATP  
CAGGCTATCTTTCTCTCTTCACTAGCTTUCATTTTATTATTAGTTCTCTAGCTTTGTTAATAGATTTTTCTTT  
ACTATCGTCAACAAATTTGCTCACCATATCTTTAATAGATTGGTTTGCTTTAGGATTATTGGCTTGCATTTCTGC  
AAGACTCAATTTAGGAGGCATACCAGCAATTTTCTTAACCAACTACTTTTGAACAAACTACTTTTGCATAACGGA  
AAATATCGAGTTAACAGCAAAATACAAAATAATAGCAGATGCCAAACCCCTTTAGTAATGAAAATAGAAGCAATTGC  
AACAACTGATGACTTTTTCATACCTGCTGCCATGGCATGTGACCAGTTTCCACCACCTCTTAACAACAGC  
AATGATGGCAGCAGCAGAAATAGCTTGTAAATCCCAATATGGATCAACTTCAATCAAATTTTGAACCAAGCATA  
CCCTTGATCAGAAAACCCCTTCAACATTTATGATTAGCCATTTTCTCAAAGCTTGGAAAACCCATATGCCAATGG  
TAATTCGACCCGACCGAATTAAGTGGCTAATCTCGAAGACCCATTTTCTTTCATAATAAGCTCTTCTTTTTTCCA  
AGCTCTCATTTGGTCAACTGTATCACCAGTCTTAATTTGTTGTAAATTAATTCGTCATTTGTGCTTTTATTTTAGA  
CATCTTAGTTGCATTAGATGATGCTCTCAGATATARTGGAACAAAACAGTCTAACAGCAATGGTAGCAACRAC  
AATAGTACCCCAACATGGTAACCCAGTATAAACATGAGTAACCTTCTAATAATCTTCAATCAAACCTTGTTTGGTCC  
CCAACTTTGAGCTAGACCGAATGATTCGAAATATCCAAATGATCAGAAATGTAAATTTGTAACATTTTCAAGTAT  
AGCAGAGTGGTGGTACCATCAAATGAAGTCAATTTATCTTGGATTTCAGTCCCACTAGTTGTGTGCGATGAATT  
GAATCTCATTTGATGAGTATATTAAGCTCACCCGCTGCCATCTTTAGAGGGAATTCACCCCTAACCGTTTTCAA  
AGATGCTGAAGTTGCTTAAATGAGCGGGTCAACCCCTAATCTAAGCATTTATGGGTGCTAATATAGTTATAGTAAT  
AGTTCTTAGATTTACAGTTTGATCAAAAAATGAAAAAATAAAAAAATAAAAAAGAATTATTTGTGAAAAATTTT  
AAAAGTCTGTCTGTCTTTACACATTTATGATTTGAGTGTCTCTTTTAAAGAAAGTCTTTTTCTCAACCAATGTT  
ATATAGCTGATTTGGTTTATTTGACAGATCAACTCATAGAAATGAATATTGGCGCTGGAATACGACCGGAGGAAC  
TACATTTGAGATTATATTCTCAAGTCAAAAGTCCGTCATTTGGAACCTCAATAACTCTTAAACAGGTACAG  
ACATTTTACCTCATTTTGTTCATTTACCAATTTGAAGAACAGATACATTAATTTGAAAAACATCTTAAATTACTCA  
ATGTACAATTACAAATAATGCTATATTTGAACTGGATAGTTTGAACACATTCAAATTTATTTGTAAGTACGGTC  
AACATTTGCAATCAGAAATTTATTCAGATATTTATTTACAATTTACTTTTATCAATAACCTCAAGCAACAACCTA  
CAATTAATGCAATCACTTTTACACGAAAAATAAGAGTTTCAATGTCAAATGAATTTATGGGCATTATATATGCATA  
AAGTCTCTTATATATGGGGGATTATCTTGGGGCAACAGCATATATCATGAATTAAGTTGATAACGTAAAGTTTTATG  
AACAAACAGTTATTTTACTACAAACAAATAATCTTAAGCCATTTGATCAATGAATCTTACCTTGGTAGCTTTAG  
CATATATATTTAGAAACAAACAGACCGCTCAGAGTTGGTGGCATAATACAGTATTTTCTCTGATTTTATTCAT  
TTTTACGTTTACAAATATATTTACAACTCTTTATTTGATTTTGCAAATTTGAATCATATGCTGAACTTGGAGACCTAG  
AACATGTTTTAAATTTATTTACAGCTTTTGGATTTAATCATAAATCAAAGTGAATGTAAGAAACAGGAATGTGC  
AAGCAGGATGGGAGAAATATACAAACAGACATGAAGCCATCCAAACCAATGAGAAATCCATTTATATACAAAGATT  
CAAAATATGATTTGGATATTTACCCAGATTTATTTACCTCAATTTTSTAATACCGAGTTATTTAATCCATCATTC  
ATAGAAATGTCATTTCTTCACTTAAACTGGACACAACCCAGTTATCAATGGATCTATATCTGTCATGATTTGC  
CAGCTTTGAAACGTTAATCACTGAAAAAGTGGCTACCATGGAATGAGGGAATTTATTCATCTAACAAAAATGT  
CTCATCAATCAATTAATCTTTTCAATAGTTGCTGGATTTATGCAATGTCAATAAACCAATATGGCACTTCAGTATT  
TGAAACATTTATCATATATTTTCCCACTATATCAAGGAAAAATCTTTATTAAGAAATCAAAATTTTATTCGTATT  
TACATGCTACACAAGATGTGGAATCTGCCAAGGAAGTGAATGAATATTTATCTCATATTCATATCACTACATTA  
ATGTTCAAATGTTTACAGCGTAATTAATCTGTTTTGTTCTCTAATGAATCACTACAGTTTCAGATCTCATCCCTA  
GTTTCAATTTGCTTGAATCTTACCAAGATGTTAAATTTGTTGTCATCTCTGATCAATACCAAAATTTTGTAAAT  
TACCAAAAAATACCAAAAAATTTGACTTTTATCTCATTTGATAGTTTAAATTAAAAAATCTTAATTAAGAACTG  
AAATGAAATATAATATAATAATACTACCAATACTTTTAAACGTAAGTTTGTCTTTTAACTTCATTATTTCTCT  
CTAGGGGCAGACATTTTCTCAATTTTCACTCTCTTTATCACTTAAATCTCCACACAGCAATATCTGAGGAGTA  
ATAAAAATATTTCTGTATTTTGGATATCTCTTTAATCTCTTCAATTAACAAATTTAATACTAATAGAACGATTCACT  
GAATCUATATAAACATCAAACTCATCTAAACCTCTAATACGAGAATTCATCACTTTCCAAATACATAACAAATAAG  
GCAATTTGTGAAAAATGATTTTTCACCAACAGCATAAATGATCCACGGTAGCTTTCTTTTTCATGTTACCAAGTTTGT  
ACATTTCAATGTAATGTTTTTTTCCGCAAAATCAAAATTTCAAAGTACCTTTGGAATCTCTTAACCACTAGGCTTTT  
TCAAAAGTTCTTTTTTGCCTCTTGAATTAAGATTGGATTATAGTATGTAAGAAATGAATCTAGCATTAACCTTCT  
GCATTTAAATTTCTTGATSCAGAATCAAGATTTCTAATTTCCCCCTCGGCTTTGTACATTTTGCCTTTGCTTTT  
TCTAGTTGGTCCAAAGCTTCTTCCAATGAAGTTCCAAGAGCACTTTCTGCTCTTTCCMATCAAAACCACTCTCT  
TGATAATCTTGTTGCTATCTCTCTTTGGGTATCATTTAGGGTATATGGTAATCTATCTCTGCTACAAATGTTCTTCA  
GTTTGGCAACAAATTTCTCAATTTACGATTCCTTTACGCAAGTATATCGCTCAGCTCTTTTGATCTCATCTTCC  
AATTCAGTTATCTTGATATAATACGTTTTTAAAGTCTCTTGGGTTTCAATTTGAGTTTCAATTTCAACTAAC  
TCTTTCACAAATTTTCTCGAATGGTTTCATGTTTAACTTTTTGGATTGCAATCTCAACTTTGTGTTTCAAA  
TCTTTAATTTTTTCAATTCATCTCAGAAAGATTTTCTAATAATGCTTCTGTTCAAAGCAACCAATCTACGGATTTGT  
TCAATATTTCTCTTCTCTCTTCTTCTTCCATGTGGTGTATTTTGAATTAATCAACTTCAACTTCCAAATGATCTCT  
AAAGTACTACCAATTTCTTTTCAATGATCTAATTTCTCTGATGGCAGGAGATTACATACAAATTTATCTCTC  
TTGGCATCCAAATTTCAATTTTATACTTCTGGCCCGTCTTCTAATTAATTTTGTATCTCTATGTTCTTCAATCCAA  
TCAAGTTTGAATCACTGATCAAAATCTCAGATATAGCGACCCCAACCTGGCCATTCATTTTGGTAGTATATA  
GGTCTTTGTCTAAGCTCTGTGTTTTGATAACTTATCTTAAGCCGAACTCTTCTGAAAGAACTAAAGAAATTT  
TGGACATTTCTCTCTGCTGATGAATCTCTAGCTTCACTGCCAGATTTTACTATAACATTTTTTTCAATGGAATTT

209/251

ATATCAATCAAAGCATAACAAAATCGTATCATTTCACACATTTAACATGTCTAAAACAGTGGTGAATGCCAGATCT  
 OCTTTACCGGAGCAGTATCAATCTTCTGTCTTCTTGACAAATAATGTGCTACGTATTTGATATTGCTTGACT  
 AATCTCTCCAACCTACTCTATCACCTTCATTGGTAAACAATAAATGANTCCAAGGTTTATTCAAAATGCTAGAT  
 AACAAAGGTTTCCAATTATTCTATTGATTCTTTACATGAATATAGCTACCAATAGGACCGGATTGGCTCTTGCACC  
 CAATCAGGATGTCTTTAATCGCTTTTATCAATTCAGCCATACCCAGAACCCCAAGGCCAATATTTTGATACAGAC  
 TCTTTCTGTAATTGACGCTTTTGGTTTGTAAATCGCAATTTCTGTCTTCATTCTCCCTTTGTGACTTACA  
 GATCTCAACTCGGGATCAGGATTATCTTGCATTTCCACAAGTTGTTTTC/AAATTTTCCAATTGACTTTCCAAAC  
 TCATCAATTCAGAGTTTAACTTTTCCAATTCCTCAGCCATTTCTTCTTCTTTTCCCTTTGTAGTCTTCAATT  
 CTTCTCTCTCTCTCTCTATCTTAGCTCTGGTCTTAGTAATATCTTCTTCAAACATTCATTTCATCAATATTC  
 TTTTCTGTTTCTCTTTTATTTCATTCTTAACCTCAGATTTTCATCTCAGATCTTTTGGCTCGAAGTCCCTCAAATCT  
 TCCACATATCTTTTATTTGGCTTTCCACTTCTTAACTTGCTCATCAGCAGCATCTCTTTCAGGAAATTTTCTCT  
 TCAATTTCTTTTTCACAAACATCAACCTGGTTTGTGGCTGCTCAATTTCTTCCAAAGCAACTCTCTTTTGTGGA  
 TTTCTCTGATCAATTTTCTCTCGATGGTTTGAACATTTGAACCAATAGATTTTGGCAATTCACATTTCCAATTTG  
 TTTCTTAATGCATCATTAGTTCTATGCGCAATTATGAACCTTTGGCAATTGCTTTGTATTCTTGTTTAGCCACCTTG  
 GTCTATTCTTCAAGCTTGACGCACTTATTATCAACACTTTGGCAATTTGTTGCAAACTACTTGTATAGTTTCAAGC  
 ATATCAGTGATAAATGCCCATTCUATAAAATATTATACTTCTTTTATCACTCGATGATGTTAAGAATTTCTCTA  
 GCTTTCTCTTGCAGACAGAGGCGAGTGGATTATCAATGGTGAAGAAACCTTCTAAAGCAATCTCATCCAAAACA  
 CTCTTTTGTGTTGACACTACTTTTCTCTGCTTCAATTTTAACTCTGTATGTATTGGAACCAATCTCTTGTAAATTT  
 CTTTCAATAATGATTTTCTTCCCGAAAACGCTGGTTTATACCGGTTTGACCTTCAATTTTGTAGAACCACTCTG  
 ATTCGAGAAGTAGAATTCACACTTGTGATTAATCTCTGATAGCGCTTCTCTATTTGTATGAGTGGTTTGGCA  
 CCTAACCCCTACAGATATACCAATGAAGATTGCACTCTTCTCTGACCCATTTCTTCCAATAATAAAATTCAACTGG  
 GGTCCCAATTTCAATCAAAATGAATCTGTGGCACATAAAGTTCTTTAAAGTTAATTTCTCAATAACCCCGCTTTGA  
 GCCGATCTGAACCAACGTCATCTCATCATCTCTCTCTCATCATCATCTGCTGCTGCTCTCTCATCTCTCTCATCA  
 TCATCTGATTTCCCGTCCAGAACTCGAATCAGCACCTGAATATACATTTCACTTTCTGATGCACTTTCACTGCTCATTT  
 CTACTAGGGGCTTGAGTCAATGTTCTTCTGTTTCTGGGTTGATCAGATGAGTTAATCAATAGTTTGTACATATAT  
 TCTGACACGCTTCCACCACCTTCTGGCATCGAATAAAGAATTCGGGTCATGTTTCTTTTATAGGGTACACTC  
 ATTTGGATAATAATTCMACTAACNTAAAATATATACCACCTATACACCAAAAGAAGTTTAAATAGASTGTAGATT  
 TGTGTCTCTCTAGATAATTTGATGACTTTTGTGGGTGTTCTGTGTTAACTTTTGGGATTCAATTTCTTTCTGA  
 AATCCAAAAGAAGAAAAGAAAATTTCTGTGAACCAACCAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG  
 GCGTCTCAATTAACAAAAGATAAAAAATTTGTTTGAACGTGACAAGACACGATATGCCCTGCTTACATAA  
 TCAAAAGATTATTAACCTTTCTTTCAGAGAAAATTTATCAAAAGCAAGGCTGCTATCTCTGATGCAAAATACAG  
 GGAGCATATGCTGTTAAGAGGTTTCTTTTCTAGTCTAGTCTGCTAATAATAATGATGTTGGTTGGAAATA  
 TAATAAATTCACAGACAACCTACTACTTCTTCTGCTGGGGGAGGACCAACTAAATTTTCTCTCTCTATTGT  
 TGTTGATGTTGGTTGTTGATGAACAAACAAAAGAGGTTCCATCTCTCTCACTTTGCACTATCTCTCTATCTT  
 AAACCTTACTATACAGAGAGAGAGAAAAGTTTAGTTTATAAGCATCTTTCACTCACTTTTCTCTTTTACC  
 CACTACTACTGAATGCTCTAATTTCCATTAAGATCATAACCTCTTAAATATTATTTTTCGCAATTTTGGGAAAT  
 GTCTTATGTTACCCACAGCCATTTCTCTCATCAAAATATCTCCCAAGTGATGATAGTATCAATGTTTCAGCCA  
 GAGGAAGAGGCTGAGCTTCAAAAGTTGATTTTCAACACAACTCACTGTTCCAGGTTTACATCCATTATATCCA  
 AATGTTCAATCTACTTCCAATTTGATATTGTCAATTTACCACTGCGCAACAGGAATAATGCTCACTGATTTCA  
 ATAGCATTTTAAATTTCAAAATCAAAATTTGATTTCTTCAAAATTTATTTGTTGTTAGCAGGAATTGGCGGTGCT  
 GATCTGCTAAAGTAACCACTGATCAGTGACATTTGCAAAATATGCTATACAAGTTGTTTACAATATCAAAATA  
 GATTCTCGAGAATTAACTAACCAATCAATAAGAGAGGTTGGACTTCTGGATTTTATAGTTATGGAACAAAACAT  
 CTTCAAGATTACCTGATTCGTTTATAGGTACTGAAGTTTCTCAAGTCAATGAGAATTAAGAGATAGAGCCATG  
 GAATTATCTCGTAACAAATGAAAATTTCTTAAACCTGGGTGATGACGATAATGTTAGTTTAAAGAAAGTTGATTTCA  
 ACTCTTCCCAACAAAATCCCAACCTTTAGCTTTGTAAGGTTTGTAGTATGATAATTTATTTTACCGACATGTT  
 TTGAACGATTATTTTAGTATTTATCCCAAGTTGATTACCAATAGTTTACGCAAAATTTGTTCTGAGTGGCCAAACA  
 GAAAATGCTACTTTGGAATCTTTATTAAGATTGCCAAAATGGCTTGATTGATTTATGAAAGATTGTTATTTG  
 AGAACAAATTTCTAATTTGTTGCCAAACCTAAAGATTATCAATTGATCCATTTGAGTTTCTCAATGAATATCT  
 AAAGGTGATTTCAACATGCAATGATAATTTGTATATTGGTGGTTGGCCATTTCTTGAAGATGCTGCTCAATTAAT  
 TGGGATAGTTTATACAAAGATGGTCAATCTTTTAGAGCAGAGAATTATTTAGGTGATATCTTAAACACTCTTGAC  
 GGTCAAGGTAAGATTTTGTAAGATTTCTATCAATTCAGTTGATACCAAGATTTAATAATTAACCTTACTACAG  
 ACATATATAAGCAACATACATAACGATTTTGTATGAAGACGGTCAATTTAATCAACAATTAATAATTAAGAAGTC  
 AA/AAAATTTGCTAATTTTTCATATATTGATTAATTAACAGAACAGATATAATGAACCTACTTTTGTATGCT  
 TACTCAAAACGGTTCAATTTAGTAAACAAATTCAGATCAGACCTAAAGAGTTTCAACAACTAAATGCTCTACAA  
 ATCAATCACAATTAACCTAAGAACAGTACAATACCGTTACATTTTAATGTATACCTAAGTTGACTTCTTCTCTCT  
 GTTCTCAATAAATTTAATTTCTTATCTATTGATGCTGCTGCTGCTTTTAAATATAGGTGACAAACCTTCTGGA  
 TCTATTCTCCCGAAAGTGAGAAAGTTTGGCGTTTCAATTTGGAATAATCGGAACATTTCTTACAGCGCAACAAAACA  
 ACATATCTTATACAGTTTCTCAATTTGGGAACAAAGCTAATACGATTCTTTAATTTATCATTTATCAACAGTT  
 TAAAGTTACAGTAATTTATTTACTAAGATAAAGGAAATACCCATTTAATACAAATGAATGAACCTGGGCT



211/251

ACCCAATCTTCAGTTTTTATTCCTTGTAAACACAGCTAATAATTGTTGAATTTATACAAAACTTTTCAATT  
 TTATGAACATTTCTATGACTTGGCAAATTTCTATTGATGGGCAGTTGCTGAAGTGAATTTGTTGAATCTAAATTC  
 GAAATCAAAATTTCTATCAAAATTTTCAGCACTTCAACTGGTCGATAGTTTTTTTTCACABACAATTTCTTCAATTTT  
 TTATAATAASTTACCAAACTCTCAAATGATTTCTCCAAAGTATTATCGATTTTCTTTGAATTTGTACCAGTGTAAA  
 ATTTCTATTACTGAACAATTTGAGTAATTTGATTAAATATGTTCTTTGTTGGCCAAATCCAAAGAAAAATTTGGAGTAA  
 AAATTATTTATCAAAAACAAATCAACACTTTTAATATATTGATCTGGATCTTGAGTAACAATTCATAGTCAACGCTCT  
 CCCACTTCATTCAAATCTACTGCAGTATCCAAATTCAGTTTGGGAAATTCATAGCCAATTTGTGGGTTTCTTTGG  
 TTAAAATTTGGTTCCATTTTCGTCCTTTGTCGATTCATGATTCANTTTTTTGAAGTAAATTAATCTTTTTTATACCC  
 GATATCACCCCTCTTCTGAATTTATAAACCTGTGAGCTAATTTATCTTAATAATTTCTTTGTTGTCTATAAATGAA  
 TTGTAGTTTAATAAAAAAACAAATCTATATTCAAGTTAAATCAAGGTGGACATCACGGTGGAAATATTTTGGATCA  
 AGCAACAACAAGTCAATCAACCTGTCAACGGTAGCATATTAGGGATGAATTTGTAAATTTTTTCTATACATTTCCA  
 TCCATGCTTAATTTCTCTTTATTTAGATTTTGAATTTATAGCTTTTTGTTGACATCAGAAAGTTTGTGAATTTATCA  
 GAATTCAAAATATCATCAACATCAATACCCCAATCTTGGAAATCATCATCTGTCATCCCCCTCCGGCAAAATCGTCA  
 TATCCACCACCCGGCTCCACAGCACCCACCACCACTAACAGAACTACTAGAGCTATTATCTAATTCAGATATAAAA  
 TCATCAATTTCTAAACGTCATTTCTATTGTCATAAACAAAATTTGTGTTTGTTCACAGATGGATCTAATGCTGGTGG  
 TCTTTTTTATCACCTGATTTCTCAACTCATCATATTTGCCCAATCAATTTTGAAAAATTTGTTATTAAAACTA  
 GGAATTCGAGAAGCAGGGTTAGATTCACTCAATGGAGTCTCATCCAGAGAAGCTGATGAATCAATTGAATGGACA  
 GACAAATTAGATCTATTAATATTGCTTTTCAATAATGTTGATTTCTTGCAGTGTGAAGGGGCAACGGAAATGGAA  
 GTGCTTCCATCCAAATATGCTTCAGGAAGTTCTGCTTCCAAAGTCTATGCTAATTTTCATGATTTTCTCATATTT  
 ATCGAATCAAAATTTAATTCAAATCAAGCGCAAAAGCTTATTCTTTATATCATTTGTTTACTTCTCGACGTTTTATT  
 GGTGATGTTGGATTTTCAAGTTGCCCTTTCGTCATATTATTGGCACCCAAAAACAAATACTTCTTTAAGCTCTCA  
 TTAGAAAATATAAATCCCATAGAAATCATATCGAGCTAAACATCGTCATTGTACTTGATAATTTTCATCATAATTG  
 CTCAGTTGGTCAAAATAGTCATCTCATCTATCAAGGAATAAATTAATCTTTTCCATATCGATTCAAGTTTCATAA  
 ATATCAACACTCTTATCCCTAGCTGTTCCCACTGTTGTTGATTACTAAATCTCCAAAGAAAGGAATCACTCTTTCT  
 TTACGATAAACTTTCCCTAAACCTCTTGGTGGCATGATATCATAGGAGCTCTTTAGTCTCTCAAACTCTGGATCT  
 TCGTTACCTCTCTAGATGGGTTGACTTCCCATGATCAATAGTAGACTCATTAACCAAGTACCTTCTATCCAACTCA  
 AACAGACAGGTTGACCAATCGCTTTTCAACAATCTAATATAMTCTGCTCCCACTAACGACCAGATTTTGGTTAAT  
 CTCAAAACCTGGCTGTGATAAATATAACAGATGATATACCCCAACCAGGATGACATGTTACCTGATTTTATCTAATAAG  
 CATCTAGATCAATCCATTTTTCCAATAATCTGSCCTTGTTTTCCAAATTTGGCTGGAATCATGTTCTACTCGAA  
 TTTTCCCAAAACAAATGATTTACCAACAATCTTGACAAATATGAATGTCATANTCATTTATTGAATTTAAAGGG  
 TTCCTTTTATAGAAAAATCTCGATTAGTGTCATCCGCTAATTGAAGAATATAGCAATAAGGATTTGTCTAATATTA  
 GAGTCTCCASTTACTAAAAAACTTTAAATCAATTTCACTAATGGTATAAGCAAAATCAATCAAAATTAATTTCTTCT  
 ACAAACACAGCTGGATTTCAAATCTTGGAAATGGTTGAACATTAAGTGTAAATTTATCATTTATTGAGTAAATCTATC  
 AACACTTGTGCTTTTGAACCATTTTCTTTTTTGAAGATAGTGATATCTTCAATGTTGTAATGATTGATCATTTCC  
 AATACCTTCAAAATATAGGGGGCAATGTCAGATTTTAAATAAAATCCATCAAAATGTTCTTCCAAATCTTGGCAAC  
 ACCATGCAAAATCTTGGAGACAACCAATTTCCAAGTTTGTCTATGCCCCCAATTTCTCTCAAAATATAGTGTGCGCG  
 TAAACAGAGAAAAATTTCTATGATTTTCCCAAAATCTGGTGAATATAGGCAAAACATCAACTATAGTGTGATCGGTA  
 CCGGTATCCAAAGGATCTTGATTGAACAATAAAAGTGGAAAAAGGCTTCTAATGAATTTTCCCATCTTCTTCTGAAA  
 AATGGAGCTGAAAATCGATGTGTATCAAAATCAATTAATAAGTCTGGATGTGGCACCTCAATTTTGTAAATATGTA  
 ATCTTCTCTCTGATATATCTATAGAAGAAGTAATGGGTAAATGTAGCTGGAGCAGTTACTGGTGTGTTGGGGATA  
 CTACTAGAATAAGGTGTATGAAATACATTTCTATTGACTGGAAATGTTGTGCTTTCAATGGTGGAAATTTTCCGC  
 ATCCCCAATGGAGGTGGATGTGCTGTTGGGATATTTGAACAATGGGGCTACTGATTTGTGAACAATCAATAGGT  
 TTGATATCAATTAGAGTTGAAGCATTAGTTTCAATGTTGCAATTTGTCATTATTATGTTTGAAGGAGGATCAGAAACG  
 ACATTTTCATTAATGCTATTACTGTTACCTAATGAAGTGGAACTATTATTGAAATTAAGGATACCTCTGCTACTG  
 TCAATTATTATCTTTCATCATTTGCTTCAACTTCTTTGGGTATAGGAGGTTCTTGTAATCCGAACTTCTTTGACATTC  
 AAATTTGTTGGTGGCTTCTAAAGATATAAATGTGATCTTTTAACTCGGCACCGTACAATTTCAAAATTTATTTCA  
 TTGATTTTCAGTCCCACTGAAAACACCAATTCACCCACGAATGTTTCCCAACAGTTGTATCATGATCATGTTTAAT  
 AAGGAATTTCAATTTTCATATTAGTCTCAACTGACGATTTGGAATTTGGGGAGAACTGAGTTTTTTTGTGTTACCGCCA  
 CCACCACCACTTACCCTATTTCTGTAGCTCTTACCTTCTTAAATAGATGTAGATGTGGATTTGTTGTTGTTGTTGTT  
 TGATTTTACTTCACTGTGCCCCAAGTAGAAGCAGCAGTATGTTGATGATAAGGTAGATGTATGATTTGTTGTTGTT  
 TTATCTGATAACGAAATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT  
 GATTCAGTTTGGACAAGGTT  
 TCAGAAATATTGATCGGATCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT  
 TATATATTTGCTGAACTAGTATCGTGAGAAACACTCTTGGTTTATCTTTTATCTTTTCTATTCCAAATCTTTCTC  
 ATGATGGTTGATTTAAATATTTAATTTGATATATTTGTTAGGTATTTAATAAATAAATAAATAAATAAATAAATAA  
 AAAATGGATATGATGTTTGTAAAGATCCCAATAGATTTATAAAGAACAAAGACGGGAAGGAAAGAAAGAAAGAAC  
 AATTAATAAATGAATCAATAAAGTGAATGAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTT  
 GAAATGAATGAACAGGTTGTAAAGAAATTTTTTAAATAAACCACCAACCAATTTAAGATTTAAATTTTGAAGA



213/251

ATACCTTTTAGGAAAAAGGATACACGAGCTTGGTGGGGAGACGTTGATTCAAAATTGCTGTTTAATAAAGTTTGAA  
TAGTTTATTC TCATTACCATATAATTAATGAAAACAAATAGTGATAAAATATATATCAACACATGGTTTTTTTTTTA  
TATTCCTTTCTCCTCCCTTTTCAATTGAGTTATAATAGTTGACTGTGAC TAGTTGATAAATTATATTGAGAAAAATTG  
AAAAAAGAAAAAATTTTACCGTGGTGTGATTTTCATCTAAATCTATGCGGAGATCGGAGAAATCCGAGCCGA  
AAGGAAGATTACTACTAGTAGTAGTTGTTTAACTGACTAACTAACAACTGGAGTGTGGAGTAAGAAAACAATA  
AGAAAAAAGAAAAACAAACAAAACAAGAAGATCGTTGAGTTGCTCGGAGTTATGCAAAAAAATTTTGTCAACT  
AATATTATCTTCGGAGTTAATTTCTTCTCTCCCAATATTAATGCCATGTCATATTAATTGTCTATTGTTATAAAA  
TAAATTTAAAGATGTAAACCGTGTGTGTATGGAGCATTGTGAATGTGATATTTCTTTCAACGTGTATCAAGTTAA  
CAGAGAAATAACAACAACAACAGCAACAACAAATGAAACACGTTTTATTCCTGTTTCACTGTACAACTGATTGATA  
TTCAACTTTAAAAAAGAAACGATTTGACATGAAAAATAACGCAATACATATCTATTGTTGTATAGTCTTAAAGGA  
GGAAGAACTAACCTTTTTTTTTCAGATATTGTTATATAGTTTTTGTATGAAAAGTATAATTTCTGTTTTGGTTGTTGG  
CCACAGTAAGTGTACGTTGTTTACGAAATAAGATCAATTCATGATTACATTAAGATGGTCCACATAATATC  
TAACGATTTTTTACGATTTTTTTTGTGTTTTCTTAGSTGTATTCGATTCTCAACAAGGACTTTTCAAGTTTGTGATT  
GGTATAATTACTTCTCATCATTTTAAACAAATCATATTACCATAGATAATTTGCTTCCAAAGTATACCTTTATTCA  
AGTAAAGACAAATTAGGTGTTGTTTGTATTACTTAGATAATTTTCCATCTGAAAACTGTAATCAACACAGATT  
CAACAGGCTTTAGTAAATTATACCATGCAAGTATGTTAGGTTGTTGTTGTTTAAATTACCTTCTACCAACGTAT  
ACAGAACTCTTTTCAACATATCAAGGCGGGTTTTACTTAAATAATCATTTTTGTTAAATAAGATTAACTGAAAC  
AAAAAGGCTTAAACAAGGGGAACTTATTGTTGTTTTCTTTTGTGTTTGTGAACTCTGTATTATTTATTTTTAAAC  
TCTCTGGGTTTTCTTTTTTTTTTTTGTGCAACATTTACACTTTCCATGGGCTTAAAAAAAGCTTTTTTTTCTA  
TGTTTTTTATTTCACATGACAACTCAAAACAAAACAGTGTACCAAGAGTCAATTTTGGAAATATCGGTGTTGAA  
ACTGTTTTATTTCATTGTATTAATATCATCTGCATGTGCTGTGATGTTGAATGTTGGTGAATGTGAGTGTGGTTTGA  
TTTGAAGTTTCCGTTTACCTTGTTTTTTGGAAAAATAAGCTCTTCTATAAGTGACAATATTTGTACCTCTTATTT  
TACTAATGATATTTGGGCAATTTCTTCAAAACCAAGAGTATGCTAAAAAGTTAAACCTGGTTATGCGATGACTT  
CATCCGAATATAGAAATTECAGCTTAAAAAATAGTTTGAAGATGCAATTTTGGCAATTGATCATTTGGTAGTT  
TCTCTGGTCCATGAGCAACATTTTTCTATCAATAAGTCTTCTTGAAGTCAATATCAGTATTTCTATACATAAG  
TATCAAAAGCCACAAATTATAGTTTAAATCCATAAGCTTGTGTTGTTGTTCTTCCCTTACATTTGTATCGATCAAAAGT  
ACGACAAATTAAGTTTCACTGTTTTTTTTTTTTTTTCTGTAATGTAAACAAATTTGTTCAAAATCAAAACCAACCCAC  
ACACAAAGTATCTATATCTATGATTGAAGATCAATTTGTACAATATATTCACCTCCCCCTGTACATGTACGGCCACAA  
ATTATATATATGAGCAGTTATCAGTTGTTCTGSGATGATGTGCAATGTATCAACAATAGTGTGGTTGTTGTTATG  
TGGTATTCCCATTCATATGGTGTCAATTTGTTTGCATTTTGTGTTGGCTAIGTAGGTTTGTATTTGTTCATTTGAT  
TAGTACACTCTATTGATCTAAATTAAGAGAAGCAAGTTGTGTAGGAATTAGTCCCTCTTACCTAACACATCTGTG  
AAAGGAAGGAACGAAAAAGTTATATCCGAACATGCAATTTGTTGTCTGAAATCATGTAAATCATTTGGGCCATG  
ATGAAAAATGAAGAAATACCTTTCTGCTTAAATGCAAAAAAATAAAGTGTCTATATTATTAATAATTAAGTAAT  
TGTCCTATATTATAAATATATATATATGCTGTAGTTGTTTTTAAATTTTTTTCATCTTCTTTTTCAAGGAGGGT  
ATTAATTACATTTGTTTCTCCAAAAAATAATAACAAATGGGTATTTGGCCCTCTTATTTTCAAAAAACAAAGGCCAA  
TTTTGGATTATGACGAAGTGATTTACCATATAATAGAAAAACAAATGGCATTGCAAAAAATTAATAACCAATACA  
CCCCAAAAATTTGATTTGCCCCATTTAATTGTTAAATTTGGTAAACATTTTCTCTGGCAAAAAAGTGGGAAACAGCCCC  
AAATCCAGATCTAATAAAGCTGTATACCAAGCCAGGCAAGTGGCTGCATATAACAAAGTAGCAATCAATAATATAAT  
CAACATATGCTAACAATAACATTAACCATTAACCAATATGCAAGCAACAAATGAGGAGGACATCCCAATGCA  
ATGTTGTGGGTAAATTACCAAGTCCAAACCAAGCCAGGAATACCAATAACAAATGTGAATCCACCAACUATCATGGG  
TTCTAATCTTTTTTCCGGGATGATTTTACCACCAATTATCTTCCATGGCTTTAATGTATCTTTTTTCAAAACAAT  
AATCATACCAACCAATCAAAATCCCAACCAACATGCGCCAAATATGTTAATTCACCTACCTTTGAACAAAAATG  
ATATTCACTCAAGAAATCAATGGAATAGCAGTTAAAAACAATAAAGCATACCATAAATAAAGCAATTATTAAG  
ACTGACCAAAAACAAAATTTGGTTCGGTGAAAGCATTTTAAAGTGAGCAACCAATATTTATTTTCAACAATTTCTTT  
CATACTTAATTTCAATTCTTCAATGTGGAGCATATAATCCCCCAATTACCTGTTCTTCTTCTTAATTCCTGAGCTCT  
ACGTTGTTAAATCAATGCAATGAGCTTTCTTGTAAATAAGAATGTATTCTATAAATAATGCCAAGGAACCAATAAT  
CCCCAGAAATATGAAGTCCATCTCCAAACCAAGCACTATTTTTCACAGTGAATCTCTCCCAAAATTTGGTGAAG  
CATAGGTTCTTCAACAAACAAATACATGGAGAAAAATGGCAATTTGCCGTACCTCTATAACGATTATTAACATATCGGC  
CATACGGGAGGAGCCACAACCAATGAGCCAGCACTAATAAACCAGCAAAAGAAACGACAATCATAAATTGTTTG  
AATATCTTTTACCAAGTTGGCAGGCTAAATGAAAAACACACATTAATTAACATGAAGGAACCAATTAATTTCT  
ACCAAACTAATTTCTGATAAGGCACTATAAATAACTGGACCCGAAGCAACCCAAAACAAACAAATGACGTTGTTAA  
AGTTGCTGGAGTCCAAACCAATATGATAAATTTCCATTTATATCATGCAACCTGCTTGAAGAAACATTTGCTGATCCCAT  
GAAATACCGATAGGCAAGCAAGCAACAGATGCAAAATATAAATTTTTTTTCCAACTTGGATAATTATGAGGATG  
ATCAGCATCATCGGACCATCAAGGCCAAACACATAAGGATCTCTGTAACCAAGCATTTGGAGGATATCTCTTACC  
TCCACCCATTTGCTGCAACCTGTTTACTCGATGAGAGCAGCAGTACGTAATAAATTTTCAATTTGATTTGATAACTCT  
CGTGGCTCTTCTCGATAATTAATATTTGATTTCTATTCTACTCAATTCATCATCAGGAGCTAATTTACCAACUAC  
ATTAGCTTCACAACTTTTGACATTTTGTGCATTTAAACTATTAAATTTCAATTTCTTCTATCAGCAGTGTACTACT  
GGATTCCAATGAATCAGTAGGTCACACATAGCTTTGTACATTCACATATTGTTATTAGTTATAGTTGTAATTC  
GTCAATAGAAAAAGGAATTTGTAGTATTTTGTAGTGTGTTGCTTCCAGGACCAATATCTCTCTGATTTGCTGTTGGT

214/251

ATTGTTATTCATTGTTCTATCAATTTAAATAAAAAAGAACTAATGGATAATGAATTTTCCAAITCAATTTAGAAAG  
AAGAATAAAAAACCCCGAAGAAATTTTTTTTTTAAATTAATTACGACTATTCGTTTATATATATATATATATATCT  
GTGGGTAAAGGAPAAAAACGGAAAAATAAAAAATTCATTTTCTTACTGGGGGTCTATAATTCCTAAATAGAACT  
AGTAGTAGCTGTTTATTTTCCGTGCGATGGGCGGCGGCGAAACAAGAAATTCCTTTTTTGTCTCTGCTTTTTGCT  
TTTTGCTTTTTGTTTTGTTTTTCATCCTCGCTTGACTAAGTTAATGTTAATGTTAGGAATTAATTTTTTCTTTTCC  
GCCCTCCCGTTTTGTGTGAATTTCTATTAGTGTGTGTGTTTAAATTCGATGTGCTAAAAAATTTTATACTAAAAAC  
AATTACTAGTAAGACGTTACTTTCTTTTTATTCTACTTTCATCTACTTAGTTGTTCACCTTCTGTTATATAAATTG  
TTAGGTTTGACAGTCCGGTTAGTAGCAAAAAGGGCTGAGCTTCATCTTTCATACAATACACAAAATTACAAAACAC  
AUCGGAGATATTATTGAACATATTTTTTCATATTAAATCCGAATAGATGAATTAGTAATCAGCATCATTATCACCT  
TTTGTTACCACACCAGTTTGATTTTGACAGTATATCCAANTACTTCTATTICAACTGTTTCGGATAAACTCTAAA  
AGCATAAAAACATACATCAAGGTTTTTGGAAAACTATTTCACCAAAAAGTTAATCAACAATTTGTAATTTCTCAATT  
ACTTATTAGTAATATCATCTAATAATATCACTAAAGAAAGGCTATAACTTAACCTAATTTTCATTGGTCCCTTC  
TCTTCTTTTTATCTTATCAGACGTTCAAGGTTTAGTGAAAAATTATGATTAAATAAGTTACAAATTATTCGTCAAC  
CAACCAACACCGCATGCACACATCTAAACCAACATCGGCTATTAATTTGCTTTTTTCAGTAATATCGGCAATTAA  
ATATTTGGCATATACACGACTAGCATTGTCTATGTACAAAAATTAGTTTCTGTTTAAATTTAGCTTGATATATTCAA  
GTCAAGATTAAATGTGTGATATATGATTTCCCCAAAGGGCTATGTCAATTTGATGAATTTTATTGGCGCTCGGTGT  
TTATATCTCTTCGGAGTTTAGTATACGAAACAGAAATGAGGGGATTTTATTATTCTCTCTCTCTCTCTCTCTCTCT  
AATGCATTAACCTTATTAACCTGTAGCCGTGTGTGTAAAGCCGATTTGTTTCTATTCTTCTGTTATTTTGGCTCAT  
CACAACCTATATAACTCCAGACATTGTTTGTAAATCCTCGGTAGTAATAATAGTAAAGAACCAACCAACCAACCA  
ACCAACTAGAAAGTGACAGAAACTTCACTCCAAACAAAAGGATGGAGTAACAATCAGATTCCCTCCCCCCCCAA  
AAAAAAAAGCTTAAAGCCCTACCTGGCTACTAAGCTTAAATAACAAAGATGCTTGTCTCTTATCTCTCGAAAG  
ACTTTCTATATTTGGCTGTGGAGAAAGAAAAAAGTAAAAATTAAGAAATGTCTAGCATTAAATAACGTACATA  
CATATTTATATATATATATATCTAAAAAATCTAGAAATCAATCAATCAATTAATTTGTTTAAATGAATATAAA  
CTTTTTTGAATTAAGCAACAAAATAATAAATAAATAAATCTCTAGTCTGTAATAGTAGTAGTAGTAGTAGTAG  
TAATGTCTATATATGTACAGTATAATGTGAATATCCCCATTTAAACAACCTCTTGTCTTCTCTCTCTCTCTCTCT  
GGCCAAGGCAACAATCCCAATGACACCAACTAAAGCACCACAAATCCAAATTTGGTACTGCCGATGAAGTATCAGA  
ATACCAAGCAATTAATGGGACCATTCGGGTAGAGATTCTGTGAAAAACAACATTAACAAATTTCCAGTGGCTCT  
AGCAGCTGAATGCATTAACCTCTGGGTTATAAGCATACATAACUCCATAATATATATACAAAGGCAACAATAAAGTGC  
TGATGTTAACTCCACATTTTGAGCTCTGGTTCTCAGCGCAGTATAACCAATAAATATGCCRTGGTAGTGACTCC  
ACCAATAAACCAATACCCCCCTTTCTACCTAAAGCTGGTAATAAATAAATAAATAACCCAGCAATAATGCCACCACC  
AATTAACCTACATTAGAAATGACATAATCTCGTATATCTCCACTAGTGGTATCAGCAGAGATATTTGGCACCAGG  
AGTAGCTAAATATTTCTGGTAAAAACGCTGAATATATTAATGGATTAACCAATACCTAAACAAGCCCATGAGAAAAACA  
CAAGGAACTTCAACCAAGCTGATTTTTTGGTTGCAACAAATTTTCAATGTTGAACATTAATGACAAATGTCCC  
ACCAAAACTGAATGTTTTCTATAGTCATCATTTCTCAATTTTACCACATTTCAACAATTTGTTCCAAAGCTTAG  
TGAACATTTACGATTGATTTTGTGGGCAATTTCTTGTAATACTTCAACTGCTTCAGCATCAGCATTATTAGCCAC  
CAAGAAATTTAGGAGTTTCTTTCAATTTCAUUAATGTGAGTCTTAGTATGGCCATGGCCAAAACAATTTGATCCATT  
AGTATAAAACCATATCTTCCAACCAGGATTTGACTGAGATGGACAATAATCAGCTGATTACAACTATTATTATTTGG  
TAAAAATCCATTAAGCTAATGCACAGCAATAGTTTGACCAATCCCCCAAAAGAAATGGCAAAAAAGTTTAAATACCA  
TTGATCTTTATGAGGTAAATATTCAAAACACACAAATTTCCAAACTAAATTTCCACCAGCAGCAAAATGAAT  
TAATAATACAAATAAACAAATAGATGCCATATGGCCATCATCCCCGTCTATGTTGTGAATAAGCACTTAATAA  
TAATGATAAATTAAGGCTAATCGTCTACCAATTAATCAGCTCCAAACCCCTACTAATGCTCTCTAATAATCAT  
CCCACCGGCATAACATTCACTACTAACGGGGAATTTATAACCAAAATGATAATTAATAATGTACGGACACTACT  
TDCAGATAAATCAACATACAAATCACTACAAATAACCATCATTCAAGAAAAATAATTTCAAAATGATAAGGAGT  
AAACCCAAATTTATCAATGECATCATTAAATTAATTTCTATTTATTATCTAATATCTATCATTAGCTTCTAAACC  
AACCATATCAAAATTCAGCGATGTGCAATCTTCTAAATAGTTTTCTTATGAGAAATGAATCTCTCTTATCATC  
ATTTCTATCATTTGTTGATAGAAATGTTTAGAGTGGTTTTGGTTTTGGTTTTGGTTTTGGTCTCTGGCCAAAGTTTTG  
CTTTGGGTTAGTATTTCTTTCAATAATGACATGATTAGCAACTAAGTAAATTAAGTGAATGAATAGCTGAATAT  
GTCTAAATTAAGAAATAAATGAATAAGAAAGCTATAAGTAAATAGGAACCTTTGATAGTGAATAAAGG  
AAAAAGTGAATAAATAATCAGGGGGAATAAGGGAATAACCGAAGAGTTAAATAATTAATTTTGTACTTGTAT  
TTGGTTTTGTGGGACTCAAAAGACAAAGAAAAAATAATTTCTTGTGTTAGTATTTAATTAATTAATTAATTAAT  
AAGAAACTAAATATGAATATACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
AAAAATTAATTTTGAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
AGAAAGAAAGTACAGAAAAATTTTTCAGTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
GTACATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
TGACTAAGTACTACATTTCCACAAATGTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
TATTTCTTAGTATTAATAAACCCTCTATAGTAGTTTTTGAAGACACAGATCTCTCTCTCTCTCTCTCTCTCTCT  
AGTCTTAATCAAGTGTAATAATAGTACTTGGCAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
TTTGGGAATTAATTAATTAATTAATTTTAAACAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT





216/251

CAGACATTAACTACTATCTTCAICCAACACCAAATCAGTTAACCCCTTCCTCCCATATCATTAAATGAAATCTGAACG  
 TTCAACATTUAACTTAGATCTAATCTTCTCTCAATCTTGATAATTTCTAATACTACGTAGTTCTTCCCTCGCTC  
 TTCCCTCTTCCCTATCACGCTGATATCCCTTGTTGTTGTAGCACATTAAATTCANITTCCTTTTGTC TAATACCATC  
 AGGAGGCCAAGGTAATTCATTTGATCATCTTGTTTATAATCTTGGGAATTTGTGGTTGATATCCATTACTCTT  
 AGGTTTACCGAATGGTATTAAACACATATAAGGATAACCCAAAGCATTTAC TAATTTCTCCATATTTCTTAAAT  
 ATAAGGAAATATCAAATCATCAATAGTGAAATTTTGTGGGCACATTGTTTGAACCTTCATTATTATTGGTTGCTTAA  
 ATTAATTAATTC AACATCTCATCCCCATCATCATCACTATCTGTTATAATTGACATTATTGGTGGTATTAGTCCA  
 GGTGTTCAATTCAGGAATGGTTTACCTTTATGTAATCTTCCATAATGGAATCGAATCAATCTCCATAATCGTTT  
 ACTTGAACCATTCGAACCTCTAATCTTTCCCATTTCCCATATTTCTATTGTTGTCATCCCTTACATATATTAATCAA  
 ACATCGAATGAAACAAACCAATATACTAGCAAGGACAAAAAATTTAATGGAGTATACCAATTATGCCCACTAA  
 TTCTGTCTTGTTGAATAAATAGTGTGGCATATTCAGATTTTCATAAATAATTAATTAATTAGTTTAAATCAATTGAAT  
 CATTAAATATCCTGTACCCCAATGATCCATCCAAAGAAATCTCATGAAATGAGGTAATTAATTAATTTCCACACA  
 ATTTCAATGTCCAAAGGCAATGATCCATTTGTAAAAACACATTGTTGACAAATTTACAAATTTGACATTGACTTCTTGG  
 TGGTTTATAATTATTACATTTCTTACAATACCTTATCCATTACACATCTATCTCCACTGATIGGTTCTCTCCTTAT  
 TACGCTTTCTATCTCTCTACATTTCTAGACCTAACCCATCAGAATCACTCTGGGTTTGTTCATTTCTTGTAGACGA  
 CGCCAAAGATGGTCTATAAATTTTGGGACTCGTCCGGGATTTGGTATATATTCOCANTAAATAACATATTCATAT  
 CATAGTCACATAAAATTCATAAATCAATTTGTTGTTTCAATCTTAAATGGTGTCCGAGAAATAAATAATGTGATCC  
 ATAAGATAATGAAAAAATGATTATACAAGGAATAATCACTCCCAATATGSSCCATTTTAACTGTATGCCATGAT  
 TATTAGTAAAGTATTGTTTACCATCTAATTTATGAAAC TATTCAACCTAGCAGTTGTTGTATAGATTGAACCTG  
 TGGTTGTACTAATAGTTATTAGTTAATCTTTAGGAGAAAGTGAGAGAGAAATCAGAGAGAAATGAATCAACGA  
 ACTCAACCATAAAAAATAAATACCTTTGAAAAATAATCTCAGTGGCAATCAACAAACTTACTCTCTCTCT  
 CTTTGTGAATCATTACAACATCTTTATATACTAATATTTATCTATATCTATCTGTCATTTTGTACAACT  
 AAACACAAATTCATTTGCTCATGTATACTAATGATTTATAGACTTCAATTTGTTACAGGTTACGATTTATCCAAACAG  
 TGTCTTCTCAUCAGGATGTAATCAAAATCAAAATTAATTAATTAATTTTTCCTCTATCTCTGTTATTGCAGTATA  
 CTAATCTATATAGATGGGAGAAATTTTCAAGTTGAATATGCCATGAAAGCCGTTGAAAGGGTGGTACATCAAT  
 TCGTATTAAATCTAAACATCCGATGATTTGGCTGTGGAAAAAACTCATTCAATCAAAATTTAATTCCTCAAGAA  
 AAACAAACGAATTCAAACTGTTGATAGAAACATTGGAGTAGTTTATTTCGGGTTTGTATCCCGATGGACGTCATTT  
 TGTAAATAGATCTCTCTGATGATGTCATTCATTCAAATCAATTTTCAAACTATGATGCCAATATCTAATTTAAT  
 GGATAGAAATGGGTATTATGTTTCAAAATTAATCTTGTATTAATTCAGTTCTGTCATTTTGGTATAGTATCTATTAT  
 TGGTGGAGTAGATAATGAAGATGGGAACCATACTTGTATATGATGAACCTAGTGGTAGTATTGGGGGTATAA  
 TGGTCTCTCCACTCGTAAAGGTGGACAAATTTGCCAATCAGAAATAGAAATTTGAAATTTGAACAATTCACCTG  
 TTTAGAAAGCAATAAACTCATGCTTCCAAAGATTTATTCAATTTGAGTTCATGAAGATAATAAGATAAAAGACTATGAAT  
 GGAAATTTCTTGGTGTAGTAAAGAACACACTGGAGGTAAACATCAATTTATTTCTGATGATTTATTAGAACCAAGC  
 TAGAAAACTTCTGAGAGAGAGGAGAGAGAGAGAGATCATGATGAAGAGAGAGAGCTGCTGCTGATGATGAACA  
 AATGCTCTCCATAATGTAATATATAGGTTCAAAATTTTGTCTTGAATGAAACAAAAAAGAAAGAGAGAGATGAAT  
 TATTATTAACTTAACTAGATACAATTAATAGAAATACAACTATCAATTTCTTCTTTCAACCTCTCTCCATCTTA  
 ATTTGATGAGTCTAAGAAAGGGGGGGGGAGTCTCTATCTCTGCTGCTGCTGCTGCTGAGCAAAAAAATAAATATTT  
 TCTTCAACGTTGAAAAAGTAACAAATCAATTTGATAGTTAAAGAAAGAAAGTTAACACCAAGTCTATACCTTACC  
 AAATCAAAAGCTCTATATGTTGAATAGACAACTAATTTTATTTTGAACATTTTAAACATTTATAGCTTACCTT  
 GAAAGCTTTTATTTTCCATGTTCAAAATTTATCAATTAATGAATCAAAATGATTAATTAATAATTTTACTG  
 AATAAAAGTGGTCTCAAGTAGTACTAATACTACTCTAATTTATTTGTTTAAACCACTGAAGATTTATCA  
 ATTTCAATTAACAACAACAACAAGGAACCTCAAGAAGTACACCAGAGAGAGAGAGAGAGAGAGAGAGAGATG  
 GAACAAATAAUCGAATTTGGAAGTTCAACAAGGAACCAACCAAGACACTTTATCTTCTAGTCCATTTATTTCAAGT  
 CCGAATTCACCCCTTGATGATATAATTAGACCCCAAGGCAATCTTCAACCATCATTGACTATTAGAGATTCTTAT  
 TCTTCTCAACTACATATCAATATATCTAATTTACACAGAGCTTGAATGAGATGAGATTTATCAACTGATCCAGTT  
 GACAAACAACAACAATAACACAAAGTCAACAPAAACCAACCTTCCCAATAGTGATATACTAATGATGATATCAAT  
 ACCATCGATAATTTGACTCCAGTAGAATACAAACAAAAACATATCGCCATGGACAGCAATTCGGCCCTACGTTA  
 CGTGGTAGTCCAGAAATCAACGCCACGGCTGTGTTTCAAAATAAACCCAAATTTGAAATTTAATAATGGTCTTACT  
 CCTACTAATGGTAGTAGATATGGTTCAAAATAATATTGCTTACAACAACCAAACTCAAGAGAGAGAGAGATTTGAAT  
 AAACGAATAGTTAATTAATAAATTTCAATTAATTTGATGAAGAAATTTTTCAAAGAAATTTGATAGAAATAAT  
 CTTGATCTCTCATGAATTTCAACATTTATTAAGAGAAACAAATCAACATCATGAATAACGAACAAACCAATTA  
 TCAACCTCATTTCTCCCAACCTTCAACTTTAGAAATTCACACTCAAAATTTCAAAATTTGAACCTAGATGAAGCACTT  
 GAATTAATAAACAATTTGTACAAACAAATAGAACTCCAAATAAGGAATCACTGATAAGGATTTGCAAAATTTCT  
 AATTATGAATCAAGAAATCAATTTAATTAATTTCTGTTGATGAATTAATTTATATTTTCTATCAATCAATATGAT  
 AAAAAATAATTTATTTCCACGGGGGGGCAACACCACTAGCCCGGGTAAAGAAATTTTACAACAATCCATATCGGCA  
 CAATTAGAAGTTAAATTTGAATCTTTTGAATTTGAATTTGATGACTAGATTGGATCAACTGCATCAAAATAATTAAT  
 AAACCATAGATTTATTTACCTCACCATACACATCATCTGAATATGGTGTAGCAACCAACAAATGTCCTAAATGAAG  
 AATGATTTGGAACCATATATTCATATTTATCGAAGATTTGATTAAGAACTGATTAAGAACTGATTAATTTGTTGAA  
 AATTACAAGCCAAATAAGAAATGAATTACAAATCAATTTAGTTCAACCAATAAATGAATCGACTCGAATTAAGAAAT









[illegible]

YJR115W\_homoLog\_1 63aa PathoSeq: 1..63 (SEQ ID NO 660)  
TTTITTSAINSSSOPOMSGAOTVILASKVRSKLTREADSPKSSLENLVQANMLDNIMDYISD

YDL075W\_homolog 513bp PathoSeq: 1..513 (SEQ ID NO 661)  
 ATATATCAATGACTATGATTGGATTGAATGGATAGTAGCCAAAATCCCATCTTCTATCTCCATCATCAAATAAT  
 GTTTCCTTTTCATCTATTATACATTCTGACAAATAAATCTCAAGGAATATCAAAATCTACCAATCGTTTGT  
 TTTTCTAGTTCACACGGTGTCATATTTCAAAAAGAGAGCTCCAAAAGCTGTCABAAGAAATCAAGAAATTCCGCCACTT  
 TACACATGGGTACCACTGATGTTAGATTAGACCCAAAATTGAACATTTGCCATTTGCAAAAAGAGGTGTTCAAGGTG  
 TTGAAAACAGATATGAGATTAAACAAATTTCCACAAAAAGAAATGATGAAGAAAGATGCTAAAGAAATTTATTTTGCTC  
 ACGTTGAACCAAGTATTGTCCCATCTCAATAAAGTTTACAAACCGTTGTTGTTGAAGATGTAATAGATGATTT  
 GCTAAAATATATTTATATGAGCTTAGCATTTAATGTCATTTATTGAGGGGGTATTTTAAAT

YVL075W\_homolog\_1 93aa PathoSeq: 1..93 (SEQ ID NO 662)  
LHGVNFKKRAPKAVKTKKFKATLHMGTDDVRLDPKLNIAIWKRGVQGVENRMRRLRISPKRNDEEDAKKELFAIYE  
PMIVPSTKGLQTAIVEDD

YDR064W\_homolog 5975bp PathoSeq: 1..5975 (SEQ ID NO 663)

CCCTATTCACTGTCTGAGGTTTTAAATGTNGGAGATCATAGGCTACAAATGTGTGCCCAATTCGAATGCAGATGG  
GGAUCTCGAAGCTTTAATTCTTAGTAAAAGAAAAAATTATATCGCATCTTGATACAAGATTCTGATGCTTAGATTTT  
TCAGAAATCGCAATCTTCAATCGCGTCAATACCCAAATTTATTTCAAGAGTCTTACTTCAAAATACAACGACAGC  
ATGCTATGTATACACAGACTAATCAATTTAAAATGAAATTGATTTATGTTATGGCAACAATATTAACATTACATCT  
TAAGCCACCAAAAAAGAAAAACGAGAAATCAACTACCACTTCTCAAGTGAAGAGATATACATCTACTTTTATCT  
AACGATTGAACCATCACACTCATAGAGGATACCAATATCAATGTGTGAATATCAACCAACTCGCGAGGAT  
ACCTGCAATTCAGACCTGGAGGTGAAGAACGAACATGAAGAAGATATCCCAATCCCAAAATCAGAATACATCGA  
TGATGTGGNTGAATCAACGCAAGACTACAAGACGAGTCGGCATAACTAAGGTACCTGGTATGATATACGAGT  
GGCCTATCCAAAGATTCAACTCAGCCTTATTCGAATAACTGGGATTGAATTTAGTGAAGATAGTGATATGCTGA  
ATTAAAGTTAAAGGATTTCGATATATGGCTTTTCCATATGCTTCCGACACAACAATTTGAATTTGTTGAACCAAC  
TTATGAAGAAAGCTTAATTTAGAAAAAGATATAATACACGAACAGCTCTATAGTTTACATATCTTTAGTATACAT  
GATTTAATGAAGCTGAAGCAAAAAAGAAAGATAACAAATAACAAATAAAGACAGGTTATCAAAAGAAATGAACT  
TAACATACATCTCACTACATATATGTTTCTTCCACTTAACTTTCTCACACCACAGAGTGTGCTCTTGATGTTTGTG  
AGTTTCCAGAGCAATCTATTTTGGGATCTGGCTTTAGACACCGCGCAAAACATTCGTGGGGGATGTACCTGGTG  
GAGATCAATAATCTTTCATTGACTGTTTTTGTGTGTTGTGTGCTTGATATATCAATTCATGCTGACTAGATACAC  
TGTGTGTTGATATGTATCTCAAACTCTCGAATCAGAATTATCTTTGTTTGTGGTGTCTGACTCATACCTTG  
CTGGTGAGCTTTGAATTATATCTTCACAGCTGTTTTCATCGTCAGAAATTTGTTACCACTTCTACCTCGTCAAT  
CTTCAGAGTCTTCAAAATATTTCTTGGTGTCCAGGAGCTCGATAGGTACACAGTTGGATTTTAGATAGCCA  
AAGAACCACTTCACTTACGTCTTCTAATCGGGGATTTTATACAGAAGAAATACAGAGTGAGATGTCAATTCTT  
CTTGCAATTGCAATCTTCTCTTTTGGCTCTTTTAGCTTTGTTTATAGTCTTCATAAGAGCACAAATGGGA  
ACAAGTTGCCAATTAAAGGATCGGGTCTATTGTCTACTATCATTGTATGCTCCAGCTCTTAAATATCTCTCT  
GCAAGTAAAGCCAATGTTGTTGAGGACCAACAACCACTTCTTGGTGTGATCATTCTCAATGTACCGGATACATTCT  
TGCTGTAAATTCATGATGTATATGAGATGGGCTCCAACTCAAAACAACCGGTTCTTCTTAACCTGCTTTACAAT  
GTACTGCAATTTTTCAGCTTATATGGAATTAACACTCTTACAGCAACCAATTAATTTTGAAGCTTATCCAAAGAT  
GACAAATTCCTATCCCAAAATCATATCAATGTGCTTGAATTTCTCTTGAAGAAATTTTGTGCTCTTATAGT  
CAGAGTTTAATCTCACCAACAGCTTCCAGTTGTTTCCACCAAGTACTCCAAACTTTTGAAGATGGTTCTGTTA  
ATCTCTCTCTGCTTGTGTTGTTGAGGAGATGCAATGCAATGAAATCTTNGCATATAACGTTAAAACTCTCTTGGT  
CGACTCTTTCTGACTGTTCATCTCTCTTAAATCAAAATTTGCCAAGTCAATCATACCTCTCTCTTTAGCTCTCC  
ACATGGCTATCACTGACATCTTGAATAGTTATTTCAATAATCGGCACTGCTATATCTTGGGCTCTCTGAAAGCTTGT  
AAGGTTGGGCTGATTTCAGCAATACCTTCCAAACTTGATGAGGAGCCCAATCTTGGAGCAATATCATGTAACAG  
ATGTTAAACATGCTAAATTTGGCTCTTTCTTTACCGGATGCCAATATATATCAAGGATCTCTCTCTCTTGGT  
AGTCTCTCTTTTAACTTTCTGTTGTTAAAGAACTGCAAAACGATATAAATGCCCAATGTTCAAGGTCGGAATCT

TGTAATAATGCATTATATGGTAATCCGCTTCAACTGTGAAATATGCCAAATCTTCGTATCCCTTTTGTGATCAT  
CATAAGCGCCAAAGGTATATTCTATCTGTAATGGAATTGTTAGTATATAATGTTATCAAAGGTAGACAAATCAAT  
TGTGAAGTAGATTTCCTCCAACTACTTTTAAAGAACTCTATAAGAGGCACATGAACCAAGTGAACCTATGCATCGGAA  
AAGGTGTTTGTGATTATTAGGTAGTTTGAACGGTATGGTAGAAACAAACGGTGTNTTGAATGAAAGACAAAATG  
TACTTATATGTACAAAATCAAAATGAATGTATAGACGCTTGAGCTTAATTGGCAAAATTTGAAGACATAAAATAGAAA  
TTCAA AAAAGATCTCTCCCTCAAAATTTATCTTCTTTCACTTTGTTTGTGTTTTGTTCTTTCTTTGATTCTTT  
TTCTTCTTTGAATCGCTCAATCCAAACCGTACTGTTGTTCTTTGTTTTCTTTTTTGCTCAATCGCGTAAGATTGTA  
ATATTGTGCACTACTGTAGCAAACCTCAATCCAAAAAAACTCCAAATCTGATTGTGAGAAATCAAATTTTAGG  
TGTATTAAATCCTTCATAGCAAGGAAAGGAAAGCCATGGTAGCTTCAACATACTATTTTTATAAAGCTTGTTCTG  
CTTTACTAACCAGGACCAATTGATGATAGUCATCTCGTTATATACATTTCTCCAGAAACACATACAGCATTAACA  
AAGTTTATGATTTCAAAGTCCCAAGTGGATAAAGTTCAAGCTGTTATATATGTAATGTAATGTAATGTAATGTAAT  
TTTCCGATTGTTTAAATTTTCAATACTATACCTCAATCTAGACATGATGACAAAAAGCTGATGTAATGTAATGTAAT  
AAGAAGATGAAATATATAGATTTCCATAGAGAAATGTTTGAAGAAATTAACCGACACCTCTCTGATGATCTCATCT  
TATCATATCCCTTCAAACTGGATGATGGCGGATTGAAAAACACCAATTAGTTATGTTTATACTGGATCCCAACCA  
CTGACACAAGAAAGTAGAATGCTCTATGCTCGTCCAGTTGAGCAATTTAGAGATAAAGCTGGAGTCTCAAAGTACG  
TATACAGGTAAATCTCGCTTTTAGCTGAAACACATTAGTGTACAAACATCCATTTAGATTGATCAAACTTGAAGA  
AGAAGAGGACCTTTCATGATTTGAAGAACAAATTTGATTTAGACGGGGGGTTAACAGTTCTCTGATTATATAAAATGAA  
TAGCTTCTAATCTGCTCTATCTATCATACCTCTCCCTTTAGTCTATAATCTGATCTGATCTGCTCATATTGCTACT  
CATTTAAATTTTTTGTACAAAGTCTGTGTGCACTACTATTCTGTAGAAATGAGTAGAGAAAAAATTTTCAAGTTGT  
TCTTCTCTTTTAAAGGAAAAAATTTTCAATTTCTCTTTCTCAATCTCTTTCTTACCCTAGTCAA  
TCAATAAAATATAATCAGTCTCATGTGCTGTATGCATCTCATCTGTATGTTATCAATCAATCAGTCACTAAATCA  
GCATCACATACTATTAACATGATAGTGGGAAACAGGAGTTTAAAGGAAAAAATGGATTGTGTTGGCTTTAAACAAA  
TGAAGAGGCTTGTGCTAAAGTAGAACATTTCTCTACGGTCCGACATTAACCACTACCTTGAATGTTTACTATATAC  
GCTTAGGATTTCTGATACCTTTCTTTGATTTATCTAGGATGGAGAGGAACACTGGATGGCATTAATGCTCTG  
GTGCTCTCTCTTTTCTTAAATTTCAAAATCTAAGTAATTTCAATTTACTTTTTTCTAATATGACATGCTCAATA  
TTGCTCCAGATGTTAATTGGAATTTTTCTTTCTTTGCTTTGGGTTAAGTTTACTAACATCTTGTGTTTGAAGCT  
AAAGGTATTTCTCTCTCCGCTCTTCTCAATACCAAGAAACGCTCCATCTCTGTTCAAAATTTCTCTTGAAGATGTT  
GTTGAACAAATCAATCAAAATCCCCACAAAGGTTTCACTTCCATCTCAAAATTTGGTGTATCTTAAAGAGATGCTC  
GGTCTTTCTCAAGCCAAAGTTGTCTCATCTGTAAGAATCTTGAAGATTTAAATCTTAACCGTTTACCGCTCAGAA  
ATTTCAAGAAATTTATACCTTTGATCAAGAAAGCTGTCTGTGTCAGAAAGCACTTGGAAAAAACAAGAAAGAC  
AAAGATTTCAATTTCAATTTAATTTTTGATTTGAATCAAGAAATCAAGATTTGCTTCAATCAAGAAATGATTTGCT  
GCTTTACCACCAAACTGGAATACGAATCTGCTACTGCTCTGCTTTAGTTGCTTGAAGAGGTTAGTTATTTGTA  
TATCTTGTCTTTTCTTATATATATAAATGATATATTATCACTAATTAATTTTTATATCAATACGAATGGA  
AAGTAATCGTTTAAATATGATGCTTCTCBAAAATTAATTTGATGTTTGAATAGCAATGCTGTTGCAAGAT  
ATTAGTTTGAAGAAATATAAGCAACCCAAAAAACAATTTCTGAAGATTTCTGTAAGACATTTGAACATCTTT  
TAACTACTCAACAAATTTGAAGGACCAATCCGATAGACATTTTAAAGAAATGCAAAACAGTATGAAGACGCTG  
AATGATGACCCATCATTTTGAATATTAATCTAGATCTTTCAATGAAAGGATGGTATAACATCAAGAAATGATTT  
TCAATACAAGATATCAACCAATCAATTACTAGTTTCTTTGAATGGAATTTGTCATTAAACAAATAGTAATCAAGTG  
CAATTTTTAGTCAATTTCTACTATGCGCTCTTAATTTTATATCTCCGATTTAACTATGGTTGGAACCCCAACG  
AGTGAACATTTCTGAACATTTCTGACATGTTGATCTGCTTTAAATGTTGACCAATCTGCTGCTACAACTAATG  
AACGAGTATATTGAAGAGATTATCAAAATCGAGACAGGAATGAAAAAAGGTTTCAATTTGCTTGAAGGAGGAC  
ATGAGTATGGCTTTAAAGTACAAATAGAAATGTAAGTTTAAAGTTGGAATCAATCAATCAATCAATCAATCAAT  
ATGACACCTTCTAGGCTTGAAGTACATCAACCAACAAATTAATCTAGTGGCACTAGTGGATCATCTAGTACCTCA  
TCTAGCACATCGATGAATCAAGATTTTGAATTTGTGCTGCTAATGATCATGACCATCTAGGTTATATTCTCATTTG  
ATGAATGATATATTGCTGCTCCAGAAATGAAAGTGTCTATTGACGTAGCAAAATTTGGGCTATAACCACTCATCT  
TACTTCAATAAAGCTTCTGATGCTACCAAGGGGGTTATTTACATATTGAACATCCAAAGGGAATATTCAAGTT  
TTGCTCAACCGCATTTTCTATAGCAACCAACCTACGACCATCAATTTTACCTACAACTCAATTTCTCAATTT  
CGACCGAGTTGTTTCAATCTAGGGAATCACTAGATTTGGATATGTTG

YDR064W\_homolog 143aa PathoSeq: 1..143(SEQ ID NO 664)  
GKGISSSALPYSRNAPSWFKLSSDEVVEQIIKYARKGLTPSQIGVILRDAHCVSQAKVVTGNKILRILKSNGLAP  
PIPEDLYYLIKKAQSVRKHLEKNRKDKSKFRLILIESRTHELARYRTVAVL PENWKYYSATASALV

YKL156W\_homolog 2002bp PathoSeq: 1..2002 (SEQ ID NO 665)  
ATTCCTCCCCAAAATAAAAATAAATATGGAAGAGAAATTCCTATGATACATATATATATTACCAACCTTTCTTTTCT  
ATCTCTCTCTCTCTCTCTATAATAGTTATTTCTTCATCCAAATTTTCATTTCATTCTTACTTCTTGGTGTTCT  
CTTTATTGTTTGATTGTGTATGTGAGTTTCTTTTCTCTTAAAAAGCGTTTACTTTCTCTGAAATGAACAACCT  
TTCACTCAATTATACCTTTTACCACAGTTGGGGTACACAAACAGTAGACAAAGAGTCACAAGTGCACGACAGTTCTC  
ACGGTGACGAAAGAACAGTTGGTGTATTAAGACATCTTTGACATTTAACGTCCATAAAGAAAGAGATCTTGGTTGTCTC

YKL156W\_homolog\_1 8Laa PatheSeq: 1..81 (SEQ ID NO 666)  
VLVQDQLHPSFATPEAKQIKLKLPLVQQPRGFFMDVKCGCLNITTVFSHAQTAVTCBSCSTVLCTPTGGKAKLTSG  
CSERRK

[illegible]



[illegible]

225/251

CTTTGGATACCAAGTTTCAGCACCTTAATTGGGAACCTCTATTTTCACCTCAGCATGC AAAATTTGGGCAGAGCATTTTC  
 AAGCATCTTTTATCTCGTGCAGTTAGAGAATGTACTCCACACATTTGTAACAAAGCTGTGGAAACTGTTGTTACCA  
 CCACCAAAGCTTTAATCACTAAGGATTTTGGCTACGGAACGTGACATTTAGAAAAATTTCCGAAACAGTTATCAGAAAT  
 TGGCATTTGCTGTTGTTCTCATCCAAATGGTCTCAATCCAAATGGGAAGAAAGCATTTAGTTGAAACCAATCGAGGCTACTA  
 TGTGTGCAGTTATTTGGGCAACAATCCAAATGAAGTACCTTTAGCTGAATTGAATAGTGC CATTTCAAGCCAAATGTTG  
 GTTTATGTGTTGATATTGTTGATGTGTTGGTAGGTCAAACCTATTCTTCACATCATAGACCCAAACAATCCAGACAG  
 AAGTGTGTTTTCGCGTGACATCACACTGCCACAGCTCCAAATCAACCATTATTTGTCAGAAACGGGGCAGTGCATTACT  
 CGTTGACATTACCAAAATCCTTTAGGATTAGCACTTACCGGATTGAGTGCACAGCAATTGAAGATTTATGAACATT  
 TTGGAGAAGCAAGAGTGGATCAAAATGTACCTCCTCCAGGAAGTACCGGTATAACACAACAACAACAACAATCAT  
 TAGCAACCATTACAAACAGCAACAACAGCAACAGCAACCAACCAGTATCTACAGTAGCAGCGGCACACCAG  
 CACCAAGCGUACCAACAACAACAACAACAACCTGAAGAAGCCATTGCAACAAGCACAGGTGTTCTTGATGATATTG  
 TTTCTGTTTGAACAATTGTTTACTGCTATTACTCCCAACTGTGCACAAAGCCCTTCAACTTGTTCGAAGTCACAG  
 AAACCAAGTTAGCACATTTGCCACCAAAACCAATTCCATTTATGGCGGCATTGACTCAAGCTTTGGTGATTGCACAGA  
 CCAATGCCATATAATATCCTGAGTTGTTATTAAGGCTGCACAATATGCAGTCAACTGTTTGTGTTTACTCAGACAC  
 ACGAAAACCCAATGAGTAATGAATCTATGTTGTTATTTTACACAAATTTGTGTGAGTATTCACCTTCTACCGCCA  
 AAGATGTTATTTTGGTGGCTTGTACACTCATCTGAATCAACGTAAGTTTAAATATGCCAGTATAGCTTTCAATTATTGA  
 AAGTTCGAATTAATCCAGCCAAATTAATTAGATTATCTATTGGGAAATTGATTAAAGAAACAATAATCCGGTTG  
 TAGTAAAGTTTGCTGCTAGTTTGTGACGAATATTTTACTTCCGAAGACATGCCCTCTATTCCGTTACCGATCG  
 AATTTGCTAATACATTAGATGCTTTATCTAAATACCAAGCAAAATGATCAAGTGAAGAAGACAGACAAAGCAAAAC  
 AGGCAACTAGTACATTGTTTAAACTCTTGAGTGAAGCCAGCAACCCGCTTCAAAACCAATTTTGTCTCAATTGGGTT  
 ATATATTTGCTGAATGGGTAAAGATTGTTGACTCATGGAGACGATGCAACAAATGAATTACAAATGAATTTGTCA  
 AGGGATTGATTCAATCTGGTATACTTAATTAATCTGAATATGTAAAGACTTTTTCAAAGCGGCCATTGAGATT  
 CCATTACATCCGTTTCCCACTGAACATGAATTACCTTCANCAACTCAACATGAACATACCTTTGCCCTTCATACAT  
 TGCTATGTTGATTGTTTGGAA

YLR038C\_homolog\_1 74aa PathoSeq: 1..74 (SEQ ID NO 668)

DPATFKFETPPQFDPREFPNQNSKHCAQAYVDYHKCVNVKGEPEPCKIEFKTFTSLCPLDWVEKWDDQRAAGRF

YNL131W\_homolog 15251bp PathoSeq: 1..15251 (SEQ ID NO 669)

TTTAAATCACAAAAATGTATCAATATTTTCTGAACAGATACAAACAACAACAACAACAACAATTTGTGATAA  
 ATATTAAATCAAAATTCATATTCATTTAGTAGAATTCATGACAAAAAGAAATCAAAACCAAGANTTCTCATCCTGGTA  
 TTAATAATATATCTATAACTAATGATACCAATAAGATCCCAATCCTAGTAATGGTTTAATAAAATTAGCAACAC  
 AAGAAATAGATTAAACATTTGTTGATTCTGCTAATTTGAGTTTCCAGGAGAAGACAAAGATAGATCTCATATAT  
 TACTTCAACATGTTCAATCAAGTTACAAATTCGGTCAATTTCAAAATAGATCTGATTAAACTTCAAAATACTATTTC  
 AATTACAACTTAACAAAAATCTATCAATTTCAATAAAATTCACCTTCATCAACATTTTTCAAACATTACCAATA  
 TTGGATGTTATCAAAATCCATCAACTAAACAATGTAAATTCGTTTAGATTATCCAAATTAATGAATCAAAATAT  
 ATCCTGTGAAACCAGATATTAATATTAAACCAAAATTAACAATCCATTTGTTTTATACCTGGGTGAAAAATTTATCTA  
 TCCCAATTTGGAATTAATTAATAAAATTTCTATCATCAATGTAATAAACAACAACTTATCTCATGGCAAAAAATAAAT  
 CCCCAGTACTGCTACTGCTACTAATGATGTGTGCTGCTAATTAATTCGGATGGATTAAAGATGATGAACCAT  
 TAAATTTAATCAAAATTAACAAGAAATGATANTATTGATACATTATATATTTTACCAGGAATTCGAATCAAGAA  
 ATTTAAATATTGAATTACAACTTATACTGAAATGAAATGAAATGGAATGAAATGAAGAAGAAATGACA  
 AGGACCAAGATCAGGATGAGGATGAGGACCAAGCTTGTGCTTTATGATATTGCAACTTTTACTATACCAATATTAT  
 CAAAGCCATTTCTTGTCAATATGTTATAACTCCAGATTCGGTGATAAAGCCACTGATATGCCATCACCATTTA  
 IATTAACCTAATAAACTGATCATATATGCTATTGCGGTAGATTATCGGGAAGGTAAATTAATAATCATTCATG  
 AATATAAAGAATTTATGGAAGAAGTTTAAGAAATAAAGAACAAACAACAACAACAACAACAACCTTGAATTTG  
 TTGATATTGAATTTAATATTGTTTCTAAAAAATCTGAATTAATCATGATTTAATAAATAATGATACCAATAATA  
 CTATTGAATAATCAACAATTTATAACAAAGAAGTAAAGTGGATTTAGTCATAGAAATGTCACCTGTTGTTAGTTTCAG  
 CTATTATTAAATGGAAACGTAGGAATCATATGATAATTAATGATGATGATGAATAATTAATGAATTTGAAA  
 CTCCAGAAATGGGAAATCACTTTACCATTAATCTGAACCAAGAGTTTATTTCTGATATTATGAACAAGAACAAGAAC  
 AAGAGCAAGAGCAAGACCAAGATGCTAAACACAATTAATGGTTATAAATTAACAATATATTTTAGAAAATCCAACTC  
 CGAGAGTATTTACATTTACTACCCAAATGACTGATTATGAAGATCAATGGATATTCACCAATTTCAAAAAATATTG  
 TCCCTTGATCCAACTCCATTTCCCGTATTACCATTTAGTCCACATTATATGGATTTCATAGGTGAATATTAC  
 CAGCACTGGAAGGTATGAGTGAATTAATCCCAATTTAGGGTGTGGGTCTGAGTCTGGGTGGGTGGGATTGA  
 AATTAACCTAATTTAAAGTATTTGATCTTCAATATAAAGTGAACATTCCAATTGTATCAGTTCTGAAAGATATCA  
 CCAGCATACCTAAGAATACTGGGAATTTATATTACAAACCAAAATAACTAAACTAATAATCTCTTTGTGTTTAT  
 ACATTTCTCAAAAAATAAATAATTCACACATATATTATCAATAGTGGGTCTGGTCTGGTCAACACACATAATTA  
 CTCACCATTAACACCAAGTAATTCACCTTCGAAAACAAGAGTTTCATTAGCACCAATAATTTGGTGGGATACCTCT  
 TGGACCATAAAGCCAAATTTGGTGGAAATAGTTAAATTTGCTTTAGTTCCCTTTGAAATTTTAGGTAAATTAGCAC  
 ACCTTTACCATAATTTTAGTTTAAAGAAATATCCCAACCTTCAATAACTTGACCAACCAACAACAGTACAAGTAA



[illegible]



229/251

YNL131W\_homolog 150aa PathoSeq: 1..150 (SEQ ID NO 670)  
MVKLTQIDDETQQQFENQSVAKNNHIIDASSEESDDDDSDDDDFDENETLLERIVALKQIVPPEQRE  
SIYNLESTIGDLFKSSVQNGGKFLNLTLSSSLLLGVPALAILSETQLQEWERGMSLFXSAQDVTAPCSFA  
AFQNNKK

[illegible]

YDR544C\_homolog 1700bp GeneSeq: 1..1700 (SEQ ID NO 673)

CTAAAGTCCAAAGTTGGTTCAATTTTGGCAGAAAAAGAGAGGAAAAATTCACCTGGAGCTGATTCAAATTCGTG  
AAGATGAACCAATATCTCAGGTTCTTTGCCACCTACAAGAACTAGGAATTCAATCGGTGTTGCTCTCCGAGTAAAC  
AATAGAAAGATCTTTTATTTGACCGCTTCCATAGAGATGAGCTAGCACTGGCATTAGCAGACAACTAGCAGCAGC  
CAGCAGCCTTTGATGATCTTTGCCCTACCGCAGAGAGGCTCAACGGAAATCCCAATCACCAGAAGCTCCAC  
AGGCCAAATCACTAGAGCCTGTATCAGAAGTACTAAAAGAACTGTTCCCACTTATGCAAAACCGGTCGGAAGGAA  
AGGTGAAAATCAGCAGTCGAGAGTTGATGTATCCTCTCAAACTTGTACCCAGTTACTCCTACTCAGGATGGATT  
GTTGGTTCTGTTAAACCAATTAACAGAACCCTGTTGATTTCTCCAAATGTGATTAAATTAATGACCTGGACACTCTT  
CTACAGAAGAACCTAGAGGCTCGTTACTTGAAGAAACACAATTTAGAAGTACAACCTGTATCTTCCCAATTCAATAC  
TCAACCGCCACCACTCTGCCACGAAGAACTCCAGATCTAGACAAAGCACTGATGCCAATTAATCTGTTTGAAGCGGGT  
GATGATTTCCAAACCAATCTCGGCTACTCCAAAGATCCGAGCAAAATGTGTTTGGACAGATGCCAGACCCAAATTTGT  
TCTCTGAAAGAGACTTTGCTCTCCACCACCACCTTTCGAGAGAAATTTTGCACCATGAAGAACCACTGTAAAGGGA  
TTCAGCTCTTTTCCACAAATTTACCTGCTGCCCTCCCACTCTGGAAGAGATTGGGTAATGGCTCCATTACCAAGTCAA  
GACAGGGGTCATTCTTTTCAAAAATGATTTCAACACGAAACCTTGGCATCCACCTCTGGATTGAGCTCTCTCTA  
TTGCTGAAGTCATCAATGCCAGCTTTAAGGATGGACAGTTGATTAAATCAACAGTAGTTTGTGAAGTGGCCCTCAA  
TTATAATGGTAATGCTTTCCGATCCCACTTGTGGTCACTATCCCTAATAGTTTTCGATTAAGATCTCTGTAACAGACT  
TTTATTTGAGATTTTAGGTCAAGCAAGTATAAAGTGAACCTCAATTAAGTCTAAAACCTTTGGTGGCTTGA  
ATATCTTTTCAAAACCAACACAGTACCAGTGAATTAACCAATATCGAAATTTGAACCTCAAGTCAAGTTT  
GATGGTTAGCATTCGTTCAACTACACCTTTGGTATTGGAAAATTTGTTGTCTCTGTAGCTTTGAATCAAGACATT  
GAAGCAACATCTGCTTCTCCTCAAGGCTCAAGGTGCGTTTAATAAAGAGAAAAACACAATAACATGGAGATATCCAC  
AGTCCCTCGCATTTGAATGGTGTAGAGCGTTTGATAGCTAGATTATGACTAATGGATTGGGTTCCGACATGAGTC  
TGGTGTGCAGATTAATTTCAAGTTAAAGGATCCCAAGTCAAGTACTGTATATTTACAGTGAAGATGGCGAGAG  
ATTCCTACGTTTATGAAATTTGGTTAGCGGTAGTTATAGTGGTCATCTTTAAGTTATCTGTTTTCAGATTAGCTCTCT  
TGTGTAATTTGAAAAAATTTTGGTGA

YHR094C homolog 1653bp public: 1..1653 (SEQ ID NO 687)  
 ATGTTCATTAGCATTAATTCACAGAAAACCGTGATTTTGGAGGAAAAGGAAGAAATCCAAAGAACGAACAT  
 AACGAACAAGGCGAACAAAAACGAGAACAAATGAGCAATATACCTACCTTTGGGAAGATTAACCATTCGAAGGAA  
 TATATTTGGGATTAGTATATCTGGTGTTCCCTTATTCGCTTTGGTGGTTTCGTTTTCGGTTTCGATACCTGGT  
 ACCATCTCTGGTTTCATCAACATGATGATGATTTTATGAAGAATTTGGTGGTACTAAAGCTGACGCTACT  
 CTTTACCTTTTCCAAACGTATGAAGACTGGTTTATGTATGGTTTGTTCGAATCTCCCTTCGCCAATTCGTGCA  
 TTTATTCCTGTCTAAAGTCCGCTGATATGTAATGCTAGAACACTTGGTATCATGACCTGCTATGATCATTAT  
 ATTGTTTGGTATTATTCTCTCAAAATTCCTTCTCAACATGCTTGGTATCAAATCATGATTGGTAGAATTATC  
 ACTGCTCTTGTCTGTTGGTATGTTATCAGTTTGTGTCCATTATTTATCTCAGAGTTTCTCCCAACAT  
 TTAAGAAGTACATATAGTTTATTTGTTTCCAAATTGAATGATTACCTTTGGGTACTTCTTTGGGTTACTGTACC  
 AGTTACGCTACTAAGAAATATCTCTGACATCCAGACAAATGCAATTCACCTGGTTTATGCTTTTGTCTTGG  
 CCGCTTGTGTTTGGTTGGTATGGTAAGAAATGCAAGAAATCTACCTTACTTTCCTCCCTAAGACATAGA

231/251

ATTGACGATGCTAAGATTTCACTTGGCCAAACTAACAAGGTTTCTCCAGAGGACCCCTGCATTATACCGT  
 GAACCTTCAATTAATCCAAGCTGGTGTGAAAGAGAAAGATTGGCCGGTAAGGCATCTTTGGGGTGGCTTTA  
 ATCACTGGTAAACCAAGAATCCTTGAAGAGATTATCTTGGAGGTATGTTGCAATCATTTGCAACCAATTG  
 ACTGGTGATAACTATTTCTTCTACACAGTACCACCATTTTCAAGTCTGTCCGGTTTAAATGATTTCCTTC  
 GAAACATCTATTATCCCTGGTGTCAACAACCTTTGGTCCCACTTTTCTTGGTATTTATGCCAATGAAAGA  
 TTGGGTAGAACACTCTGTTTATTAACITGGTCCCGTTGCCACGTCCATTTGTTTCTTAATTTACTTCATTG  
 ATTGGTACTCAACATCTTTACATTGATCAACCAGGTGGTCCAAACAGAAAAACCAGATGGTAACCGCTATG  
 ATTTTCACCTACTGCACCTTTATGTTTTCTTCTTCCGTCTCTACATGGGCTGGTGGTGTCTACTCCATTGTT  
 TCTGAACCTTATCCATTAAAGTCAGAAGTAAGGCTATGGCTTTTCCCTAATGCCATCTAAGTGGTTGTGG  
 GGTTCCTTGATTTCTCTTCTTCACTTCATTTATCACTGATGCTATUACCTTCTATTAATGGTTTATGGT  
 ATGGGCTGTTTATGTTTTCATTTCTTCTTGTCTTACTTTATGATTACGAAACTAAAGGCTCTTACTTTA  
 GAGGAAATGATGAATTATACTCTACCAAGGTTGTTCCATGCCAAATCAGCCGTTGGGTTCCACCTTCT  
 CACGAAGAAATCCTTCTTCTGCAAAAGGCTATACTGGTGATATCCACGCAGATGAAGAGCAAGTTTAA

YHR094C\_homolog 550aa (SEQ ID NO 688)

MSLDNSTENRDLEEKKEEIPKNEHNEOGEONENNEHIPTLEDKPLKEYIGLSILQFLIAFGGFVFGFDTG  
 TISGFINMTDFLERFGCTKADCTLYFSNVRTGLLIGLDFNVGCATGATFTSKVGDMYGRRVGIIMTAMLIY  
 TVGTTIVQTASQHAWYQIMIGRTITCLAVGMLSVLCPFLSEVSPKELRGTLVYCFQLMITLIGIFLGYCT  
 SYGTTKYSDSRQWRIFLGLCFWALCLLGGMVRMPESPRYLVGKDRIDDAKISLAKTNKVPEDPALYR  
 ELQLIQAGVERERLAGKASWGALITGKPRILERVIVGGLQSLQQLTGDNYFFYYSTTIFKSVGLNDSF  
 ETSEILGVINFASTFVGIYAIERLGRRLCLLTGSAVMSCTFLIYSLIGTQHLIYDQPCGPTTRKPDGNAM  
 IFITALYVFFFASTWAGGVYSIVSELYPLKVRSKAMGFANACNWLWGFLLSFPTSFITDAHFYYGFVF  
 MGCLVFSIFVVFMIYETKGLTLEIDELYSTKVPWKSAGWVTPSDEEMVRAKGYTGDIHADEEOV

YBL099W\_homolog 1344bp public: 1..1344 (SEQ ID NO 717)

ATGGCTTTGAACTTGAAGCTGACCAAGTCCGCGTTCTCTCTTCCGTTCTGATAGATTAGTCAAAAGAA  
 GGTGAAACCGTCAAGAGAACTGGTCAAATTGTTCCGTTCCAATTGGTCCAGAAATTGTTAGGTAGAGTT  
 GTTGATGGTTTAGGTAACCCAATTGATGGTAAGGTCCAATCAAGGCTGCTGCTTACTCCAGAGCTCAA  
 GTTAAAGCTCCAGGTATTTTACCAAGAAGATCCGTCCACGAACCAATGCCAAACCGGTTTGAATCTGTT  
 GATGCTTTCCGTTCCAATTCCCTACAGGTCAAGAGAAATGATCATTTGGTGATCGTCAAACCTGGTAAACC  
 GCGCTTGCCTTGGATGCCATCTTGAACCAAAAGAGATGCCAACAATGGTCTCTGACGAAAAGAAGAAATTG  
 TACTGTGTTTACGTTGCCGTTGGTCAAAAGAGATCCACTGTTTGGTCAATTTGGTCCAAACTTTTGAACAA  
 CACGACGCTCTTAAATACTCTGTTATTGTTGCTGCTACTGCTTCTGAAAGCTGCTCCATTGCAATACATT  
 GCTCCATTCACTGCTTGTGCTATTGGTGAATGGTTCCAGAGACAATGGTAGACACGCCCTTGATTGCTTAC  
 GATGATTTGTCCAAACAAGCTGTTGCTTACCGTCAATTGTCAATTATTGTTGAGAAGACCACCAGGTAGA  
 GAAGCTTACCGTGGTGTATGTTTCTACTTACATTCCAGATTATTGCAAGAGCTTGTAAAGATGCTGTAT  
 GCTTACGGTGGTGGTTCTTTGACTGCTTTGGCCAGTTATTTGAAACCAACCTCGTGATGCTCTCTCTCTAT  
 APTCCAACATAACGTTATTTCCAATTACTGATGGTCAAAATTTCTTGGAGCTGAATTATTCTACAAAGGT  
 ATCAGACCAACCTATAACCTCGCTTTCTCCGCTCTCCGCTGCTCGGTTCTGCTGCTCAAGTTAAAGCTATC  
 AAACAAGTTGCCGGTTCCCTTGAAATTCTTCTTCCGCTCAATACAGAGAGTTGGTGGCTTTGCTCAATTT  
 GGTCTCTGATTGGATGCTTCTACCAACCAACCTTGAACAGAGGTGAAAGATTGACCCAATTATTGAAA  
 CAAAAACAATACAACCCATTGGCTCCCGAAGAACAAGTTCCATTGATTTTGGCTGGTGTAAACGGTTTC  
 TTGGACAATCTTGGCTCTTGACAGAATTGGTGAATTCGAAGAAGCTTTCTTGGGTCACTTGAANTCTAAC  
 GAAACTGGTATCTTGGATGCTATTAGACCAAGGCTGATTATCTAAAGATGAATTAGAAAATTGAGA  
 AAGTCAACCAAGAATTGGTGGCTTCTTTCTAA

YBL099W homolog 447aa public: 1..447 (SEQ ID NO 718)

MAINLEADQGVVLFQSDRLVKEGETVKRTGQIVSVPIGPPELLGRVVDGLGNPIDGKGPICAAAYSRAQ  
 VKAPGILPRRSVHEPMQTCCLKSVDALVPIGRGQRELIIIGDRQTGKTAVALDAILNQKRWNNGSDEKKKL  
 YCVYVAVGQKRSTVAQLVQCLEQHDALKYSVIVAATASEAAPQYTAFTACATGEWFRDNGRHALIVY  
 DLSKQAVAYRQLSLLLRPPFGREAYPGDVVFLHSRLLEAAKMSDAYGGGSLCALPVLETQGGDVSA  
 YIPINVISITDGOIFLEAEIFYKGRPAINVGLSVSRVGSAAQVKAKQVAGSLKFLAQYREVAAPAFQF  
 GSDLDASTKQTLNRGERLTQMLKQKQYNPIAAERQVPLIFACVNGFLDNVALERICEFEEAFLCHLKS  
 NDTGILLDAIKTKGELSKDELEKLRRKVTDEEVASF



232/251

YF032W\_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)

AUGGATGAACGATTTTGTGAATCCACCACCTACAGCTGATCAAGATGATACTAATCAGCCACTTGATGCC  
 ATCTTTGGTGATAGAGTCAGAGAATTTCAAGAGTTTTTAGATAGAATTGATTCTAATACAGGTATAGAT  
 TACAGATCTATTATCAAAGATATGTTGATCAACACTAAGTTTACATTGAGTGTTCATTGATGAAAATA  
 AGAGAGTTTGACAGAGAATTTTGGTTTGGGTTGCTCAACCAGCCAGCTGACTATTTACCAGCTTGTGAA  
 AGACCTTTGAGAGACACAGTTTTAGCTAATTACGACCCACAGGATCCAAGTTTCCACATGACAGTTAT  
 GACCCTAACCAGCAATACTATTTATCATTCAAGGGAGCATTTGGGGGACATTCGCTCACTCCTAGATCG  
 ATTGATTCAGCTATCTTTCCAAAATGGTTTTCTATTGAAGGTATTGTGACTAGAGCTTCATTAGTTAGA  
 CCAAAGGTTATTAGATCGGTTTCAATTATGCTGAAAAAACTGGTAGATTTTATGCACGTGAATAACCGAGAC  
 CAAACAACATCCTTTGATGCCAATTCCTACTCCCGCTATATATCCAACCTGAAGATATGGAAGGTAACTAA  
 TTAAACCACAGAGTATGGTTATTCGACATACAGAGATTACCAGAAGATCTCTGTACAAGAAATGCCTGAA  
 ACAGCTCCTTCAGGTCAATTGCCAAGATGGGTTGACGTTATTTTGGATGATGATTTGGTGGATTTGACA  
 AAAACCGGTGATCGTGACAAATGTTGGTGTATTCGTTGCCCTTAGGAGGTGCTGCAAACAATAGTTCT  
 TCTTTCAAAACGGTTATCTTAAGTAAATCTGTTTACTTGTACATGCCAGATCAACAGGGGTTGCTTCA  
 CAGAAAAGTTAACTGATCAAGATATTAGAAATATAAAATAAACTTCCAAACCATAGAAACATTTTTGAT  
 ATTTTATCCCGTTCTTTGGCCCTTCAATTTATCGGTTTGACTATATTAAGAAACCTCTTTTACTTATG  
 ATGATGGGAGGTGTTGAAAAAAATTTAGATAATGGTACACATTTGAGAGGTGACATTAAACATTTTGAATG  
 GTGGGTGACCCATCCACTGCCAAATCTCAAGTATTACGGTTTGTGTTGAACACTGCTTCATTAGCTATT  
 GCCACTACTGCTAGAGCATCGTCAAGTGTAGGTTTAAACAGCTGCTGTTACTACCGACAAGGAAACACCGA  
 GAAAGAGAGATTGGAGGCTGGTGCATTCCTATTCGCTGACAGAGGTATTGTTTGTATTCATGAATTTGAT  
 AAAATGTCAGATATCGACCCGAGTGGCCATTACGAAAGTTATGGAACAAACAACTGTCACTATTGCTATAA  
 GCTGTGATTTCACACCTTCATTGAATGCTCGTTGTTCTGTTATTGCTGCGCAAAATCCGTTTTTGGACAC  
 TACGATGTCCATAAAGATCCACATAAAAAATATTTGCTTGGCCGATTTCATTATTGCTCTCGTTTGTATTG  
 CTCTTTGTTGTTTACAGATGATGTCAACCCAAACAGAGACAGGGTTATTTCTGAGCATGTTTAAAGATG  
 CACAGGTTTGTTCCTCCTGGATTGATGGAGGGAGAGCCCAATCAGAGAAAAATCAGCAGTTACATTGGCT  
 GTCGAGATGATGAAACCAATGAACAAGAAATTATTAGAACAGCCCAATGTTTGAAGAAATTAACACATTA  
 TTGCATGCTGTTATTCAAAACAAAAAGTCAAAATAAATATCTTTTCGATTCCATTCTTTGAAAAAATATGTC  
 CAGTACGCCCAAGCAAGAGTGCACCCAGTGTTCACCAAGGGTGCATCCGACTACATTGTTACTACATAT  
 TCCTCCTTAAGAAACGATTTCATACGCCAACCAACCAACAAATACAGCTCCAAATAACTGCTAGAACTTTA  
 GAACCTTTGATTTCGTTTACCAACAGCTTCATGCAAAAGTCCGTTTATCCAAAACCTCTTCATCTGAAAGAT  
 GCAAAAGTTGCCGAGAGCTATTGAGATATGCATTATTCAAGGAAGTAGCCAAAAGACAAAAAGAGA  
 CAAAAAACTACAAAGTATAGTGGACTCAGAGAGGAGGAGAGAGATGAGTCTGATGCAGAAATGGAAAT  
 TCCGATAACGAAATAATGCCAGAGAAAGTATAGAAAGAACAGAGCTACAGCAAAACACAGACTCCCA  
 CAACAGCAACAGCATCTCCTTCACTAACACCCGAAACCCCACTTTGGACATCCGGACCATGGAGATGAC  
 GATGGAGTTGGTGAAGAATTAGAACAATTCATTTTGTCATCATCTCAGCAACACAGCAACACAAATAT  
 TTGCAACCATTCAGTGCAGATCATCAAGTAACTTTGTATCATCTACCGCCACAAATGCAATCAGCGTT  
 GAGAGATTGAATAATTTTCAAAAGAACTACTAGCCAGGTGTCAAGTTCTGCATTATTTGCCAATGATCAA  
 GCTGCGGCAAACTATCATGACGTTACTGCTGCTATCAATGAACAGATGGAACAAGAAGATATTTTCTCA  
 GAGCAAGAGTTGAGTGTGGATTTGAAGTGTGAGTTCTGAAAACAAGTTTTACCTAGAAAGTGATAAG  
 ATTTGGAAGATTAA

YEL032W\_homolog 878 aa public: 1..878 (SEQ ID NO 720)

MDERFVNPPPTAQDQDINQPIQATFGCVRVFQEFLEDRIDSNQIDYRSIIKMDLIKSKFRLSVSIDEI  
 REFDFEFWLGGLNQPAJYLPACERARCTVLAIYDPQDPSPPHDSYDPNQYYLSFKGAFGGHSLTPAS  
 IDSSYLSKMSVIEGIVTRASLVRPKVIRSVHYAEKTGRFYAREYRDQTTSFDAIATPAIYPTEDMEGNK  
 LTTEYGVSTYRDYQKISVQEMPRTAFFGQLPRSVGVLEDDDLVDLTKPQDRVQIVGVYRALGGAANNSS  
 SFKTVILSNVYLLHARSTGVASQEKLTDDQIRNINKLAKDRKIFDILSRSLAPSIYGFQYIKKAVLLM  
 MMGGVYKNNLVNTHLRGDIINLMVGGFSTAKSQVLRPVLNATSLAIATTGRGSGGVLTAAVTTDKETG  
 ERRILEAGAMVLADRGIVCIDFDMSDIDRVAIHEVMEQQTVTLAKAGIHTSLNARCSVIAAANPVPFGQ  
 YDVHMDPHXNIALPDSLLSRFDLLFVVTDDVNFTRDRVISEHVLRMHRFVFPGLMEGEPIREKSAVTLA  
 VGDDETNEQELLEQPMFEKFNLLHAGIONKKSNNILSIPFLKKYVOYAKORVQPVLTKGASDYIVTTY  
 SSTANDLICNNQRNTAPITARTLETILRLATAHAKVRLSKTVDVKDAKVAEELLRYALFKEVAKKTKKA  
 QKTTGIVDSEEEDESDAEMENSDNEIMPRESRRRTRATAQTQPFQQQASPSLTPEPLGHRDOGDD  
 DGVGEELECFHLSSSQOQOQOQYLOPLTERSSSKIVSSTATNAISVERLNIKFRILAQVRSALFANDQ  
 AAANYHVDVTRALNEQMEQEDIFSEQELSGAFVMSSENKFYLESDKIWKI

233/251

YHR135C\_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)

ATGACAACAAACCCCTGCTTTGGGUGGCTGCTCAAGCAATCATAAATAATATTCCTACAAAGCAAAATGAAT  
 CATTCACACTTCATCTTCAAAACCGTAACGGTAGCAATAATTCATCCGTGGTTGGACTTCACTACAAGATT  
 GGGAAAAAATTTGGTGAAGGTTCTTTTGGTGTCAATTTTGAAGCTACTAATATAATAAATGGAGTACCC  
 GGGGCCATAAAATTTGAACCTAGAAAGACTGAAGCTCCTCAATTACGAGATCAATATAGAACTTATAAA  
 CATTTACAAGGATGTGACGGAATTCCTAATGCATATTATTTTGGTCAAGAAGGATTACATAATATTTTA  
 GTCAATTGATTTATTTGGGTCTTCTTTAGAAAGATTATTTGATTGGTGTGGTGAAGATTTACTCTTAAA  
 ACCGTGGTACAAGTTGCTATACAAATGTGACTTTAGTAGAAGAAGTTCATCGTCAATGATTTAATCTAT  
 AGAGATATCAAACCCGACAAATTTTTTAATGGAAGAAGAGGTGCTACTGATGAAAATAATGTTCATTTG  
 ACTGATTTTGGTATGGCCAAGCAATATCCTGATCCCAAGAACAAACCAACATATTCATATAGAGAGAAG  
 AAATCTTTGAGTGGGACAGCTAGATATATAGTACTTAACACTCATTTAGGAAGAGAACAATCAAGAAGA  
 GATGATTTTAGAAGCATTTGGGTCAATGATTTTTTTTTATTTTCTTTAGAGGCCAAATTAATTTAGGAAGGTTTA  
 AAAGCTCCCAACCAATAAACAAGATATGAGAAAATTTGGTGATAAAAAGAGAACTACACCAGCAGTTACA  
 TATGTGATGGCTTACCTCAACAAATTTGCTGAATATTTAGATTCAAGTTAGATCATTACCATTTGATGCT  
 GAACCTCCATATCAAGAATATAGAATGTTATTTATTTGTCAGTGTGGATGATTTGGGTCAAGCTTGTGAT  
 GGAGATATGGATTGGATGTCATCTTAATGGTGGTAGAGGTTGGCATCCTACATTTAATAAAAAACCCAAC  
 TGGCAGCGTTATGGACATCCTAATCCACCAAAATGAACGTGAAGAAGACATCGTGATCAAGAAGAACAA  
 AGACAACATCAACAACACTGCAACAAGTACAACAACAACAATTACAAGCTCAAGCTCAAGCTCAACAACA  
 CAACAACATTACAACAAGCACAAACAGGCCACAACAACAACAACACTGCAACAACATCAACCACTATCTGCA  
 GCCCAGTTACATCAACAATAATTACAGCAATTTGGTTAATCGACCATTACCACCAATTTAAACAAGATCA  
 CAATCAGCAATCAAAAGTGGTAATGGACATCATGAACCTTTTGAATAATAATTTAGGTGATCAGCATGGA  
 GGAACAACATGAAGGATACAGTTACAGACCAAGATCAATATCAACAACAACAATCGTTTGCUGAAGAAGAA  
 GAAAACAAGGGTTCTGGTCTAAATTTGTGTTGTCATTAG

YHR135C\_homolog 495 aa public: 1..495 (SEQ ID NO 722)

MTTNPALAAAQASHNNIPTKQMNISTSSSNGNGSNNSSVVGTHYKTKGKTGEGSPGVIFEGTNTITNGVP  
 VAIKFEPKCEAPQLRDEYRTYKHLGGCDGLENAYYFGQEGLEHNLVLDLLGPSLEDLPDWCGRFPVSK  
 TVVQVAIQMLTLVEEVHREDLIYRDIKPDNFLIGRRGATDENNVHLIDFGMAKQYRDPRTKQHLIPYREK  
 KSLSGTARYMSINTHLGFEQSRRDDLEALGHVFFYFLRGQLPWQGLKAPTNYKQKYEKIGDKERTTPAVT  
 LCDCLPQQFAEYLDVSRSLPFDAPPYEEYRMLLLSVLDDLQACDGDMDWMHLNGGRWDATINKPEN  
 LHGYGHFNPPNERERRRHRDQKMTQHQQQSQQVQQQQLQAQAQAQQLQLQAQAQAQQAQQAQQAQQAQQA  
 AQLHQKQLQHUVNRPLPPIKQESQSAIQSCNCHHELLNNNLGDCHGGKHEGYSSRPDQVQQCQMVAAEE  
 ENKGFWSKLCCH

YJL060W\_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

ATGTTAAGACGGCTCTTTCCAATACGACAATTGTACACAACAACCTAGAGCCATGGCCAGCAAAATCAACA  
 GACCCAACTAGTTTTCATATAATCCGTATTTTATCAAAAACCTGGGGCAAAAAGATATCTGGTCTGTTAATC  
 AACGAAACTGCGGCCCCAGGCACAACAAGAATCCGGCGAGCCAAATTTGTCAAATTGGGACAAGGGTTTTC  
 TCCTACAAATCCTCCTCACTTTGCGATTAACGCTGTTGAGGAAGCATTGACCAAGCCGCAATTCAACCAA  
 TATGCACATGCTCGTGGAAACCCAAACTTATTGAAACAAGTGGCAGAGCACTATTCCGCTATCGTATGGA  
 CGTGCTGTGGGGGTTGACGAGGTCCAAATCACCAACGGGTGCAANTGAGGGAATGTTTGCCATTTTCTTT  
 GGTTTCTTCAACCCCGGCGCATGAAGTCATTGTGTTTTGAACCATTTTGTGACCAATACATCCCCAATGTT  
 GAAATGACAGGAGCCAAGATCAAGTACGTTGAAATCAAGTATCCCAAGAAATTTGACAAACGAGGTTGTC  
 ACCGGCCAGGATTGGGAGATTGACTGGGAAGGATTGAAATAATGCCATTACCCACACACCAAGATCATC  
 GTGATAAATACCCACACAAACCAATCGGCAAAGTTTTACCGAGAAGGAGTTGTACAAGATTGGCAAG  
 CTTCGCCGTGGAACACAATTTAATCCTTGTGAGGCAAGAGGTTTACCGAGAAGTTGATATATACTGACAAG  
 TTCCCTCGTCCAGCTGCATTACCAAGTTGCTGAAATGGCTGAAAGGACGTTGACAGTTGGGTTCTGCT  
 GGGAAATCATTTTCTGCCACTGGTTGGAGAGTAGGGTATATCCAGGGCCCTGCCAATTTGATTAATAATTT  
 GTAACACGCGGCCACACCAAGAATTTGTTTTCTCGACCCCAACACCATTCACACACCCAGTATCTCAGCCC  
 TTTGAGCAGGCTGAGAAATCAAACTATTTTGGGAACACTCGAAAGGAGTATGAACACAATACAAATA  
 TTCACCAAGGTATTTGACGACTGGGGTTACCTACACCGTTGCCGAAGGAGGGTACTTTGTGTTGGTG  
 AACTTGCTGAAAGTTAAGATACCCGACATATGACTTTCCCGGAACCATCAGCGATAGAGGCACTTTA  
 GATTTCAAATTTGGCGTATTTGGTTGATCAAAACAATTTGGGGTTGTGGGAATCCCTCCAACAGACTTTTTA  
 ACCGAATCGAATAGAAAGGGGAACCGCTTACAANNCTGTGTCAGATTTGCTGTTTGCAAGATGATTCT  
 GTTTTAGAAGACCGCGTTGAGAGATTGAAAAAATTAAAGACTATTTATAA

234/251

YJL060W\_homolog 453 aa public: 1..453 (SEQ ID NO 724)

MLKRLFFPIRQLYPTTRAMASKSTGPTSLHNPYFYQKPGQKDIWSLINETAAQAQOQESGEPIVNLGQGFF  
 SYNPPEFAINAVEEALTKPQFNQYAMARGNPNLLKQVAEHYSRSYGRAVGVDEVQETTGANEGMFAIFF  
 GFLTPGDEVIVFEPFFDQYITNVEMTGAKYKYVEIKYPKKFDNEVVTGQDWEIDWEGLNNAITDKTKIT  
 VINTPHNPICKVFTEKELYKISKLAVEHNLILVSDVEYENLYYTDKFPRAALPQLPELAERTLTVGSA  
 CKSFAATGWRVCYIQGPANLIKFTAAHTRICPSOPAPLQQAVSQGFQAEKSNYFENTRKEYEHKYKI  
 PTKVTFDDLGLPYTVAEGGYFVLVNLKVKIPADYEFPGTISDRGTLGFKLAYWLIKEIGVVGIPPIKFL  
 TESNRKGNGLENCVRFAVCKDDSVLEDAVERLKKLKDYL

YML028W\_homolog 591 bp public: 1..591 (SEQ ID NO 725)

ATGGCTCCAGTCGTTCAACAACCAAGCTCCCAAGTTTCAAGAAAACCGCCGTCGTTGATGGTGTCTTTGAA  
 GAAGTCACCTTTAGCAACAATACAAAGGTAAATGGGCTCTGTTGGUUTTTATTCATTGGCUUPTTACATTTC  
 GTCTGCCCATCAGAAATTATTGCTTATTCCGAAGCTGTAAAGAAATTTCCGAAPAGGATGCTCAAGTT  
 TTGTTTGCTCTACTGACTCCGAATACACCTEGTTGGCTTGGACCAATGTGCCAGAAAAGACGGTGGT  
 ATTGGCAAGTCGACTTCCCAAGTCTTGGCTGACACCAACCACTCCTTGTCCACAGACTACGCTCTCTTA  
 ATTGAAGAAGAGGTGTTCCTTGAGAGGTATTTTCTTGATTGATCCAAACCCCTCTCTTGAGACAAATC  
 ACCATCAATGACTTTCGCAATCGGTAGATCTGTTGAAGAATCCCTTGAGATTGTTGGAGGCTTTCCAATTC  
 ACTGAAAAATACGGTGAAGTTTGTCCAGCTAACTGGCACCAGGTGATGAAACCATCAAGCCAAAGCCCA  
 GAAGCATCCAAAGCAATACTTCAACAAAGTCAACAAATAA

YML028W\_homolog 196 aa public: 1..196 (SEQ ID NO 726)

MAPVVQQPAPSFKKTAVVDCVFEEVTLQYKKGWLLAFIPLAFTFVCPSEIIAYSEAVKKFAEKDAQV  
 LFASTDSEYTWLAWTNVARKDGGIGKVDFFVLADTNHSLSRDYGVLTRREGVALRGTFLLDPKGVLRQI  
 TINDLPVGRSVEESLRLLLEAFQFTEKYGEVCPANWHPGDETICKPSFZASKEYFNKVNK

YOL100W\_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)

ATGCATAAATTTAGATATTTCTTTCGCAUCAAACACTATAGCAAAACGCAATTCAGGTGACAAATCCAAAGAC  
 AGTCCAAATTAGCCAAAACAGCAATGAAGAAAATGATTGCACTAAATTAAGTTCAAGTAGTCTTCAAGAC  
 TTACATGATGATCTCGATGATATTTATAACAATATACTTTAGCACAGGCTACCAATAACAACTCTTA  
 GATAATTTGGAATCTGAAAATAATCAAGCTATAAATAACTTTATTGATAAACCTCCAGCAATTCATGGT  
 ATGGAAACCACAACCTACCGGTGATGCACGTTTCTTCACGATTATCTTCTTAGGTAATACCACCAATGAA  
 ACCGGTGAAGCATCGCCAAAGTGCAACCAAGCAATCCGTTATCTTCACATTCATTTGATTTCAGACCG  
 CATCATCTCTGTCAGTAACCAACTCATCCCTCAATGTATTGTTAGACACCCCTAATGTCAAGTCCGAA  
 TTCAATCATTTAGTGGATCAAACACCAACCCCAATGAGTCCGTAGAAAGGTTTGACGACAGTAATAATACT  
 GTGGACAATACAGAAGAGGAAGAAAATAATGATGATACAGACGAAATAUCAAATCCGAAACATTGAA  
 CAAACCCAGCAGAAATTCGGAAATTAAGGGTGTCTGCAAGTTAAACTATCAAGACTATGGATGGAGAAATC  
 AAAACTATTTCGGCGAAATGTTACTGATTTCAAATTTGGTAAAGAATTGGGTGAAGGTTTCATATCCACG  
 GTGATTTTAGCCACTGATAAGATTACTGGTAAACAATATGCTGTAAAAGTACTTTCATAAGCGACATATT  
 ATAAAAGAAAAGAAAGTCAAGTATGTCAATATAGAAAACATGCATTGAATCGATTAAAGTAATAGATTA  
 GGGGTATTTTCATTATATTTACCTTCCAGGATAAAGATTCCGCTTATTTTGTTTTGGATTATGCTTCA  
 AAUGGTGAATTTATTGACATTTGATCAAGAGATACAACTATTAATGAGGAATGTACTAGACATTTTGGT  
 GCACAAATATTAGATGCTATTAATATATATGATGATAATGGTGTTATACATCGAGACCTAAAAACCAAG  
 AATATATTATTAGATGACAAATGACAATTCAAATTACACATTTTCTTACTGCCACATTTATTAGAGAAA  
 AAGAAATGTTGAAAGTGAAGAAATACCCAGTGGATGTAACACCAAAATCATTTCCTTCCAAACCGCTGAATAT  
 GTATCCCTTGAAATTTAGAAAATAAGTATTGTGGTAAACCTGGAGATGTTTGGGCTTTTGGTTGCAATC  
 ATATATCAAAATGATTGCTGGGAAACCAACATTTAAGCCAACTAATGAATATTTAACCTTTCAAAAAATT  
 ACGAATTTGCAATTTGCGTCTAGTGCAGGATTCCTTACAATATTAGAGATTTAATAAAGAGATTTCTT  
 GTGTTGCCAACCTTACGACGTGGCACCAATTCACAGAAATACAAAAACATTACTTTTCCAAATCCGTTCCAC  
 TTAAAGATTTTGTATCTGATTTGCTGTCTGATCTCTCTGAAATAGCACTTTATATTAATGACACGAAAA  
 TCCATGATGAAAGTACCGGAATTGAATAAGGCACCTATAACCACAGTCATTAAAGAAGAAATGTGAAGAAA  
 TCCACAAACTCAAAATCAAAATACCAACAATGTGCCCACTGCTGTTGGTGGTAGTAGTAGTAACGGACAT  
 AAAGCGCTCTACCCGACTCTTGAGAAAGAGCCGAGCCGAGCTACTATTAATAACAGTCCACAGAAATA  
 GTTAGTGCCGCTAGTGTAGCTGCATATGTTTAAACAAACCAAGCTACAAACCAAAATTCAGTACATCC  
 GAGGATTCATCTAAGCGTAGCAGCACTCCAATGAACTCCCAAACTTTGATATTCACAAACAGGATTAT  
 ATTCCGGGAACAAATATTTTACGTCCACAGATTACTACTAGACCGTCAGTAGGATCTTATGTGAAAACC  
 ACACCAATCAAGGATAGAAAAACATTAACCAAGGTCCCACTGAATATCCATCAACAACAGAAAAAGTGG

235/251

AAACUGAAAGTAAAGGAAGTGAAGCCAGCAACTACATTGGGAAGCAGCATGGGAAACCATATTTAACCCAT  
CCAGATGAAAGAATACTTCGTATTGGTCCAGTTATTGCTCATAAAGAACCAACAGAACCATTTGAAAAG  
AAGAATAAAGCATCTTTACATATATCACCTTTGGATATAAATAAAGAAACAAAGAGTAGATCCAAATACCT  
AGTTTACTTTACACAAAATTGTAATGAAGTAAACAATAACACCAGCGAATTGAAAAAGTGAAAAATGCT  
GNTGAATCACTTGGCATTATGAACCACAATAATAATGAAGAGAAGTCCAACCTTCTGATAGTAAGAAA  
AGTATGGATAFTGAAAGATCTGCATCTACTCTCGGAAGTAGAAATTAGTAAGAACCCAATTTTCAAAAAA  
TTGGGGTTTTAGTCATTTAGAAAAAAATGATAGTGAAGAAATCAAAATGGTCCTAGTTTAAACCGAAAAACCA  
CAAACTTGTACATTGGTTGTTACAACCTCATGGTCCGAGCATTACTTTTCATTAGAAATGATATAGAATCC  
AATTATCTTTTAATTGCTGAAATCAAAATGAAATATCCATTATTCATTTCCTAAGAAATTAGTTATATCA  
UAAACTAAAATTTTCTAAATTAGTACCATCAGTCGGAGTATTTGTCATTAGTTCGAATTGATAATTCATTAA  
ATTTTTGAAGTAGAAAAATTTGAAGTGAATCAATGGACTGAAGCATTAGCTAAATCTAAATATAATGAA  
ATATAA

YOL100W\_homolog 944 aa public: 1..944 (SEQ ID NO 728)  
MHKFRYSLHQHYSKRNSDUXSKDSPISQNSNEENDSTKLSSESLQDLHDDLDDIYNNYTLAQGTNNNSV  
LTLDEENNAINKFIDKPPAIGHMEFQLPVMIIVSSRLSSLGNTTNETGESIAKSAPGTFPLSSHSEFDFR  
HHPRAVTNSSLNVLLDTPNVSEEFNLVDQTPPNESVERFDSDSNMTVDNTEEEENNDDTDEIPKSETLK  
QNEENWEKKGAAVKTIKTMDEMKTIIRNVTDPKFGKELGEGSYSTVILATDKITGKQYAVKVLDKRHI  
\_KEKKVKYVNIKHALNRLSNRLGVISLYPTFQDKDSLTFVLDYASNGELLTLIKRYNTLNEECTRIHFG  
AQILDAIKYMHNDNGVIHRDLKPENILLDDKMRIQITDFGTARLLEKKNDESEBYPVDVRAKSEVGTAEY  
VSPELLEKKYCKPGDVWAFCCIIYQMIAGKPPFKATNEYLTQKITKLQFAFSAGFPTIIRDLIKKII.  
VLQPSRRATIPETIQIKIYTFQSEVDFKDFDSIWLSDPPEIGPYKMTAKSMNKVPELNKAPITTVIKKNVKK  
STNSNSNTNNVATAVGGSSSNHGKSSPTPEKEPSPATINNKSTKVSAAASVAAYVLNKPATNQNSSTS  
EDSSKRSSNSNETRKLSSYSQCDYIPGTNLLRPQISTRPSVGSYVKTTPSKDKRTLTKVPSNIHQOQEKV  
KPKVNEVWPATTLRAAWRPYLTHPDERITLRTGPVIAHKEPTEPFKEKNKASLHISPLDINKEQSRSEN  
SLLTQIVNEVNNNTSELKVENADESLAIEPQYNMKRSPSTDSSKGMIDIERGASTSGSRISKKAIFKK  
LGPSHLEXMDSEESNCPSLTEKPQTCTLVVTTTGRALLFIRNDIESNYLLIAEIKLYPFIFHQELVIS  
QCKPSKLVPVSVGVFVISSIDNSLIPEVEKFEVNQWTEALAKSKYNEI

YJL166W\_homolog 288bp PathoSeq: 1..288 (SEQ ID NO 729)  
ACGGCAGGTGCACCACATCCACATACTTATATGGGCTGGTGGGGIAGTTTAGGUTCCCCAAGCAAAAA  
TATATTACTCAATATACTATTTCTCCATATGCTGCTAAACCATTAAGGGGGCTGCTTATAATGCTGTT  
TCCAATACTTTTGAAGAAGCAAGAAATCAATTTTCTTTATGTTTGGCAATCCATTTTGTGTTGTTGTTGAGT  
ATTGGAUTAGAGCTAGAGATTATAATGAATACTTTGTACACTAAAGAAGCTAGACAAGAAATTCGAAAGA  
GTTAATGTTTAA

YJL166W\_homolog 95aa PathoSeq: 1..95 (SEQ ID NO 730)  
MAGAPHPHTYMGWMSLGSBKQKYITQYIISPYAAKPKGAAYNAVFNTFRRTKNQFLYVAIPFWVWWS  
IWTNRADYNKYLYTKEGREELKRVNV

YLR038C\_homolog 252bp PathoSeq: 1..252 (SEQ ID NO 731)  
ATGCCAGTGGATCCAGCTACTTTTAAATTGAAACTCCACAATTTGACCCAAGATTCCCAAACCAAAAC  
CAATCCCAAACATTGTGCTCAAGCCTACGTTGATTACCACAAATGTGTCAATGTCAAAGGTGAAGAAATTT  
GAACCATGCAAAATCTTTTTCAAACTTTCACTTCATTATGTCCTTTGGATTGGGTGAAAAATGGGAT  
GATCAAAGACCTGCTCCTAAATTCCCACTCAACATGGACGCTTAE

YLR038C\_homolog 83aa PathoSeq: 1..83 (SEQ ID NO 732)  
MPVDPATFKFETPQDFPRFPNQNSKHCAQAYVDYHKCVNVKGEEFEPCKIFFKTFTSLCPLDWVEKWD  
DQRAAGKFPVNMDA

236/251

**Human homologues**

&gt;YGL080W\_homolog, CDS: 1-330 bp (SEQ ID NO 575)

ATGGCGGGCGCGTTGGTGGCGAAAGCGGGCGGACTATGTCCGAAGCAAGGATTTCCGGGACTACCTCATG  
ACTACGCACTTCTGGGGCCCAGTAGCCAACTGGGGTCTTCCCAATTGCTGCCATCAATGATATGAAAAAG  
TCTCCAGAGATTATCAGTGGGCGGATGACATTTGCCCTCTGTTGCTATTCTTTGACATTCATGAGATTT  
GCCTACAAGGTACAGCCTCGGAAGTGGCTTCTGTTTGCATGCCACGCCAACAAATGAAGTAGCCCGCTC  
ATCCAGGCAAGCGCGCTTATCAACACAGAGATGACTAAAACGGCATCTGCATAA

&gt;YGL080W\_homolog, 109 aa (SEQ ID NO 576)

MAGALVRKAADYVRSKDFRDYLMSTHFVGPVANWGLPIAAINDMKKSPEIISGRMTFALCCYSLTFMRF  
AYKVQPRXWLTAFCHATNFAQLTQGGRIKHEMTKTASA

&gt;YGR243W\_homolog, CDS: 1-384 bp (SEQ ID NO 577)

ATGTGCGCGCGCGGTGGCGGAGGCGCTGCGGGCCACCTACCACGGGCTCCTCGATAAAGTGGAGCTGATG  
CTGCGCGGAGAAATTGAGGCGGCTGTACAAACCATCCAGCAGGTCGCCAGAACAGTTTTCTTCTGGGCTCCA  
ATTATGAAATGGGGGTTGGTGCTGTGCTGGATTGGCTGATATGCCAGACCTGCAGAAAACTTAGCACA  
CCTCAATCTGCTGTTTTGATCGCTACAGGCTTTATTTGGTCAAGATACTCACTTGTAATTATTCCAAAA  
AATPGGAGTCTGTTTTGCTGTTAATTTCTTTGTGGGGGCAGCAGGAGCCTCTCAGCTTTTTCGTATTTGG  
AGATATAACCAAGAACTAAAAGCTAAAGCACACAAATAA

&gt;YGR243W\_homolog, 127 aa (SEQ ID NO 578)

MSAAGARSLRATYHRLLDKVELMLPEKLRPLYNHPAGERTVFFWAPIMKWGLVCAGLADMARPAEKLST  
AQSAVLMATGFIWSRYSLVLIIPKQWSLFAVNFVGAAGASQLFRIWRYNQELKAKAHK

&gt;YGR183C\_homolog, CDS: 1-399 bp (SEQ ID NO 579)

ATGCGCGCGCGCACCTTGACTTCGAATTTCTACTCCCTGCTCTTCCGCGAGACCTCCACCTTCGCGCTCA  
CCATCATCTTTGGCGTTCATCTTCTTCGAGCGCGCCTTTCATCAAGGCGCGGACGCTATCTACGACCACA  
TCAACGAGGCTGAAGCTGTGCAAAACACATCAAGCACAAAGATGAGAACAAGTAGTTCTTGGAGGCCCCC  
ATCCAGGCGCAGAAGGACCGAGTCCACCCAGCAGCTGTTTTGCCAGAGCTGGAGCCTCAGCTTGAAGATG  
ATGCTCAAGGTACTCTTCATGGACCACCATTCGCTGTTGGCAAGAAACGGCTTTACTTACAAAACAGAC  
TCTTTACCTTCTGCTGTGTTGAAGTATGTTTAGTCAGCATGCTCAGGAATAA

&gt;YGR183C\_homolog, 132 aa (SEQ ID NO 580)

MAAATLTSKLYSLLFRRPSPSPSSWASCSSEAPSIKARTLSTTTSTRGSCGNTSSTSMRTSSSLEAP  
TQARRTRSTQQLEAQSWSLSLKMMLKVLFPMDHHSLLARNGFTYKTDSLPSAVFEVCLVSMRLK

&gt;YBR009C\_homolog, CDS: 1-312 bp (SEQ ID NO 581)

ATGTCCTGGCCGCGGCAAGGCGGGAAGGCTCTTGGCAAGCGCGGCTAAGCGCCACCTAAAGTACTG  
CGCGACAATATCCAGGSCATCACCAAGCGCGCATTCGGCGGCTTGGCTCGCGCGCGCGGCGTGAAGCGC  
ATCTCCGGCTTCTCTACGAGGAGACTCGCGGGGTGCTGAAGGTGTTCTCTGAGAAAGTGATCCGGGAC  
GCGGTGACCTATACAGAGCACGCGCAAGCGCAAGACGGTACCGGCTATGGATGTGGTCTACCGGCTCAAG  
CGCCAGGCGGACACCTCTACGGTTTCGGTGGTTGA

&gt;YBR009C\_homolog, 103 aa (SEQ ID NO 582)

MSGKGKGGKGLKGGAKRHRKVLRDNTQGTTRPATRRLARFGGVKRTSGLIYEETRQVLKVFLENVTRD  
AVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG

237/251

>YGR209C\_homolog, CDS: 1-318 bp (SEQ ID NO 683)  
ATCGTGAAGCAGATCCACAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGATAAACTTGTA  
GTAGTTGACTTCTCAGCCACCTCTGTGGGGCCTTGCAAAATGATCAACCCCTTCTTTTCATTCCTCTCT  
GAAAAGTATTCCAACGTGATATTCTTGAAGTAGATGTGGATGACTGTCAGGATGTTTCCTTCAGAGTGT  
GAAGTCAAATGCACGCCAACATTCCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTTGGAGCC  
AATAAGGAAAAGCTTGAAGCCACCATTAAATGAATTAGTCTAA

>YGR209C\_homolog, 105 aa (SEQ ID NO 684)  
MVKQIESKTAFQEALDAAGDKLVVVDFSATWCGPCKMINPFFHSLSEKYSNVIFLEVVDVDDCQDVASEC  
EVKCTPTFQFFKKGQKVGEFSGANKKKLRATTNFIIV

>YPR028W\_homolog, CDS: 1-594 bp (SEQ ID NO 685)  
CCGAGCGGCGAGACGGTCCCCCCCATCTCTCCGGCCATGAGGGAGAGGTTTCGACCGGTTCTTCGCACGAG  
AAGAACTGCATGACTGAACCTTCTGGCCAAGCTCGAGGGCCAAAACCGGCGTGAACAGGAGCTTCATCGCT  
CTTGGTGTTCATCGGACTGGTGGCCTTGTACCTGCTTCTTCCGTTATGGAGCCTCTCTCTCTGCAACCTG  
ATAGGATTTGGCTACCCAGCCTACATCTCAATTAAACCTATAGAGAGTCCCAACAAAGAAGATGATACC  
CAGTGGCTGACCTACTGGGTAGTGTATGCTGTGTTTCAGCATTGCTGAATTCCTCTCTGATATCTTCTCTG  
TCATGGTTCCCTTCTTAUTACATACTGAAGTGTGGCTTCTCTGTTGTGGTGCATGCCCCGAGCCCTTCT  
AATGGGGCTGAACCTGCTCTACAAGCGCATCATCCCTCCTTTCTTCTTGAAGCACAGTCCCAGATGGAC  
ASTGTGGTCAAGGACCTTAAAGACAACCCCAAGACACTCCACATCCCATCACTAAAGAAGCGACGAAA  
GCTAACCGTGAATTTACTGGGTGAACAAAAGAAGAGCACCTAA

>YPR028W\_homolog, 197 aa (SEQ ID NO 686)  
PSGZTVFAMSAAMRERFDRLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYL VFGVGA5LLCNL  
LQPGYPAYLSIKALESPNKEDDTQWLTYWVVYGVFSIAEFFSDIFLSWFFPYIILKCG7LLWCMAFSPS  
NCAELLYKRIIRPFFFLKHESQMDDEVVKDLKDKAKETADAITKEAKKATVNLLGEEKST

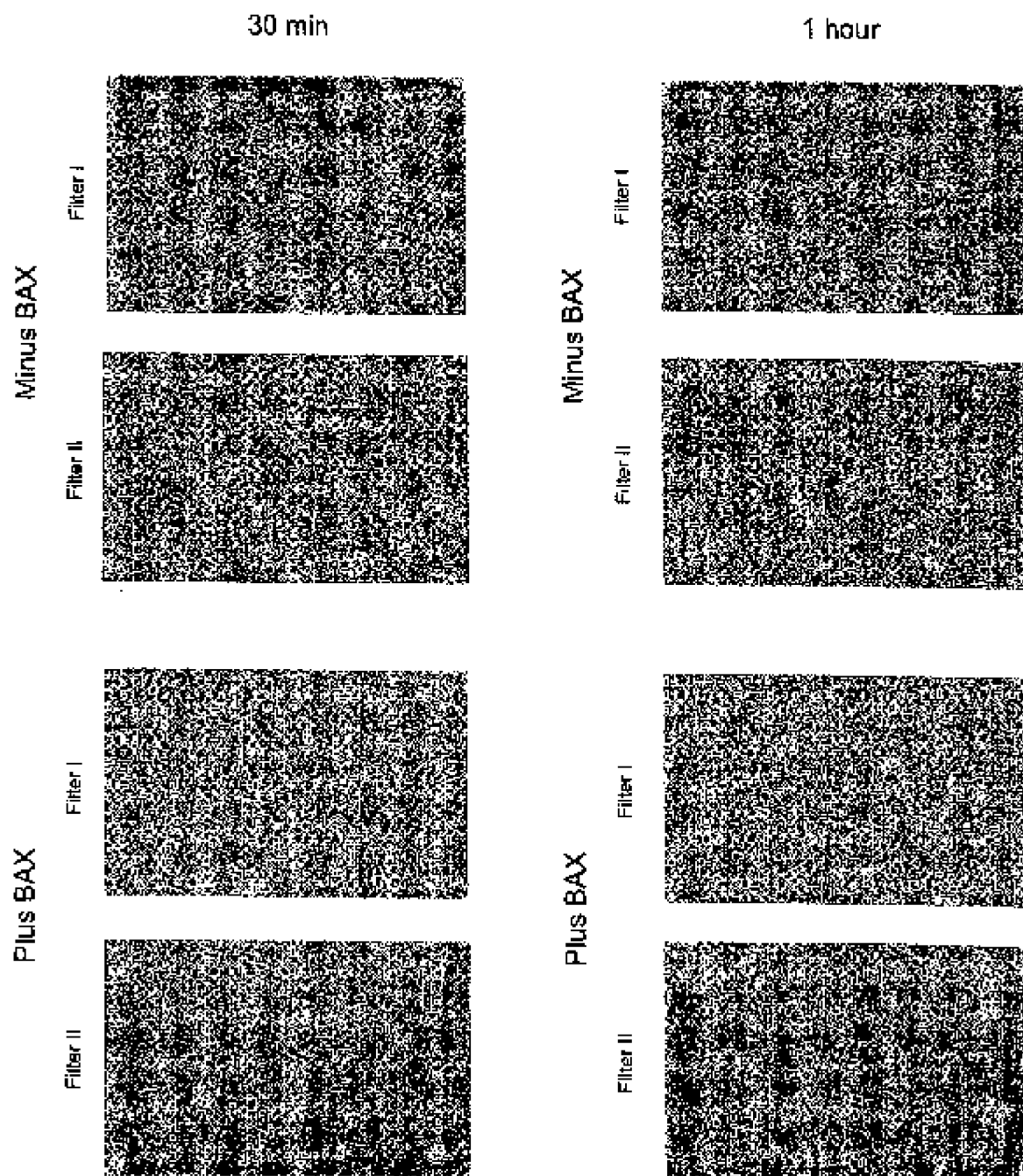


Figure 3 1

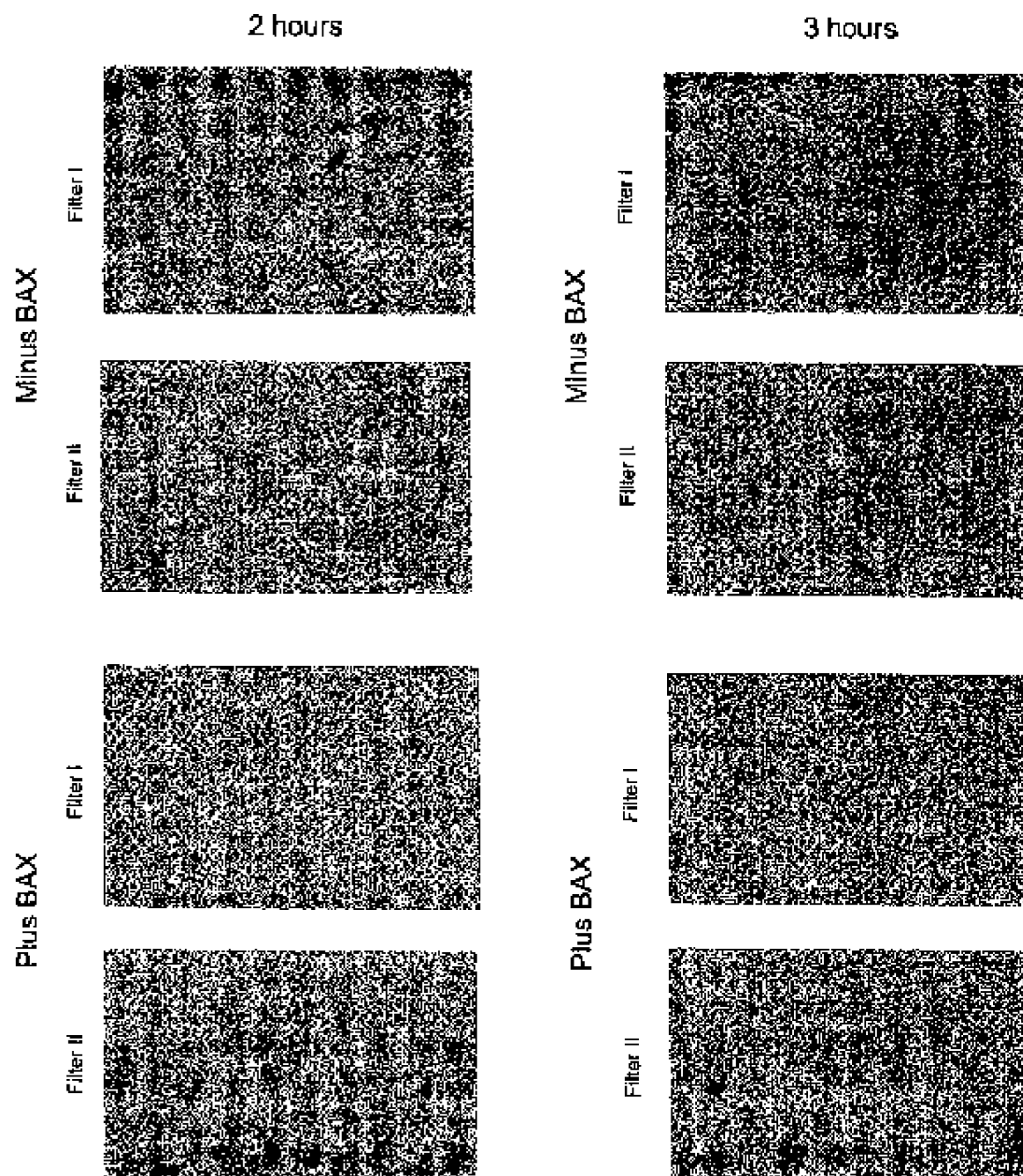


Figure 3 - 2



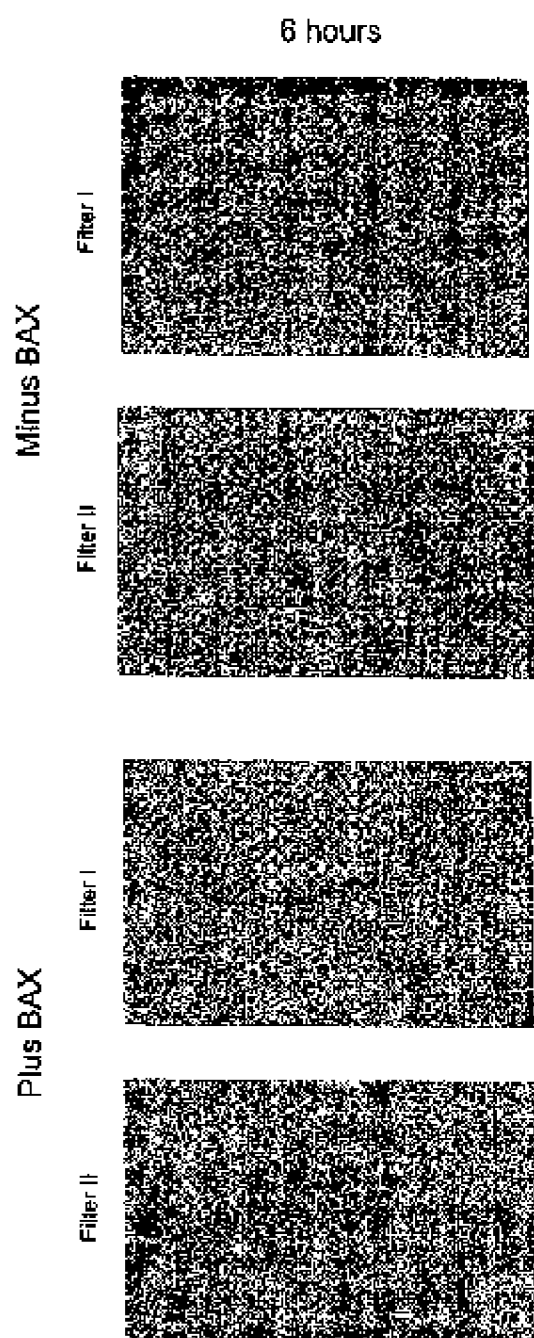
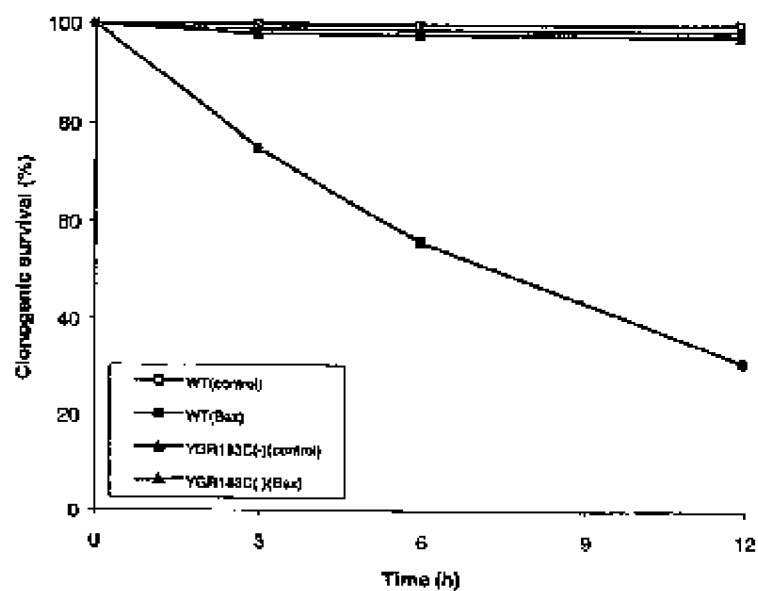
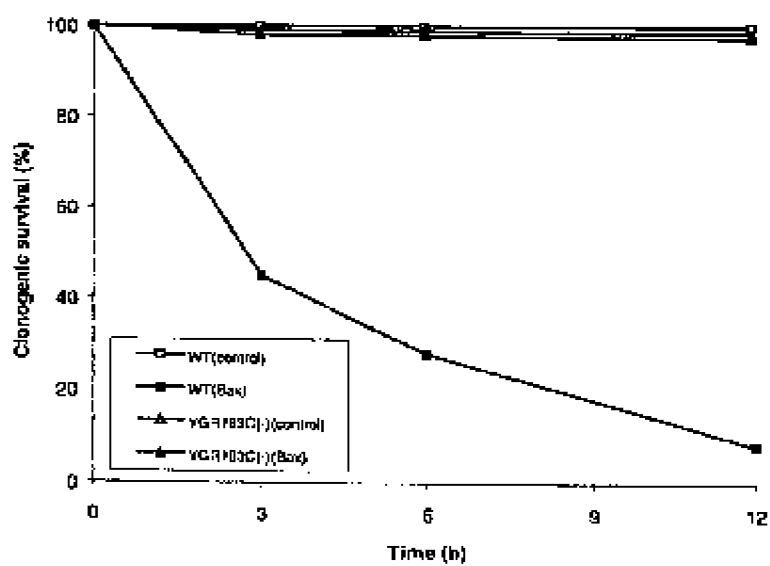


Figure 3 - 3



(A)



(B)

Figure 4

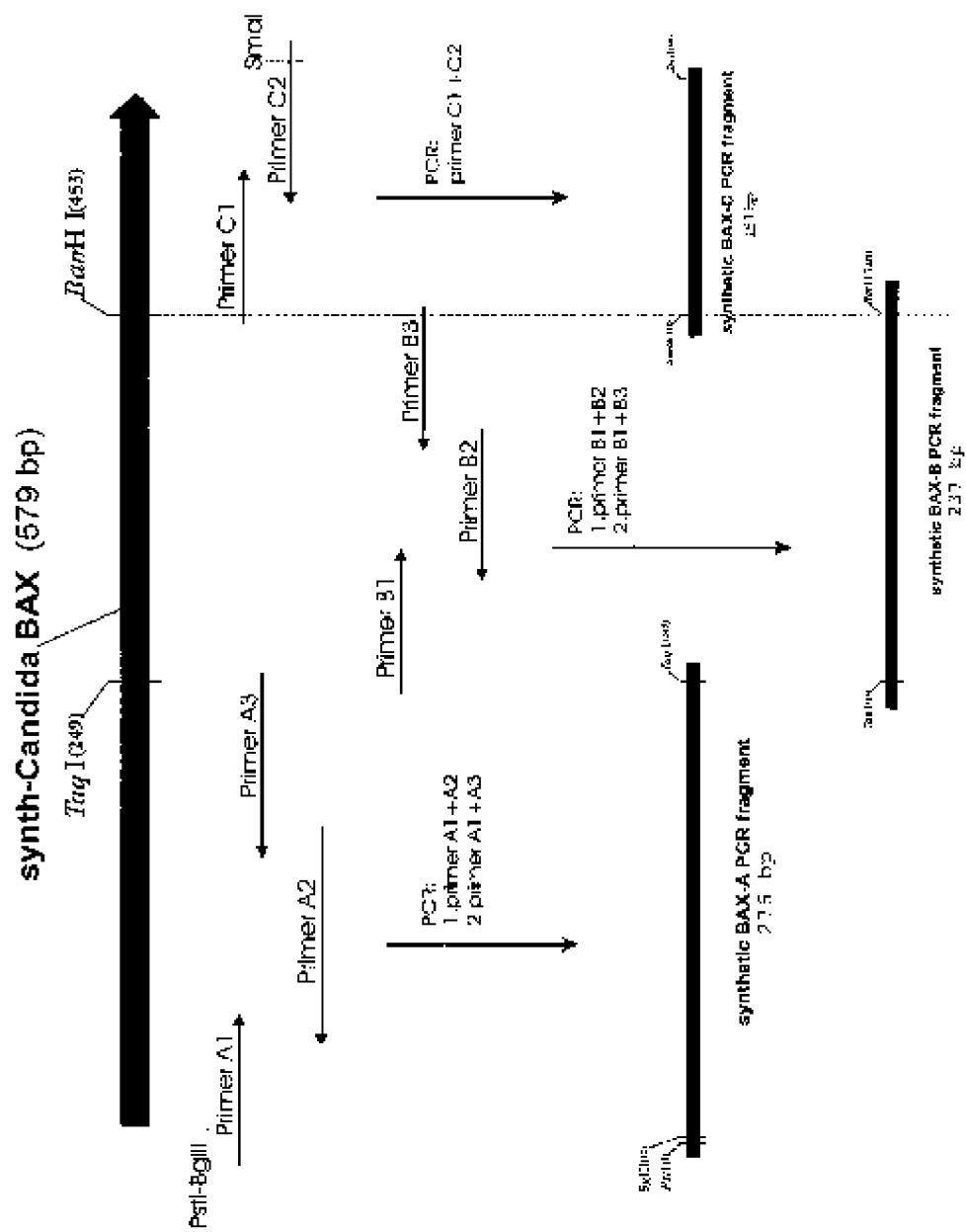


Fig. 5

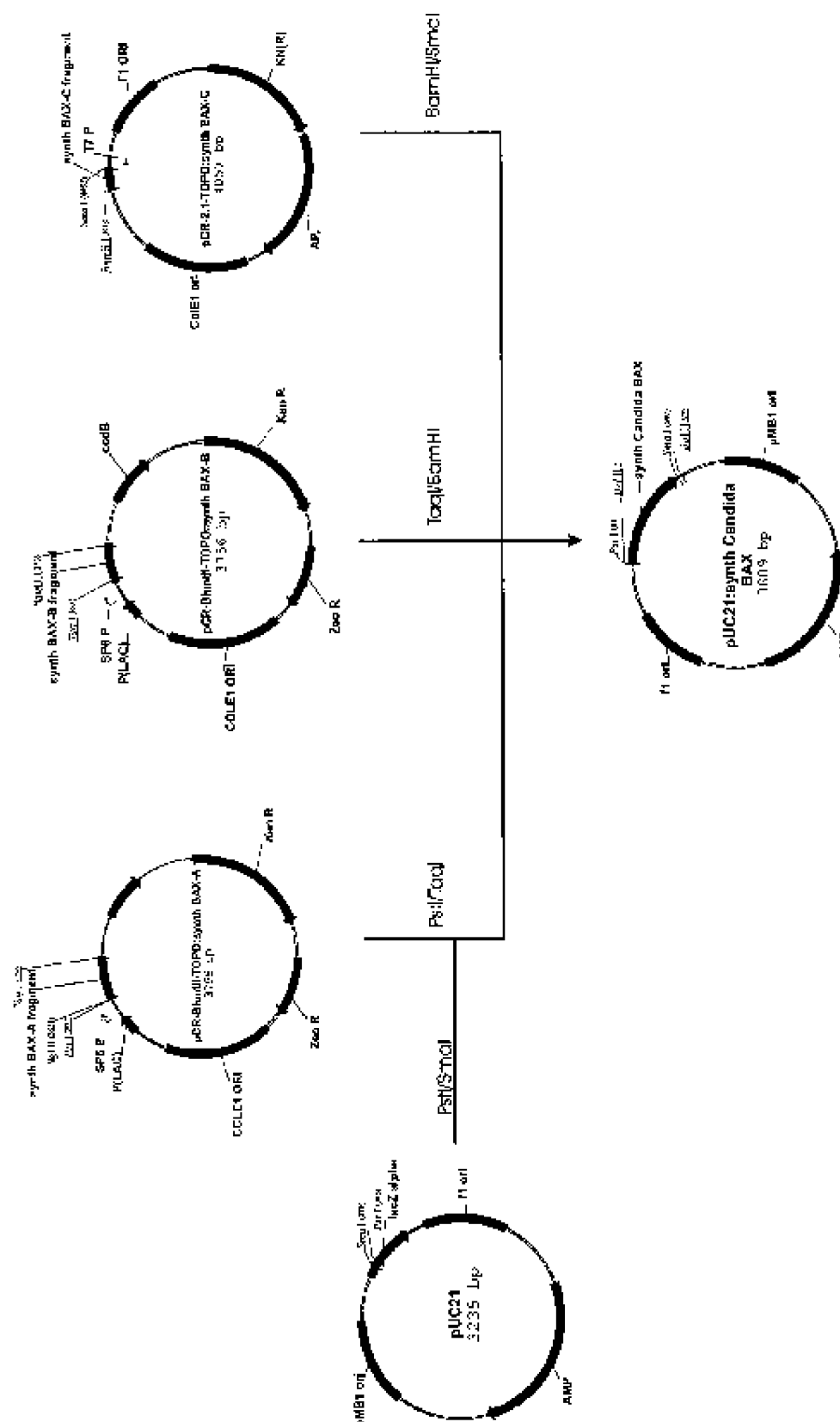


Fig. 5. Continued

```

Met Asp Gly Ser Gly Gln Gln Leu Gly Ser Gly Gly Pro Thr Ser Ser Glu Gln Ile Phe
1  ATG GAT GGT GCT GGT GAA CAA TTG GGT TCT GGT GGT GCA ACC TCT TCT GAA CAA ATC ATG

Lys Thr Gly Ala Phe Leu Leu Gln Gly Phe Ile Gln Asp Arg Ala Gly Arg Met Ala Gly
61  AAA ACC GGT GGT TTC TTG TTG GAA GGT TTC ATC CAA GAT AGA GCT GGT AGA ATG GCT GGT

Glu Thr Pro Glu Leu Thr Leu Gln Glu Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
121  CAA ACC CCA CAA TGG ACC TTG GAA CAA CCG CCG CAA GAT GCT TCT ACC AAA AAA TTG TCT

Glu Cys Ser Arg Arg Ile Gly Arg Glu Leu Asp Ser Asn Met Met Glu Leu Gln Arg Met Ile
181  GAA TGT TTG ACA AGC ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC

Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe
241  GGT GAT GTC GAA ACC GAT TCT CCA AGA GAA GTC TTC TTC AGA GTC GGT GGT GAT ATG TTG

Ala Asp Gly Asn Phe Gln Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
301  GCT GAT GGT AAC TTC AAC TGG GGT AGA GTC GTC GCT TTC TTC TAC TTC GGT TCT AAA TTA

Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr
361  GTC TTG AAA GCT TTG GGT ACC AAA GTC CCA GAA TTC ATC AAA ACC ATC ATC GGT TTG ACC

Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Phe Gln Asp Gln Gly Gly Trp Gln Gly
421  TTC GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GCT TGG GAA GGT

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Cln Thr Val Thr Phe Phe Val Ala Gly Val
481  TTG TTG TCT TAC TTG GGT ACC CCA AGC TCT CAA ACC CCA ACC ATC ACC CTC GCT GGT GTC

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly (SEQ ID NO 2)
541  TTG ACC GCT TCT TTG ACC ATC TGG AAA AAA ATG GGT TAA (SEQ ID NO 11)

```

Fig. 6

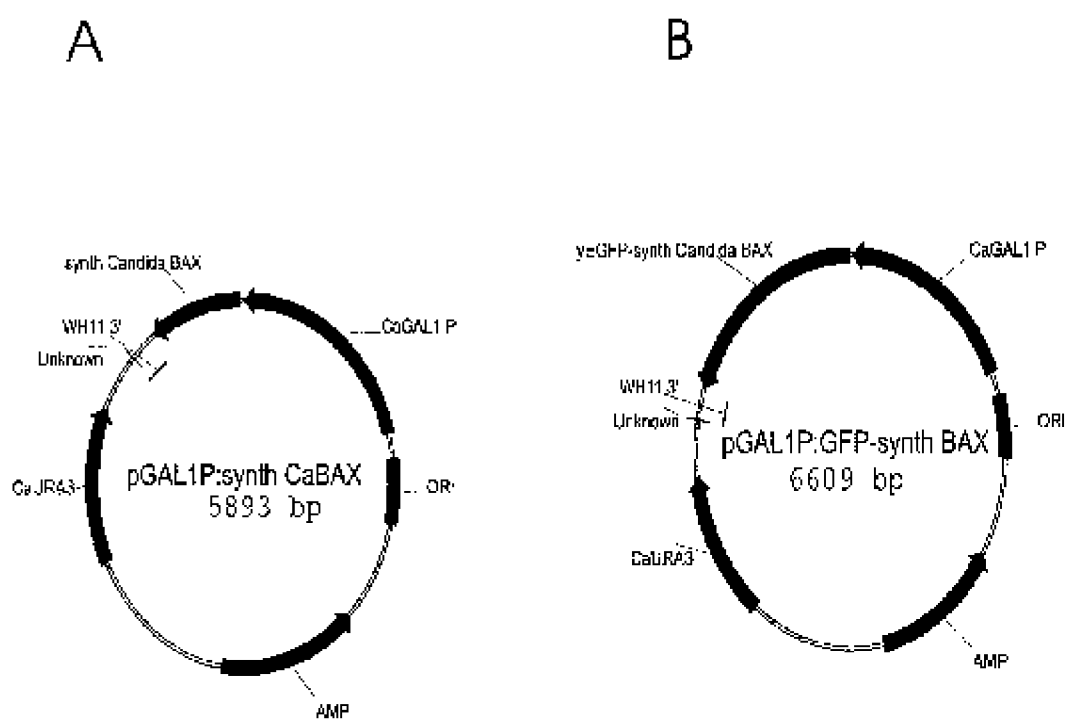


Fig. 7.

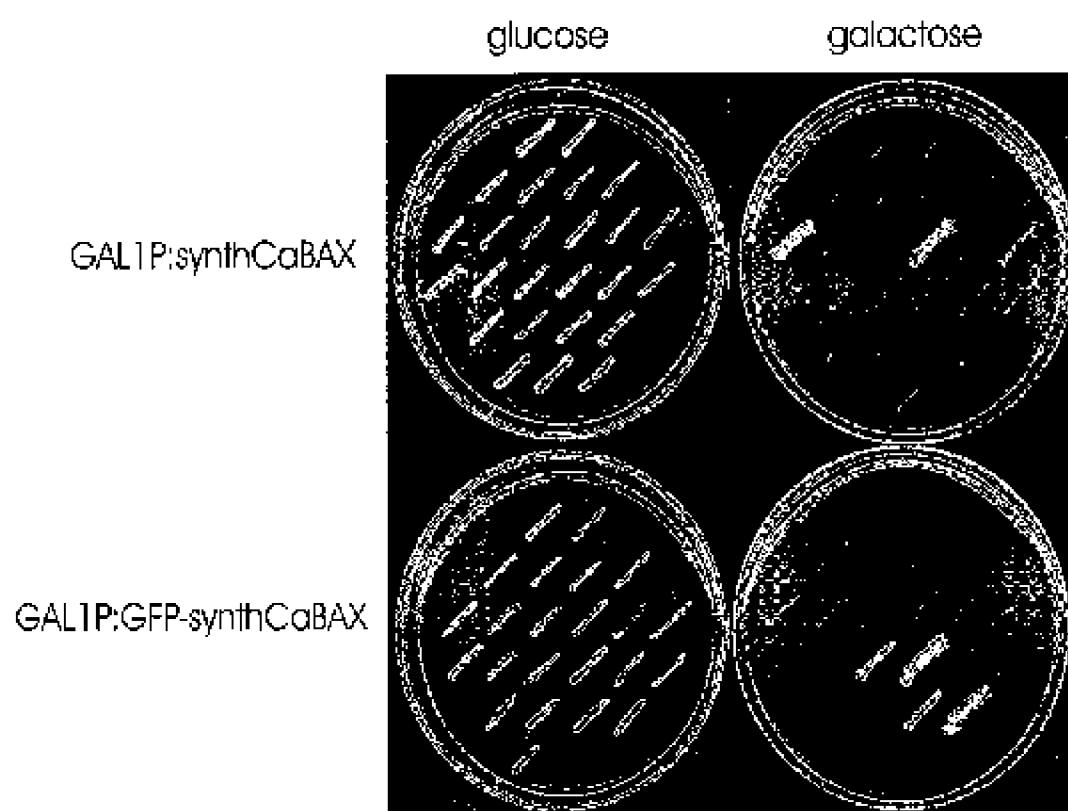


Fig. 8.

247/251

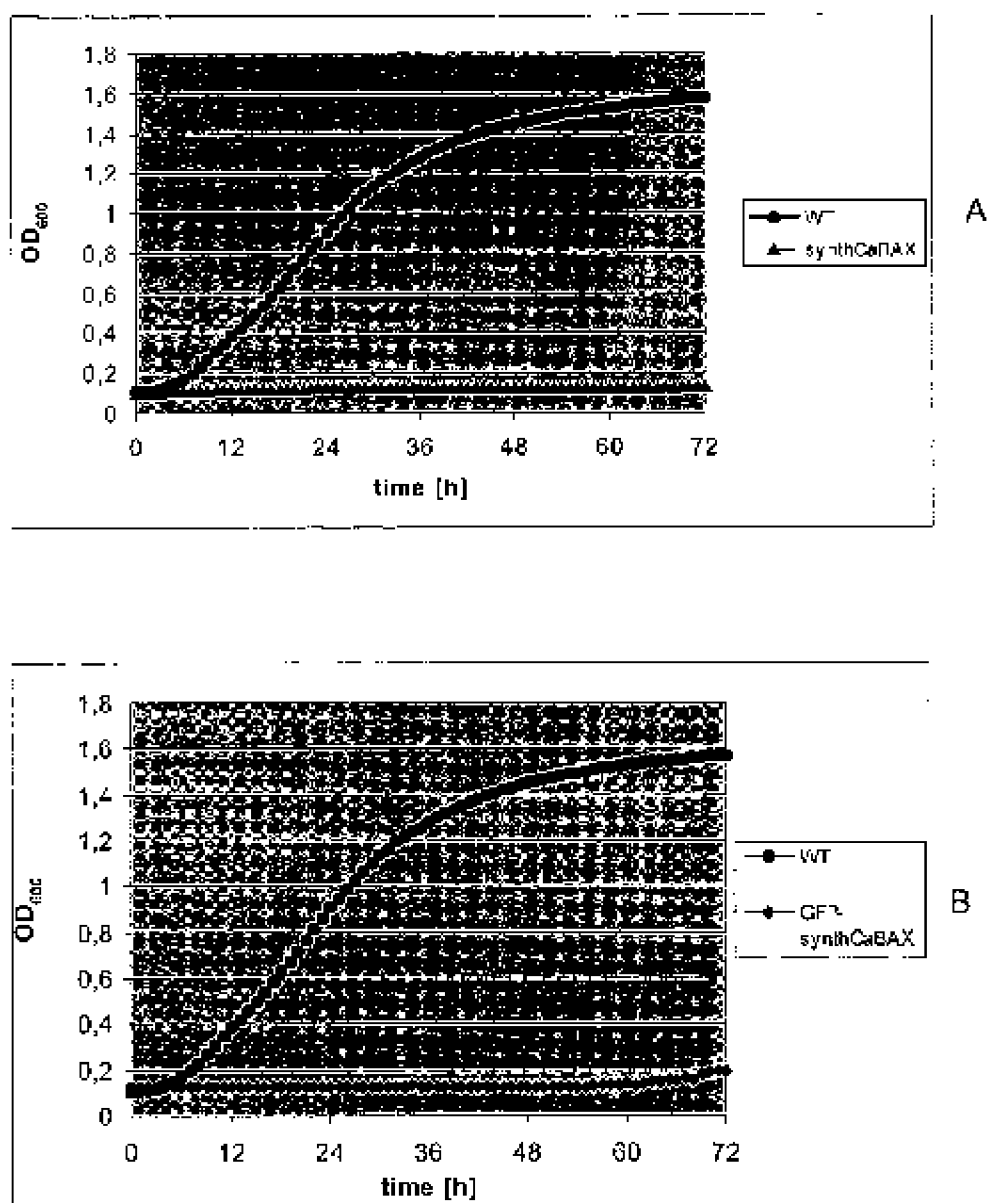


Fig. 9.



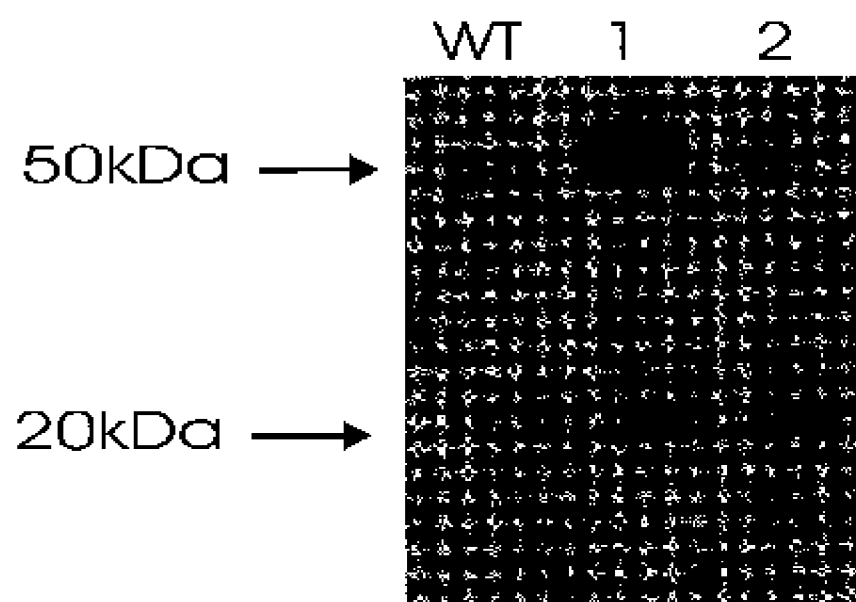


Fig. 10.

249/251

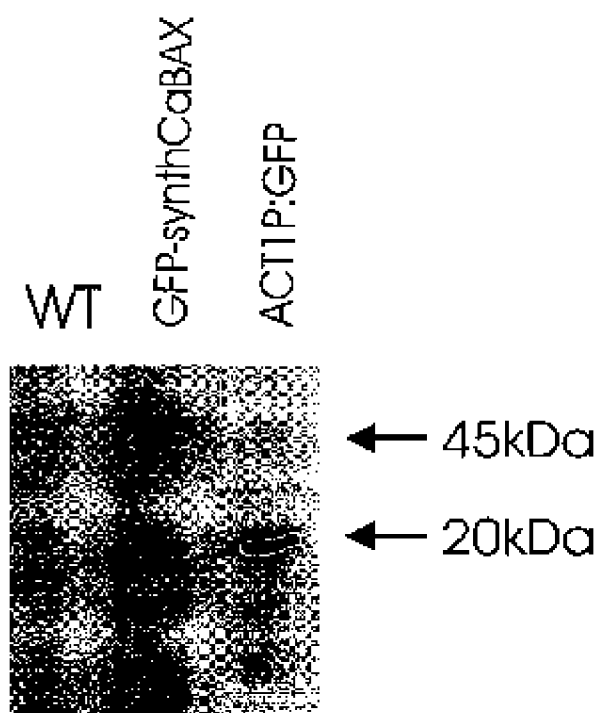


Fig. 11.

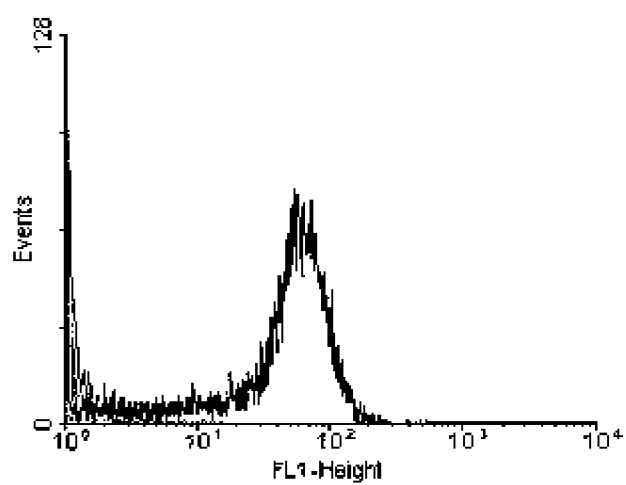
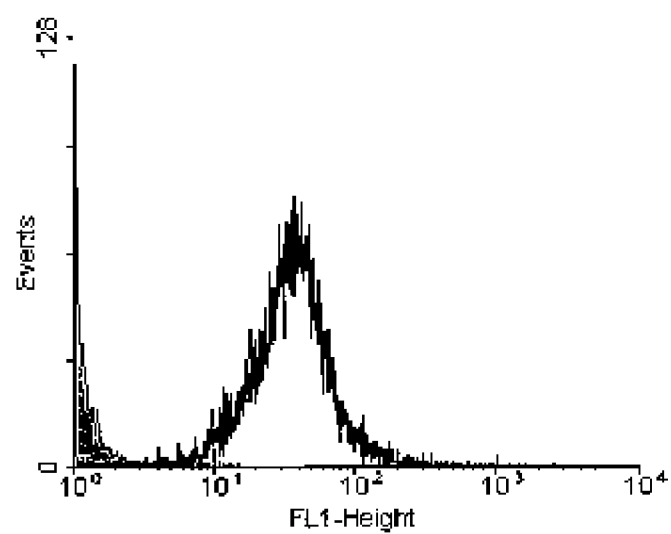


Fig.12.

251/251

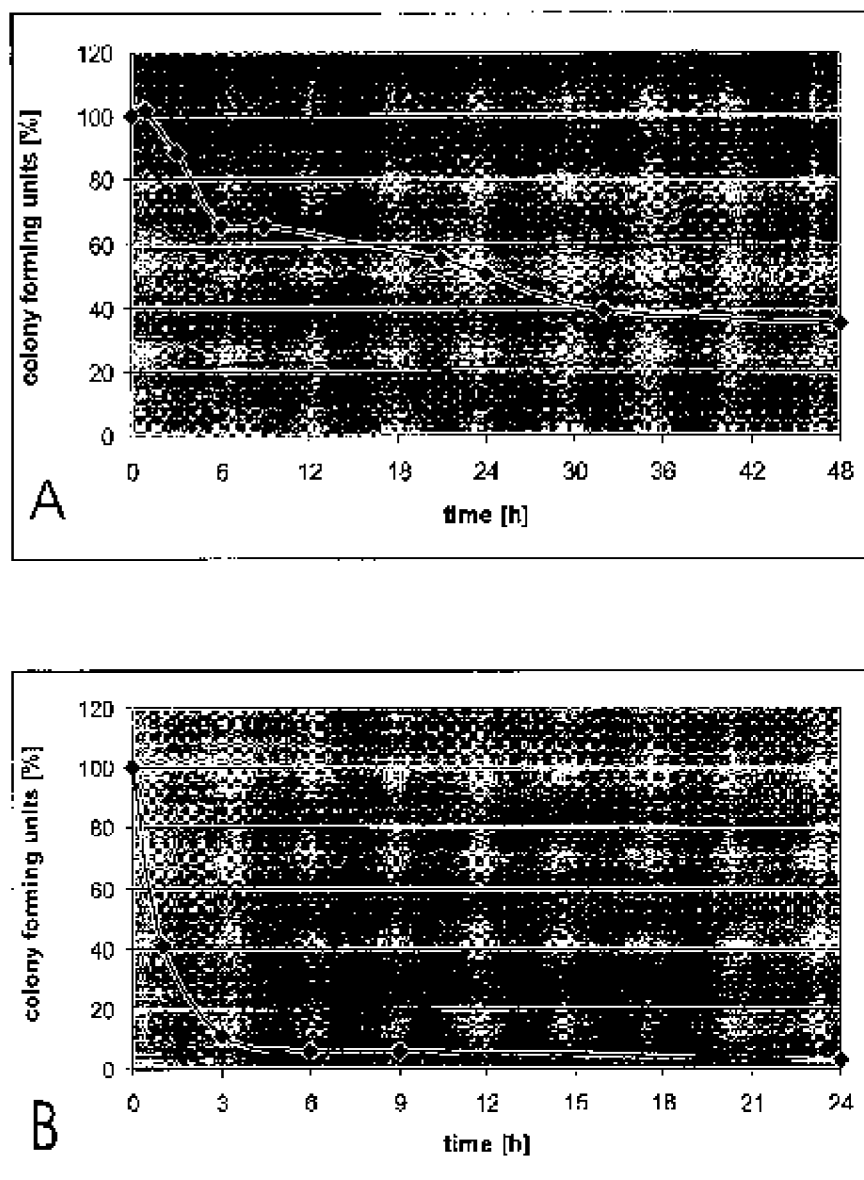


Fig. 13.